

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: February 13, 2005, 12:24:56 ; Search time 4928 Seconds
(without alignments)
17317.389 Million cell updates/sec

Title: US-10-036-342-56
Perfect score: 2242
Sequence: 1 gaatgaataacctccgaagcc.....aaaaaaaaaaaaaaaaaaaa 2242

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					%		Query		Description	
Result No.	Score	Match	Length	ID						
1	2098.6	93.6	2105	3	CR610360		CR610360 full-length			
2	1445.2	64.5	1528	3	BC004271		BC004271 Homo sapi			
3	1007.8	45.0	2814	3	AK085308		AK085308 Mus muscu			
C	4	978.2	43.6	1107	5	EX422767	BX422767 BX422767			
	5	952	42.5	1006	5	BX422768	BX422768 BX422768			
C	6	872.4	38.9	928	5	BX432016	BX432016 BX432016			
	7	860.4	38.4	913	5	BX453730	BX453730 BX453730			
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	9	774	34.5	799	4	BI754224	BG715910 602676657			
11	761.2	34.0	1054	5	BM920701		BI754224 603025522			
12	741.8	33.1	887	4	BI600248		BM920701 AGENCOURT			
13	736	32.8	807	4	BG708811		BI600248 603245955			
14	735.4	32.8	804	4	BI545916		BG708811 602673107			
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	16	714	31.8	772	4	BI489508	AI939620 tm64d04.x			
17	712.8	31.8	806	4	BG705917		BI489508 603032068			
18	712.4	31.8	763	4	BI600841		BG705917 602669227			
19	712.2	31.8	730	4	BI667149		BI600841 603244258			
20	710	31.7	748	4	BI597871		BI667149 603291543			
21	705.6	31.5	932	4	BI600150		BI597871 603245353			
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102 328.8 14.7 644 2 BF784109 602110065
103 320.2 14.3 866 7 CR409817
104 319.2 14.2 503 7 CR775127 DKFP459G
105 318.6 14.2 568 4 BI489676 603032149
106 317.6 14.2 872 6 CD302224 AGENCOURT
107 312.6 13.9 851 4 BJ727946
108 311 13.9 838 7 CK948185
109 310.6 13.9 855 5 BX705230 BX705230 B
110 310.6 13.9 1425 3 CR635434 Tetraodon
111 310.2 13.8 799 5 BU373789 603813418
112 309 1423 3 CR654499 Tetraodon
113 307 13.7 817 7 CR409263 CR409263
114 306 13.6 855 7 CR447198 CR447198
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121 298.2 13.3 827 5 BU473464 603761940
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130 287.8 12.8 939 5 BU177134 AGENCOURT
131 286.8 12.8 889 5 BU899764 AGENCOURT
132 286.4 12.8 1023 5 BX441686 BX441686
133 284.6 12.7 841 5 BU993920 EST0001 X
134 282.6 12.6 897 7 CF548195 AGENCOURT
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140 278.2 12.4 1054 5 BX417738 BX417738
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144 277.6 12.4 917 5 BQ714969 AGENCOURT
145 277.6 12.4 1032 1 AL542184 AL542184
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149 277.2 12.4 874 5 BX745177 BX745177
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166 272.2 12.1 821 5 BQ900309 AGENCOURT
c 167 272.2 12.1 859 5 BX748531 BX748531
168 271.6 12.1 702 7 CK974415 4105262 B
169 271.4 12.1 897 9 AY399850 Pan trogl
170 271.2 12.1 911 7 CK402460 AUF_frint

171 270.8 12.1 746 7 CF785757
172 269.8 12.0 852 5 BX716093 BX716093
173 269.8 12.0 1025 4 BI103493 BI103493
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175 268.8 12.0 726 5 BP689154 BP689154
176 268.8 12.0 833 7 CO887829 BovGen_16
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178 268.4 12.0 761 7 CF287146 AGENCOURT
179 268.4 12.0 783 5 BP694287 BP694287
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182 267 11.9 873 3 CNS09BV4 BX051452 Single re
184 266.4 11.9 879 5 BX737648 BX737648
185 266 11.9 790 5 BU702948 UI-M-FD0-
c 186 266 11.9 830 5 BX695126 BX695126
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195 263.6 11.8 860 5 BX439667 BX439667
196 263.6 11.8 858 5 BX743988 BX743988
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198 262.6 11.7 854 5 BX721390 BX721390
199 261.6 11.7 873 7 CF548329 AGENCOURT
c 200 260.6 11.6 763 7 CF520471 AGENCOURT
c 201 260.6 11.6 818 7 CF785758 AGENCOURT
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207 258.6 11.5 879 6 CA481013 AGENCOURT
208 258.4 11.5 967 5 BQ884782 AGENCOURT
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226 256.6 11.4 835 5 BX718173 BX718173
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228 256.4 11.4 922 6 CD326615 AGENCOURT
229 256 11.4 790 5 BP152784 BP152784
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232 255.4 11.4 831 5 BP436338 BP436338
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240 253.6 11.3 971 2 BF780587 602103131
c 241 253.6 11.3 1101 6 CD324819 CD324819
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243 253.2 11.3 803 5 BX712905 BX712905

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539	211.8	9.4	820	7	CN059607	CN059607 Salamande	612	202.8	9.0	635	7	CK967185	CK967185 4082632 B
540	211.6	9.4	805	4	BG770068	BG770068 602745196	613	202.4	9.0	622	6	CA367208	CA367208 642974 NC
541	211.4	9.4	679	1	AL658957	AL658957 AL658957	614	202.4	9.0	853	5	BU160527	BU160527 AGENCOURT
542	211.4	9.4	783	6	CB955558	CB955558 AGENCOURT	615	202.4	9.0	934	5	BQ734438	BQ734438 AGENCOURT
543	211.4	9.4	851	2	BF780226	BF780226 602103322	616	202	9.0	856	7	CN832267	CN832267 AGENCOURT
544	211.4	9.4	945	2	BF781937	BF781937 602105891	617	201.8	9.0	636	7	CK953554	CK953554 4093320 B
545	211.2	9.4	651	2	BF160757	BF160757 601769161	618	201.8	9.0	658	1	AL642334	AL642334 AL642334
546	211.2	9.4	718	7	CF704644	CF704644 CCAAC13TR	619	201.8	9.0	674	1	AL636340	AL636340 AL636340
547	211	9.4	531	1	AV615674	AV615674 AV615674	620	201.8	9.0	864	5	BU856566	BU856566 AGENCOURT
548	211	9.4	643	5	BW440526	BW440526 BW440526	621	201.8	9.0	772	6	CB952724	CB952724 AGENCOURT
549	211	9.4	1041	2	BE542903	BE542903 601068037	622	201.4	9.0	841	7	CF149212	CF149212 AGENCOURT
550	210.6	9.4	724	5	BP145282	BP145282 BP145282	623	201.2	9.0	516	4	BI314198	BI314198 daF93h02.
551	210.6	9.4	798	7	CF288087	CF288087 AGENCOURT	624	201.2	9.0	610	6	CD216482	CD216482 pgm2n.pk0
552	210.2	9.4	584	5	BP339351	BP339351 BP339351	625	201.2	9.0	783	7	CF785301	CF785301 AGENCOURT
C 553	210.2	9.4	755	6	CD629089	CD629089 56030685J	626	201	9.0	616	7	CN317268	CN317268 AGENCOURT
554	210.2	9.4	1103	2	BF343673	BF343673 602015326	C 627	201	9.0	644	7	CV026061	CV026061 3889 Full
C 555	210	9.4	874	7	CF717716	CF717716 CCAGJ45TF	628	201	9.0	737	7	CF257777	CF257777 pha015 c0
556	210	9.4	972	6	CD326976	CD326976 AGENCOURT	C 629	200.8	9.0	689	4	BJ631204	BJ631204 BJ631204
C 557	209.8	9.4	633	5	BW372925	BW372925 BW372925	C 630	200.4	8.9	584	4	BM192106	BM192106 dai24h06.
C 558	209.8	9.4	635	5	BW413732	BW413732 BW413732	C 631	200.4	8.9	844	7	CF692291	CF692291 CCAF109TO
C 559	209.8	9.4	656	1	AV899385	AV899385 AV899385	632	200.2	8.9	654	7	CK959536	CK959536 4100290 B
C 560	209.4	9.3	629	5	BW389564	BW389564 BW389564	633	200.2	8.9	694	2	BF785894	BF785894 602112526
561	209.4	9.3	685	6	CA339172	CA339172 NISC lx11	634	200.2	8.9	850	6	CD099076	CD099076 AGENCOURT
562	209.2	9.3	774	1	AL555318	AL555318 AL555318	635	200	8.9	605	2	BF787465	BF787465 602113878
563	209.2	9.3	912	5	BU184087	BU184087 AGENCOURT	636	200	8.9	607	4	BJ003826	BJ003826 BJ003826
C 564	209	9.3	646	5	BW414025	BW414025 BW414025	637	200	8.9	751	4	BG757710	BG757710 602714808
565	208.8	9.3	661	5	BX620105	BX620105 BX620105	638	200	8.9	817	6	CB198887	CB198887 AGENCOURT
C 566	208.8	9.3	721	5	BW018610	BW018610 BW018610	639	199.6	8.9	877	5	BQ220364	BQ220364 AGENCOURT
567	208.8	9.3	924	6	CD361097	CD361097 AGENCOURT	640	199.6	8.9	938	6	CD359625	CD359625 AGENCOURT
568	208.6	9.3	537	4	BI313348	BI313348 dah92c03.	641	199.4	8.9	697	7	CN058040	CN058040 Salamande
569	208.6	9.3	720	6	CA321639	CA321639 UI-M-FX0-	C 642	199.2	8.9	817	7	CF709081	CF709081 CCAHX05TF
570	208.4	9.3	961	6	CD254050	CD254050 AGENCOURT	C 643	199.2	8.9	829	7	CF702961	CF702961 CCAE582TO
571	208.2	9.3	630	4	BI475249	BI475249 fq30a07.y	644	199	8.9	643	1	AI658295	AI658295 fc21b09.y
572	208.2	9.3	807	7	CF781368	CF781368 AGENCOURT	645	199	8.9	737	6	CD494235	CD494235 CDA09-F05
C 573	208	9.3	629	5	BX713722	BX713722 BX713722	646	199	8.9	818	1	AJ455160	AJ455160 AJ455160
574	208	9.3	736	7	CF251462	CF251462 esa025_d1	647	199	8.9	927	2	BF787092	BF787092 602108628
575	207.8	9.3	678	4	BG758254	BG758254 602712435	C 648	198.8	8.9	579	4	BM192186	BM192186 dai21d10.
576	207.8	9.3	800	7	CK478554	CK478554 AGENCOURT	649	198.8	8.9	911	5	BQ734664	BQ734664 AGENCOURT
C 577	207.6	9.3	730	5	BX711668	BX711668 BX711668	C 650	198.2	8.8	772	7	CF284140	CF284140 AGENCOURT
C 578	207.4	9.3	667	2	AV958752	AV958752 AV958752	651	198.2	8.8	898	5	BU184091	BU184091 AGENCOURT
579	207.4	9.3	878	2	BF785173	BF785173 602108357	652	198	8.8	1013	2	BE731041	BE731041 601570114
580	207.2	9.2	830	7	CR764520	CR764520 DKFZp4690	653	198	8.8	1071	5	BM927649	BM927649 AGENCOURT
581	207.2	9.2	1094	5	BQ055110	BQ055110 AGENCOURT	654	197.8	8.8	547	1	AI746749	AI746749 ul07a02.y
582	207	9.2	570	2	BF787217	BF787217 602108977	655	197.8	8.8	681	5	BP457389	BP457389 BP457389
583	207	9.2	590	4	BI103102	BI103102 602889331	656	197.8	8.8	914	5	BQ670484	BQ670484 AGENCOURT
584	207	9.2	653	1	AL803718	AL803718 AL803718	657	197.8	8.8	1052	5	BM909492	BM909492 AGENCOURT
C 585	206.8	9.2	644	7	CR435969	CR435969 CR435969	658	197.6	8.8	573	7	CK331853	CK331853 H8182B02-
586	206.6	9.2	839	5	BU122336	BU122336 603144737	659	197.6	8.8	600	4	BG804189	BG804189 0252-61 M
587	206.4	9.2	772	7	CF149573	CF149573 AGENCOURT	660	197.6	8.8	688	4	BI222670	BI222670 602940176
588	206	9.2	684	7	CF734923	CF734923 UI-M-HA0-	661	197.4	8.8	785	4	BG430911	BG430911 602500207
589	205.8	9.2	989	4	BG325904	BG325904 602424645	662	197.4	8.8	836	4	BI103262	BI103262 602889223
590	205.4	9.2	548	4	BJ061984	BJ061984 BJ061984	663	197.4	8.8	978	5	BX340724	BX340724 BX340724
591	205.4	9.2	568	2	BE018795	BE018795 bb85b01.y	664	197.2	8.8	518	4	BI682272	BI682272 463308 MA
592	205.4	9.2	594	2	BE279876	BE279876 601157237	665	197	8.8	818	4	BI086355	BI086355 602849594
593	205.4	9.2	619	6	CA375085	CA375085 649662 NC	666	196.6	8.8	645	1	AL649711	AL649711 AL649711
594	205.4	9.2	761	6	CA958689	CA958689 pw88g06.y	667	196.6	8.8	646	1	AL634442	AL634442 AL634442
595	205.4	9.2	773	2	BE734822	BE734822 601568055	668	196.6	8.8	650	1	AL660944	AL660944 AL660944
C 596	205.2	9.2	697	1	AJ731920	AJ731920 AJ731920	669	196.6	8.8	724	7	CR450111	CR450111 CR450111
C 597	204.8	9.1	603	4	BG161669	BG161669 dab72c01.	670	196.6	8.8	755	7	CF149406	CF149406 AGENCOURT
598	204.8	9.1	683	7	CF288257	CF288257 AGENCOURT	671	196.6	8.8	761	6	CB014594	CB014594 AB tgz 82
599	204.8	9.1	701	2	AW993208	AW993208 RC2-BN003	672	196.6	8.8	945	6	CD324657	CD324657 AGENCOURT
600	204.8	9.1	730	7	CF547860	CF547860 AGENCOURT	673	196.2	8.8	572	4	BI101795	BI101795 602885339
601	204	9.1	638	1	AJ731914	AJ731914 AJ731914	674	196.2	8.8	617	5	BP238979	BP238979 BP238979
602	204	9.1	686	4	BJ701471	BJ701471 BJ701471	675	196.2	8.8	854	7	CK602489	CK602489 AGENCOURT
C 603	204	9.1	715	5	BP729415	BP729415 BP729415	676	196	8.7	733	7	CN440879	CN440879 BE04024A1
604	204	9.1	728	4	BI890053	BI890053 ZF637-2-0	677	196	8.7	860	5	BQ216659	BQ216659 AGENCOURT
605	204	9.1	805	7	CR769358	CR769358 DKFZp469P	678	195.8	8.7	965	4	BG421425	BG421425 602451370
C 606	204	9.1	855	4	BJ739844	BJ739844 BJ739844	679	195.6	8.7	624	1	AL675185	AL675185 AL675185
C 607	203.8	9.1	745	5	BX753467	BX753467 BX753467	680	195.4	8.7	941	2	BE796497	BE796497 601589849
608	203.8	9.1	899	5	BQ733049	BQ733049 AGENCOURT	681	195.4	8.7	746	4	BI102079	BI102079 602887820

682	195.2	8.7	888	6	CD788631	EST659992	187.4	8.4	623	4	BM767401	BM767401 K-EST0049
683	195.2	8.7	1039	5	BM920851	AGENCOURT	187.4	8.4	624	4	BM767277	BM767277 K-EST0049
684	195	8.7	566	4	BJ527376	BJ527376	187.4	8.4	747	7	CN361477	CN361477 3288232TR
685	195	8.7	766	7	CN054222	Salamande	187.4	8.4	878	7	CF698751	CF698751 CCAGSL09TR
686	194.8	8.7	581	5	BP345587	BP345587	187.4	8.4	897	7	CF715325	CF715325 CCAHL09TR
687	194.6	8.7	537	6	CB156243	K-EST0214	187.2	8.3	507	1	AI891964	AI891964 ul57b07.Y
688	194.6	8.7	948	5	BQ674071	AGENCOURT	187.2	8.3	565	1	AL797625	AL797625 AL797625
689	194.4	8.7	573	1	AL629120	AL629120	187.2	8.3	615	6	CD629088	CD629088 56030685H
690	194.4	8.7	905	2	BF344169	602017411	187.2	8.3	787	7	CF685180	CF685180 CCAHF65TF
691	194.2	8.7	583	5	BP361478	BP361478	187.2	8.3	793	7	CF715316	CF715316 CCAHL09TF
692	194	8.7	794	7	CO811744	AGENCOURT	187	8.3	887	7	CR425723	CR425723 CR425723
693	193.8	8.6	587	7	CO782995	CO782995	186.6	8.3	896	4	BI455589	BI455589 603174841
694	193.8	8.6	976	5	BQ642607	AGENCOURT	186.6	8.3	278	5	BY339110	BY339110 BY339110
695	193.6	8.6	637	7	CV221795	Le_mx0.52	186.6	8.3	577	1	AV902970	AV902970 AV902970
696	193.6	8.6	823	7	CV110304	AGENCOURT	186.4	8.3	531	6	CD629096	CD629096 56083657H
697	193.6	8.6	903	7	CO401389	CO401389	186.4	8.3	677	4	BM612766	BM612766 170006871
698	193.6	8.6	1098	4	BM460650	BM460650	186.4	8.3	691	4	BM624990	BM624990 170006874
699	193.4	8.6	724	4	BM597846	BM597846	186.2	8.3	665	5	BU401781	BU401781 603481132
700	193.4	8.6	1169	6	CD256963	CD256963	186.2	8.3	695	5	BW375130	BW375130 BW375130
701	193.2	8.6	637	4	BI193164	BI193164	186.2	8.3	750	7	CF682795	CF682795 CCAID56TF
702	193.2	8.6	655	7	CF145688	CF145688	186	8.3	639	2	BF784713	BF784713 602111350
703	193.2	8.6	870	4	BI086497	BI086497	185.8	8.3	470	4	BI867886	BI867886 ft65a12.Y
704	193	8.6	619	7	CN694924	E0357F01-	185.8	8.3	671	4	BI088042	BI088042 602850538
705	193	8.6	654	2	BF228658	BF228658	185.6	8.3	502	1	AI930268	AI930268 ul62d12.Y
706	192.8	8.6	671	4	BJ491596	BJ491596	185.6	8.3	1010	5	BQ057102	BQ057102 AGENCOURT
707	192.8	8.6	1021	4	BG335135	602403627	185	8.3	539	1	AI790788	AI790788 uk28b04.Y
708	192.8	8.6	1032	5	BQ062809	AGENCOURT	184.8	8.2	527	7	CN361469	CN361469 170006000
709	192.6	8.6	645	5	BQ419972	faa12d11.	184.8	8.2	583	4	BI533695	BI533695 fr81e11.Y
710	192.6	8.6	775	7	CO561624	CO561624	184.6	8.2	626	1	AL799212	AL799212 AL799212
711	192.6	8.6	891	7	CO808963	CO808963	184.4	8.2	616	5	BQ387495	BQ387495 NISC_mn24
712	192.4	8.6	901	7	CN317715	CN317715	184.2	8.2	667	2	BE285955	BE285955 601097691
713	192.4	8.6	929	5	BX329286	BX329286	184.2	8.2	738	4	BG481133	BG481133 602528936
714	192	8.6	711	4	BG172039	602333157	184.2	8.2	790	4	BG171680	BG171680 602322194
715	192	8.6	787	4	BI092396	BI092396	184.2	8.2	864	7	CF720182	CF720182 CCAEI18TR
716	191.8	8.6	601	1	AI259827	LP03331.5	184	8.2	607	5	BQ396656	BQ396656 NISC_ng22
717	191.8	8.6	699	2	BE159642	MR0-HT040	184	8.2	859	5	BP160379	BP160379 BP160379
718	191.8	8.6	803	4	BJ715357	BJ715357	183.8	8.2	517	2	BE757521	BE757521 211979 MA
719	191.4	8.5	351	2	BB797669	BB797669	183.6	8.2	660	6	BY745273	BY745273 BY745273
720	191.4	8.5	553	2	BE278298	601179467	183.6	8.2	874	4	BG489861	BG489861 602518751
721	191.4	8.5	827	7	CK793281	CK793281	183.4	8.2	533	4	BG016243	BG016243 de58f01.Y
722	191.4	8.5	876	6	CD361073	CD361073	183.4	8.2	1024	4	BG823747	BG823747 602726945
723	191.2	8.5	605	7	CN687811	E0247H01-	183.2	8.2	777	4	BJ723643	BJ723643 BJ723643
724	191.2	8.5	740	7	CR559690	CR559690	183.2	8.2	913	5	BQ734227	BQ734227 AGENCOURT
725	191.2	8.5	896	7	CF699888	CF699888	183.2	8.2	936	4	BI869742	BI869742 603393634
726	191	8.5	678	7	CR771708	CR771708	183.2	8.2	1034	4	BM459181	BM459181 AGENCOURT
727	191	8.5	694	4	BM6011243	BM6011243	183	8.2	649	7	CR771095	CR771095 DKFZp469G
728	190.6	8.5	621	6	CB515388	CB515388	183	8.2	661	6	BY738120	BY738120 BY738120
729	190.2	8.5	706	5	BM374533	BM374533	182.8	8.2	583	5	BP291610	BP291610 BP291610
730	190	8.5	809	4	BI100579	BI100579	182.8	8.2	598	1	AV857429	AV857429 AV857429
731	189.8	8.5	757	4	BG972086	BG972086	182.8	8.2	660	6	CD629095	CD629095 56068936J
732	189.8	8.5	1098	4	BM423500	AGENCOURT	182.8	8.2	978	2	BE563299	BE563299 601335673
733	189.6	8.5	615	5	BQ389484	BQ389484	182.8	8.2	928	3	CNS09BV5	CNS09BV5 BX051453
734	189.6	8.5	721	4	BM608455	BM608455	182.6	8.1	669	8	AO765026	AO765026 HS_3199 B
735	189.4	8.4	704	5	BX683818	BX683818	182.4	8.1	697	7	CO575451	CO575451 AGENCOURT
736	189.4	8.4	782	4	BG751936	BG751936	182.4	8.1	774	5	BP443845	BP443845 BP443845
737	189.4	8.4	824	5	BX612964	BX612964	182.2	8.1	481	5	BQ398332	BQ398332 NISC_mo06
738	189.2	8.4	805	7	CN054326	CN054326	182.2	8.1	552	4	BI535835	BI535835 415779 MA
739	189	8.4	586	6	BY704039	BY704039	182	8.1	1033	4	BG756004	BG756004 602716487
740	189	8.4	701	7	CN054966	CN054966	182	8.1	799	1	AU051366	AU051366 AU051366
741	188.2	8.4	514	2	BE302753	BE302753	181.8	8.1	606	2	BE389639	BE389639 601283351
742	188.2	8.4	646	5	BQ390223	BQ390223	181.6	8.1	594	4	BG831059	BG831059 602766794
743	188.2	8.4	664	5	BQ399549	BQ399549	181.2	8.1	658	5	BQ523740	BQ523740 NISC_n123
744	188	8.4	633	4	BI891469	BI891469	181.2	8.1	948	1	AL559600	AL559600 AL559600
745	188	8.4	636	7	CN792550	CN792550	181	8.1	529	6	CD629097	CD629097 56083657J
746	188	8.4	699	4	BG697206	BG697206	181	8.1	843	7	CO739134	CO739134 SLE04C22
747	188	8.4	809	4	BJ717492	BJ717492	181	8.1	867	5	BU192922	BU192922 AGENCOURT
748	188	8.4	892	5	EX710761	EX710761	181	8.1	1016	9	CNS06D4R	AL393361 T7 end of
749	187.8	8.4	722	6	CA958827	pw90e11.Y	180.8	8.1	513	2	BE807936	BE807936 213014 MA
750	187.6	8.4	639	6	CA588972	hab52c04.	180.8	8.1	623	2	BE278056	BE278056 601179567
751	187.6	8.4	765	4	BI107765	602892131	180.8	8.1	629	2	AW767024	AW767024 da62b03.Y
752	187.4	8.4	588	7	CR767439	DKFZp468P	180.8	8.1	1049	4	BG482070	BG482070 602527954
753	187.4	8.4	611	2	AV969267	AV969267	180.6	8.1	986	7	CF827130	CF827130 EST704512
754	187.4	8.4	623	4	BM741213	K-EST0013	180.4	8.0	555	7	CN792727	CN792727 4127630 B

828	180.4	8.0	626	2	BE734407	BE734407	601565668	901	170.4	7.6	587	5	BP311411	BP311411
829	180.4	8.0	634	6	CD692703	CD692703	EST9226 h	902	170.4	7.6	648	6	CD684533	EST1053 h
830	180.2	8.0	661	6	CD760973	CD760973	GGEZSM100	C 903	170.4	7.6	768	5	BX705231	BX705231
C 831	180.2	8.0	748	4	BJ725647	BJ725647	BJ725647	904	170.2	7.6	593	4	BJ490924	BJ490924
832	179.6	8.0	622	1	AL584429	AL584429	AL584429	905	169.8	7.6	595	4	BM192155	dai24h06.
833	179.4	8.0	583	7	CV339336	CV339336	MRO-BT300	906	169.8	7.6	627	4	BI650797	603297384
C 834	179.2	8.0	751	4	BJ722914	BJ722914	BJ722914	907	169.8	7.6	744	7	CO140990	EST835661
C 835	179.2	8.0	759	7	CF698738	CF698738	CCAGS72TF	908	169.6	7.6	717	4	BG283253	602406954
836	179	8.0	550	2	AW823784	AW823784	uE59c12.Y	C 909	169.4	7.6	681	1	AI667513	fc41c04.x
837	179	8.0	1028	2	BE735191	BE735191	601569155	910	169.2	7.5	756	7	CR557665	DKFP469A
838	178.6	8.0	673	6	CB377511	CB377511	CmaE1_37	911	169	7.5	599	7	CO334492	EK314768.
839	178.6	8.0	892	2	BF686850	BF686850	602102803	912	168.8	7.5	808	6	CB993588	AGENCOURT
840	178.6	8.0	1022	4	BM462965	BM462965	AGENCOURT	913	168.8	7.5	842	6	CD654434	AGENCOURT
841	178.4	8.0	586	4	BJ694687	BJ694687	BJ694687	914	168.6	7.5	508	2	AW732427	bb04g06.Y
842	178.4	8.0	640	2	BE273961	BE273961	601104420	915	168.4	7.5	791	7	CK483116	AGENCOURT
843	178	7.9	584	4	BI446157	BI446157	dai36e06.	916	168.4	7.5	881	5	BX713721	BX713721
C 844	178	7.9	672	1	AJ731921	AJ731921	AJ731921	917	168.2	7.5	584	5	BP366572	BP366572
845	178	7.9	849	7	CF692292	CF692292	CCAF109TR	918	168.2	7.5	748	7	CN052923	Salamande
846	177.8	7.9	652	6	BY754147	BY754147	BY754147	919	167.8	7.5	582	5	BP222244	BP222244
847	177.4	7.9	759	6	CB944443	CB944443	CB944443	920	167.8	7.5	582	5	BP358484	BP358484
C 848	177.2	7.9	903	3	CNS09BXS	CD332789	Single re	C 921	167.8	7.5	730	7	CF717962	CCAT88TF
C 849	177	7.9	519	6	CD332789	CD332789	StrPu537.	922	167.8	7.5	815	7	CF676543	CCADD54TR
850	177	7.9	815	6	CB993122	CB993122	AGENCOURT	923	167.6	7.5	826	2	BE733762	601568301
851	176.8	7.9	933	4	BI596767	BI596767	603242851	924	167.6	7.5	971	2	BE7332082	601566670
852	176.6	7.9	799	4	BM047828	BM047828	603629268	925	167.6	7.5	580	5	BP213987	BP213987
853	176.6	7.9	1020	2	BF568481	BF568481	602184489	926	167.4	7.5	729	7	CF694870	CCAI735TF
854	176	7.9	692	7	CO641569	CO641569	USDA-FP 1	C 927	167.4	7.5	499	1	AI931441	ul168d12.Y
855	175.8	7.8	788	4	BM008636	BM008636	603618290	928	167.2	7.5	500	5	BQ694592	1000735 H
856	175.8	7.8	951	5	BQ643299	BQ643299	AGENCOURT	929	167.2	7.5	559	2	AW766410	da62b03.x
857	175.6	7.8	755	5	BU415500	BU415500	603668771	C 930	167.2	7.5	621	2	BE388035	601283735
858	175.6	7.8	758	7	CN361478	CN361478	170005325	931	167.2	7.5	798	7	CF691128	CCAHX18TR
859	175.6	7.8	1380	2	BF686952	BF686952	602102727	932	167.2	7.5	1001	9	CNS07E7E	T7 end of
860	175.4	7.8	553	4	BM744352	BM744352	X-EST0017	933	166.8	7.4	795	7	CR438885	CR438885
861	175.2	7.8	736	4	BG327952	BG327952	602426975	934	166.4	7.4	786	6	CN601037	AGENCOURT
862	175.2	7.8	854	4	BG336431	BG336431	602405373	935	166.2	7.4	527	7	CN682243	E0161G01-
863	174.8	7.8	466	4	BI100777	BI100777	602886075	936	166	7.4	627	1	AV851172	AV851172
864	174.8	7.8	584	5	BP367891	BP367891	BP367891	C 937	165.8	7.4	592	6	CD215111	pgm2n.pk0
865	174.8	7.8	618	2	AW732305	AW732305	bb02e05.Y	938	165.6	7.4	723	2	BE733175	601567486
866	174.4	7.8	704	1	AU137269	AU137269	AU137269	939	165.6	7.4	638	4	BG386055	602455228
867	173.8	7.8	602	5	BP459087	BP459087	BP459087	940	165.4	7.4	554	4	BG814445	daf67c11.
868	173.8	7.8	772	4	BG468148	BG468148	602509723	941	165	7.4	637	7	CN058535	Salamande
869	173.6	7.7	500	4	BI960884	BI960884	MONO1_2_A	942	165	7.4	525	7	CN677789	E0102B03-
870	173.6	7.7	562	4	BI536332	BI536332	393256_MA	943	164.6	7.3	529	6	CD629094	56068936H
871	173.4	7.7	605	1	AI530145	AI530145	ui89f08.Y	C 944	164.6	7.3	550	7	CN694605	CN694605
872	173.2	7.7	546	1	AU167318	AU167318	601585126	945	164.6	7.3	582	5	BP359215	BP359215
873	173.2	7.7	722	2	BE792388	BE792388	601585126	946	164.6	7.3	1068	5	BX421582	BX421582
874	173.2	7.7	985	2	BE902224	BE902224	601675260	947	164.6	7.3	515	6	CD544409	B0257E10-
875	173	7.7	583	5	BU806250	BU806250	haa33c01.	948	164.4	7.3	516	6	CA870665	K0904A02-
876	173	7.7	610	2	BE836830	BE836830	ba97c08.Y	949	164.4	7.3	662	2	AV956049	AV956049
877	173	7.7	658	7	CV511319	CV511319	kc39h08.Y	950	164.4	7.3	666	4	BI485157	BI485157
878	173	7.7	968	2	BF100825	BF100825	601753760	951	164.2	7.3	496	2	AW823722	uf58c12.Y
879	172.8	7.7	495	4	BM583464	BM583464	170006872	952	164	7.3	512	6	CA545416	K0113A01-
880	172.8	7.7	716	6	BY742949	BY742949	BY742949	953	164	7.3	886	6	CB993636	CB993636
881	172.6	7.7	552	4	BI536323	BI536323	393244_MA	954	164	7.3	935	5	BQ642147	AGENCOURT
882	172.6	7.7	613	2	BE279711	BE279711	601158270	955	163.6	7.3	776	4	BI668421	BI668421
C 883	172.2	7.7	1094	6	CD325552	CD325552	AGENCOURT	956	163.4	7.3	782	7	CF717723	CCAGJ45TR
884	172	7.7	623	1	AL798428	AL798428	AL798428	957	163	7.3	712	5	BW047812	BW047812
885	171.8	7.7	554	7	CF893264	CF893264	A0121B04-	958	162.6	7.3	465	7	CF919003	CF919003
886	171.8	7.7	750	7	CO782086	CO782086	BL014A_H0	959	162.4	7.2	569	5	BP213753	BP213753
887	171.6	7.7	670	6	BY739405	BY739405	BY739405	960	162.4	7.2	575	1	AI722207	fd20d11.Y
888	171.6	7.7	892	4	BG282995	BG282995	602406184	961	162.4	7.2	601	1	AL956138	AL956138
889	171.4	7.6	808	4	BG698032	BG698032	602659177	962	162.4	7.2	635	6	BY753314	BY753314
890	171	7.6	423	4	BJ496583	BJ496583	BJ496583	963	162.4	7.2	371	8	AQ390611	CITBI-E1-
C 891	171	7.6	737	4	BJ718857	BJ718857	BJ718857	C 964	162.2	7.2	469	6	CA371834	CA371834
892	170.8	7.6	606	1	AL775869	AL775869	AL775869	965	162.2	7.2	715	4	BJ515070	BJ515070
C 893	170.8	7.6	810	2	AW331855	AW331855	S1F3 AGS-	C 966	162	7.2	887	7	CF819889	EST697271
894	170.6	7.6	621	5	BU805817	BU805817	haa22f08.	967	162	7.2	495	7	CO186932	EK024835.
895	170.6	7.6	685	7	CN058253	CN058253	Salamande	C 968	161.8	7.2	556	2	AW153789	E125f09.Y
896	170.6	7.6	729	4	BG335695	BG335695	602404349	969	161.8	7.2	561	7	CN711499	E0593F09-
897	170.6	7.6	1080	7	CF109995	CF109995	Shultzomi	970	161.8	7.2	403	6	CA043469	ssalpha00
898	170.4	7.6	457	1	AL785742	AL785742	cad90d02.	971	161.6	7.2	583	5	BP331989	BP331989
899	170.4	7.6	571	7	CN622684	CN622684	BP310616	972	161.6	7.2	662	7	CR557630	DKFP2p469N
900	170.4	7.6	583	5	BP310616	BP310616	BP310616	973	161.6	7.2				

974	161.4	7.2	495	2	BB853716	BB853716	1047	155.2	6.9	581	5	BP252798	BP252798
975	161.4	7.2	536	7	CK873786	SGP134949	1048	155.2	6.9	644	4	BM634771	BM634771
976	161.4	7.2	583	5	BP332465	BP332465	1049	155	6.9	503	5	EX560120	EX560120
977	161	7.2	753	6	CB600403	AGENCOURT	1050	155	6.9	790	7	CO958138	AGENCOURT
978	161	7.2	786	4	BI103676	BP2889170	1051	154.8	6.9	603	7	BN085398	EC2BBA25C
979	160.8	7.2	595	5	BQ667603	pb55h10.Y	1052	154.8	6.9	652	5	BW050995	BW050995
980	160.6	7.2	624	7	CK545211	rswhb0_01	1053	154.8	6.9	684	6	CA806261	ESG012c.E
981	160.6	7.2	676	2	BF059963	Hc d11_09	1054	154.8	6.9	720	7	CK505313	rswwc0_00
982	160.6	7.2	779	5	EX074911	EX074911	1055	154.8	6.9	744	7	CF702965	CAAE582TR
983	160.4	7.2	595	4	BM192252	dai21d10.	1056	154.6	6.9	584	5	BP279614	BP279614
984	160.4	7.2	602	1	AL637057	AL637057	1057	154.4	6.9	977	4	BG111505	602282820
985	160.4	7.2	692	6	CB015029	Hc d11_36	1058	154.2	6.9	427	2	BB845163	BB845163
986	160.2	7.1	790	7	CV486326	AGENCOURT	1059	154.2	6.9	665	5	BW329009	BW329009
987	160	7.1	651	4	BM581674	BM581674	1060	154.2	6.9	701	6	CA806251	ESG012c.E
988	160	7.1	670	5	BW319017	BW319017	1061	154	6.9	619	5	BU412454	603157304
989	160	7.1	682	5	BP010530	BP010530	1062	153.8	6.9	602	2	BE279251	601156763
990	160	7.1	868	4	BG325431	602424122	1063	153.8	6.9	634	7	CK621045	ml19e12.Y
991	160	7.1	915	7	CF827129	ESF704511	1064	153.8	6.9	773	7	CK352038	hggfha47C
992	160	7.1	987	5	BQ898380	AGENCOURT	1065	153.6	6.9	456	7	CF139012	UI-HF-CB0
993	159.8	7.1	460	7	CK611142	IFN1_N05	1066	153.6	6.9	655	7	CK571502	est_1_van
994	159.8	7.1	554	4	BI892283	ZF637-3-0	1067	153.4	6.8	492	2	BF706298	80602_MA
995	159.8	7.1	758	2	BE278462	601156832	1068	153.4	6.8	627	7	CK132961	RE11562.3
996	159.6	7.1	525	6	CB127230	K-EST0176	1069	153.2	6.8	647	4	BG970430	602837989
997	159.4	7.1	414	1	AJ285238	4A3B-AAH-	1070	153	6.8	581	5	BP357722	BP357722
998	159.4	7.1	601	7	CR435954	CR435954	1071	153	6.8	628	4	BJ794651	BJ794651
999	159.4	7.1	828	6	CD781861	EST653222	1072	152.8	6.8	768	7	CF694875	CCAI735TR
1000	159.2	7.1	529	1	AI874574	ul27h10.Y	1073	152.8	6.8	884	5	BQ434981	AGENCOURT
1001	159.2	7.1	650	4	BI230091	GM15386.5	1074	152.6	6.8	532	4	BJ614514	BJ614514
1002	158.8	7.1	721	4	BJ818095	BJ818095	1075	152.6	6.8	595	5	BX604180	BX604180
1003	158.8	7.1	926	2	BE780974	601469725	1076	152.2	6.8	571	7	CK491972	rswab0_01
1004	158.6	7.1	539	1	AL925409	AL925409	1077	152.2	6.8	675	7	CK514934	rswb0_00
1005	158.6	7.1	563	1	AL675098	AL675098	1078	152	6.8	834	5	BU243034	603592085
1006	158.6	7.1	647	1	AJ272857	AJ272857	1079	151.8	6.8	495	4	BI313319	daf93h02.
1007	158.4	7.1	896	2	BF784952	602110915	1080	151.6	6.8	553	4	BG814367	py31b09.Y
1008	158.4	7.1	966	5	BQ668983	AGENCOURT	1081	151.4	6.8	630	6	CB191352	BW339207
1009	158.4	7.1	977	2	BE730867	601569973	1082	151.4	6.8	637	5	BM339207	BW339207
1010	158.2	7.1	439	2	BB847422	BB847422	1083	151.4	6.8	642	5	BW359381	BW359381
1011	158.2	7.1	654	5	BW359667	BW359667	1084	151.4	6.8	644	5	BW339573	BW339573
1012	158	7.0	582	5	BP362110	BP362110	1085	151.2	6.7	681	2	BE563822	601334754
1013	158	7.0	763	8	BZ139795	BZ139795	1086	151.2	6.7	722	6	CA052384	ssalrgb51
1014	157.8	7.0	562	4	BJ040008	BJ040008	1087	151.2	6.7	752	4	BI544296	603241675
1015	157.6	7.0	583	5	BP311888	BP311888	1088	151.2	6.7	767	7	CF685186	CCAHF65TR
1016	157.6	7.0	595	1	AL780497	AL780497	1089	151.2	6.7	956	4	BG335749	602404423
1017	157.6	7.0	690	6	CA804353	ESG0113b.	1090	151	6.7	581	5	BP362398	BP362398
1018	157.6	7.0	816	7	CK174615	EST763935	1091	151	6.7	582	5	BP274868	BP274868
1019	157.4	7.0	754	1	AU133041	AU133041	1092	150.8	6.7	582	5	BP200996	BP200996
1020	157.2	7.0	505	4	BG811431	daf63c07.	1093	150.8	6.7	639	5	BW363347	BP200996
1021	157.2	7.0	583	4	BG814301	daf65f11.	1094	150.8	6.7	949	4	BG250423	BP200996
1022	157	7.0	455	2	AW430635	70387 MAR	1095	150.2	6.7	826	5	BU384202	BW363347
1023	157	7.0	491	6	CB725416	AMGNNUC:N	1096	150.2	6.7	558	2	BE018812	BG250423
1024	157	7.0	514	2	BE102647	UI-R-BT1-	1097	149.8	6.7	413	7	CK611166	603858920
1025	157	7.0	520	6	CB721101	AMGNNUC:C	1098	149.8	6.7	506	4	BG812158	BE018812
1026	157	7.0	749	7	CO565136	AGENCOURT	1099	149.6	6.7	388	4	BG812158	bb85d01.Y
1027	157	7.0	776	2	AW335650	S49G11 AG	1100	149.6	6.7	733	7	CK447267	CK0611166
1028	156.6	7.0	489	7	CO299262	CO299262	1101	149.4	6.7	595	4	BJ686163	CO296350
1029	156.6	7.0	643	2	BE977169	bs60e10.Y	1102	149.4	6.7	749	4	BM007332	CO296350
1030	156.4	7.0	428	7	CN096710	EC2CAA11D	1103	149	6.6	510	4	BG579635	CO296350
1031	156.4	7.0	632	6	CA807168	ESG016c.E	1104	149	6.6	581	5	BP349274	CO296350
1032	156.4	7.0	715	2	BF784958	602110921	1105	149	6.6	584	5	BP329637	CO296350
1033	156.2	7.0	499	4	BI312509	daf92f10.	1106	149	6.6	717	4	BJ796454	BP329637
1034	156.2	7.0	582	5	BP270540	BP270540	1107	148.8	6.6	612	2	BE279718	BP329637
1035	156.2	7.0	698	6	CB015320	Hc d11_40	1108	148.8	6.6	651	7	CN361474	BJ796454
1036	156	7.0	495	5	BY255797	BY255797	1109	148.6	6.6	481	7	CF140162	BE279718
1037	155.8	6.9	546	7	CF146611	UI-HF-CB0	1110	148.4	6.6	607	7	CF638567	601158278
1038	155.8	6.9	648	6	CA805903	ESG0120b.	1111	148.2	6.6	440	2	BB847141	CN361474
1039	155.8	6.9	770	7	CF682805	CAID56TR	1112	148.2	6.6	452	5	BY260472	170005325
1040	155.8	6.9	781	6	CB600204	AGENCOURT	1113	148.2	6.6	1022	9	CNS0761U	CF140162
1041	155.6	6.9	436	2	BB847155	BB847155	1114	148	6.6	582	5	BP313315	UI-HF-CB0
1042	155.6	6.9	566	2	BF351687	QV2-HT054	1115	148	6.6	660	6	BY732874	CF638567
1043	155.6	6.9	711	4	BJ145550	BJ145550	1116	148	6.6	779	7	CF717968	BB847141
1044	155.4	6.9	604	4	BJ699326	BJ699326	1117	147.8	6.6	602	6	CA869588	BY260472
1045	155.4	6.9	668	4	BJ690166	BJ690166	1118	147.4	6.6	448	1	AJ663133	AL430840
1046	155.2	6.9	544	4	BG814092	daf63c07.	1119	147.4	6.6	464	5	BY241339	clone XBA

c1120	147.4	569	5	BQ306973	147.4	6.6	147.4	1193	142.8	6.4	396	7	CK614195	CK614195	LPSd_H07
1121	147.4	582	5	BP346480	147.4	6.6	147.4	1194	142.8	6.4	944	2	BF786777	BF786777	602111950
1122	147.4	625	4	BI601335	147.4	6.6	147.4	1195	142.6	6.4	500	2	BB853379	BB853379	BB853379
1123	147.2	524	4	BG814412	147.2	6.6	147.2	1196	142.6	6.4	553	7	CN721222	CN721222	E0818C10-
1124	147.2	878	5	BP383262	147.2	6.6	147.2	1197	142	6.3	465	5	BY060483	BY060483	BY060483
1125	147	718	6	CD488088	147	6.6	147	c1198	142	6.3	735	4	BJ816674	BJ816674	BJ816674
1126	146.8	449	2	BB846235	146.8	6.5	146.8	1199	141.8	6.3	385	7	CF723044	AGENCOURT	AGENCOURT
c1127	146.8	597	6	CA332238	146.8	6.5	146.8	1200	141.8	6.3	385	7	CF781051	AGENCOURT	AGENCOURT
1128	146.8	799	6	CB955554	146.8	6.5	146.8	1201	141.8	6.3	385	7	CF781509	AGENCOURT	AGENCOURT
1129	146.6	390	2	AW227075	146.6	6.5	146.6	1202	141.8	6.3	385	7	CF781692	AGENCOURT	AGENCOURT
1130	146.6	509	5	BY243106	146.6	6.5	146.6	1203	141.8	6.3	385	7	CF782368	AGENCOURT	AGENCOURT
c1131	146.6	594	5	BQ387494	146.6	6.5	146.6	1204	141.8	6.3	385	7	CF783476	AGENCOURT	AGENCOURT
c1132	146.6	603	5	BQ399548	146.6	6.5	146.6	1205	141.8	6.3	385	7	CF783882	AGENCOURT	AGENCOURT
1133	146.6	902	7	CK805288	146.6	6.5	146.6	1206	141.8	6.3	385	7	CK653731	AGENCOURT	AGENCOURT
c1134	146.4	711	4	BJ726973	146.4	6.5	146.4	1207	141.8	6.3	385	7	CK654650	AGENCOURT	AGENCOURT
1135	146.2	636	1	AL584454	146.2	6.5	146.2	1208	141.8	6.3	385	7	CK655526	AGENCOURT	AGENCOURT
1136	146.2	690	6	CD305884	146.2	6.5	146.2	1209	141.8	6.3	417	4	BM771497	K-EST0055	K-EST0055
1137	146.2	1100	9	CNS06QUM	146.2	6.5	146.2	1210	141.8	6.3	581	5	BP359469	BP359469	BP359469
1138	146	445	7	CK334335	146	6.5	146	c1211	141.6	6.3	425	4	BM675848	BM675848	BJP602768
1139	146	519	4	BG552861	146	6.5	146	c1212	141.6	6.3	579	4	BJ702646	BJ702646	BJ702646
1140	146	528	4	BI314115	146	6.5	146	1213	141.6	6.3	582	5	BP360217	BP360217	BP360217
1141	146	570	5	BP291933	146	6.5	146	1214	141.4	6.3	765	4	BI770989	BI770989	603055326
c1142	146	584	4	BJ702127	146	6.5	146	c1215	141.2	6.3	581	5	BQ523739	NISC rl23	NISC rl23
1143	145.8	427	7	CF144462	145.8	6.5	145.8	1216	141	6.3	325	6	CA537596	C0255E03-	C0255E03-
1144	145.8	525	1	AU168590	145.8	6.5	145.8	1217	141	6.3	523	5	BQ520219	NISC rl03	NISC rl03
1145	145.8	756	7	CF148234	145.8	6.5	145.8	1218	141	6.3	575	7	CF638723	D06_C04 F	D06_C04 F
1146	145.6	1262	6	CD325908	145.6	6.5	145.6	c1219	140.8	6.3	705	7	CF638723	CF638723	D06_C04 F
1147	145.4	586	4	BI484773	145.4	6.5	145.4	1220	140.6	6.3	613	5	BW216183	BW216183	BW216183
1148	145.4	607	7	CK662144	145.4	6.5	145.4	1221	140.6	6.3	624	5	BW360046	BW360046	BW360046
1149	145.2	401	6	CD736173	145.2	6.5	145.2	1222	140.6	6.3	727	6	CB994471	AGENCOURT	AGENCOURT
1150	145.2	474	2	BB863141	145.2	6.5	145.2	1223	140.6	6.3	822	6	CB993805	CB993805	AGENCOURT
1151	145.2	693	6	CD783866	145.2	6.5	145.2	1224	140.4	6.3	430	4	BI541491	BI541491	455270 MA
1152	145	377	2	BF045811	145	6.5	145	1225	140.4	6.3	497	1	AL790150	AL790150	AL790150
c1153	145	593	4	BI533394	145	6.5	145	1226	140.4	6.3	544	2	AW496517	kp01c11.y	kp01c11.y
1154	145	725	6	CD759078	145	6.5	145	1227	140.4	6.3	569	5	BP331618	BP331618	BP331618
1155	145	971	4	BG336618	145	6.5	145	c1228	140.4	6.3	690	6	CA769828	saalrga50	saalrga50
1156	144.8	966	5	BUI65992	144.8	6.5	144.8	c1229	140.2	6.3	385	7	CF783475	AGENCOURT	AGENCOURT
1157	144.6	378	6	CD565567	144.6	6.4	144.6	c1230	140.2	6.3	385	7	CF783883	AGENCOURT	AGENCOURT
1158	144.6	512	4	BG553460	144.6	6.4	144.6	c1231	140.2	6.3	385	7	CN324782	AGENCOURT	AGENCOURT
1159	144.4	458	2	BB847485	144.4	6.4	144.4	1232	140.2	6.3	501	2	BF607680	BF607680	MY1_00062
1160	144.4	527	1	AL961491	144.4	6.4	144.4	1233	140.2	6.3	617	5	BW321204	BW321204	BW321204
1161	144.4	543	5	BQ389137	144.4	6.4	144.4	c1234	140.2	6.3	681	6	CA051088	CA051088	saalrgb53
c1162	144.4	626	4	BJ088512	144.4	6.4	144.4	1235	140	6.2	495	2	BE273879	601104396	601104396
1163	144.4	642	6	CB281566	144.4	6.4	144.4	1236	140	6.2	509	2	BE890822	601431269	601431269
1164	144.4	879	2	BE730937	144.4	6.4	144.4	1237	140	6.2	582	5	BP217095	BP217095	BP217095
1165	144.2	410	2	BB845512	144.2	6.4	144.2	1238	140	6.2	582	5	BP366281	BP366281	BP366281
c1166	144.2	413	7	CO312156	144.2	6.4	144.2	1239	140	6.2	586	5	BP345132	BP345132	BP345132
1167	144.2	479	2	BF041238	144.2	6.4	144	1240	140	6.2	642	7	CF131757	UI-HF-FQ0	UI-HF-FQ0
1168	144	429	2	BE688154	144	6.4	144	1241	140	6.2	695	7	CK963387	4077834 B	4077834 B
c1169	144	761	7	CF819890	144	6.4	144	1242	140	6.2	897	3	CR590069	full-leng	full-leng
1170	144	943	7	CF582410	144	6.4	144	1243	140	6.2	897	5	BX394140	BX394140	BX394140
1171	143.8	521	1	AL783328	143.8	6.4	143.8	1244	140	6.2	953	5	BU957102	AGENCOURT	AGENCOURT
c1172	143.8	572	4	BJ054399	143.8	6.4	143.8	1245	139.8	6.2	461	5	BY241683	BY241683	BY241683
1173	143.8	582	5	BP275036	143.8	6.4	143.8	1246	139.8	6.2	618	5	BW323763	BW323763	BW323763
1174	143.8	931	2	BE798140	143.8	6.4	143.8	1247	139.8	6.2	804	1	AU006345	AU006345	AU006345
1175	143.6	414	5	BQ382045	143.6	6.4	143.6	1248	139.6	6.2	521	4	BI966923	id26c05.y	id26c05.y
1176	143.6	471	4	BJ498491	143.6	6.4	143.6	1249	139.6	6.2	545	4	BI962484	id33905.y	id33905.y
1177	143.6	483	4	BG939163	143.6	6.4	143.6	1250	139.6	6.2	592	6	CD691971	EST8494 h	EST8494 h
1178	143.6	557	7	CN626088	143.6	6.4	143.6	1251	139.6	6.2	623	5	BW356802	BW356802	BW356802
1179	143.6	570	4	BJ695848	143.6	6.4	143.6	1252	139.6	6.2	633	7	CF904688	CF904688	A0425C05-
1180	143.6	581	7	CN552568	143.6	6.4	143.6	1253	139.6	6.2	635	7	CN788632	CN788632	4122987 B
1181	143.6	583	7	CO777750	143.6	6.4	143.6	1254	139.6	6.2	656	7	CF904711	A0425E07-	A0425E07-
1182	143.6	594	7	CR448177	143.6	6.4	143.6	c1255	139.6	6.2	676	4	BJ717736	BJ717736	BJ717736
1183	143.4	385	7	CF781325	143.4	6.4	143.4	1256	139.2	6.2	837	7	CV125785	OSTF30044	OSTF30044
1184	143.4	385	7	CK655430	143.4	6.4	143.4	1257	138.8	6.2	469	5	BY168028	BY168028	BY168028
c1185	143.4	568	1	AV852230	143.4	6.4	143.4	1258	138.8	6.2	559	4	BG530429	602559180	602559180
1186	143.4	596	6	CB192002	143.4	6.4	143.4	c1260	138.6	6.2	647	6	CD498917	CDA36-D05	CDA36-D05
1187	143	457	7	CF163610	143	6.4	143	1261	138.6	6.2	385	7	CF784909	CF784909	AGENCOURT
1188	143	466	1	AJ694083	143	6.4	143	1262	138.6	6.2	569	5	BP297945	BP297945	BP297945
1189	143	480	2	BF040302	143	6.4	143	1263	138.4	6.2	514	4	BM753305	BM753305	K-EST0030
1190	143	489	4	BJ692154	143	6.4	143	1264	138.4	6.2	582	5	BP283142	BP283142	BP283142
c1191	143	599	6	CA804883	143	6.4	143	1265	138.4	6.2	586	5	BP311929	BP311929	BP311929
1192	143	665	2	BE304879	143	6.4	143	1265	138.4	6.2	616	5	BX628654	BX628654	BX628654

1266	138.4	6.2	628	7	CK654683	CK654683	AGENCOURT	1339	133.8	6.0	409	5	5	BX560169	BX560169	BX560169
1267	138.4	6.2	833	6	CD171791	CD171791	AGENCOURT	C1340	133.6	6.0	581	2	2	AW333245	AW333245	AW333245
1268	138.4	6.2	896	4	BG398809	60244046		C1341	133.6	6.0	599	2	2	AW332766	AW332766	AW332766
1269	138.2	6.2	448	5	BY006317	BY006317		C1342	133.6	6.0	608	2	2	AW332685	AW332685	AW332685
1270	138.2	6.2	510	7	CF101979	hac43b07.		C1343	133.6	6.0	657	6	6	CA769622	ssalrgb51	CA769622
1271	138.2	6.2	766	2	BE788376	BE788376	601480213	C1344	133.6	6.0	686	4	4	BJ510662	BJ510662	BJ510662
1272	138	6.2	490	7	CF645035	K28 D02 F		1345	133.6	6.0	876	7	7	CF814414	EST691796	CF814414
1273	138	6.2	579	6	CB299321	ru2ic02.y		1346	133.4	6.0	579	4	4	BM603999	170006870	BM603999
C1274	138	6.2	594	5	BQ307244	MR0-BT200		1347	133.4	6.0	725	7	7	CF638800	D07 B06 F	CF638800
1275	138	6.2	605	5	BW320612	BW320612		1348	133.4	6.0	757	7	7	CR550093	DKFZp459G	CR550093
C1276	138	6.2	665	4	BU139540	BU139540		1349	133.2	5.9	445	5	5	BY314336	BY314336	BY314336
1277	137.8	6.1	557	6	CD450408	USDA-FP 1		1350	133.2	5.9	575	5	5	BW192423	BW192423	AL037548
1278	137.8	6.1	578	6	CD688220	EST4742_h		1351	133.2	5.9	612	1	1	AL037548	DKFZp564G	AL037548
1279	137.8	6.1	584	6	CA868792	CA868792		1352	133.2	5.9	994	5	5	BP224341	BP224341	BP224341
1280	137.8	6.1	585	6	CA869358	CA869358		1353	132.8	5.9	711	4	4	BJ518555	BJ518555	BJ518555
C1281	137.6	6.1	665	6	CA054355	CA054355	ssalrgb52	1354	132.8	5.9	955	4	4	BG774729	BG774729	BG774729
C1282	137.6	6.1	672	1	AU216864	AU216864		1355	132.6	5.9	582	6	6	CB019917	pw97c10.y	CB019917
1283	137.6	6.1	760	1	AV398175	AV398175		1356	132.4	5.9	475	5	5	BU113002	603131167	BU113002
1284	137.4	6.1	535	7	CF170665	CF170665	B0831E02-	1357	132.4	5.9	572	6	6	CA958096	px18d02.y	CA958096
1285	137.4	6.1	576	5	BP224203	BP224203		1358	132.4	5.9	575	5	5	BW196906	BW196906	BW196906
1286	137.4	6.1	689	7	CF099618	CF099618	rd75912.y	1359	132.4	5.9	582	5	5	BP298421	BP298421	BP298421
C1287	137.4	6.1	713	2	AW334872	AW334872	S40C1 AGS	1360	132.4	5.9	583	5	5	BP361722	BP361722	BP361722
1288	137.4	6.1	882	4	BG401715	BG401715	602466384	1361	132.2	5.9	582	5	5	BP195797	BP195797	BP195797
C1289	137.2	6.1	684	4	BJ018050	BJ018050		1362	132.2	5.9	591	7	7	CN949923	CN949923	Ha mx0 28
1290	137	6.1	461	5	BX335262	BX335262		1363	132.2	5.9	747	2	2	BE535610	601062334	BE535610
1291	137	6.1	583	5	BP359681	BP359681		1364	132	5.9	408	5	5	BY159750	BY159750	BY159750
1292	136.8	6.1	404	7	CN361475	CN361475	170005319	1365	132	5.9	446	5	5	BY259061	BY259061	BY259061
C1293	136.8	6.1	418	5	BX636866	BX636866		1367	131.8	5.9	802	5	5	BU601711	AGENCOURT	BU601711
1294	136.8	6.1	588	7	CR548022	CR548022	DKFZp459C	1368	131.4	5.9	298	6	6	CA537586	C0255D04-	CA537586
1295	136.8	6.1	615	7	CK575046	CK575046	IST WT5 7	1369	131.2	5.9	598	2	2	AV963279	AV963279	AV963279
1296	136.6	6.1	391	5	BY233021	BY233021		1370	131	5.8	413	2	2	BB845543	BB845543	BB845543
C1297	136.6	6.1	399	7	CO304710	CO304710	EK245832.	1371	131	5.8	582	5	5	BP313480	BP313480	BP313480
1298	136.4	6.1	516	7	CF639420	CF639420	D15 D12 F	1372	130.6	5.8	583	5	5	BP313480	BP313480	BP313480
1299	136.4	6.1	582	5	BP271240	BP271240		1373	130.6	5.8	746	9	9	BX996483	Reverse s	BX996483
1300	136.4	6.1	599	6	CA780034	CA780034	MPL384 4	1374	130.4	5.8	634	6	6	CD749276	CD749276	CD749276
C1301	136.4	6.1	603	7	CR448178	CR448178		1375	130.2	5.8	778	7	7	CF270676	AGENCOURT	CF270676
1302	136.4	6.1	607	4	BG971414	BG971414	602840137	1376	130	5.8	425	5	5	BY040553	BY040553	BY040553
C1303	136.4	6.1	673	6	CA057172	CA057172	ssalrga50	1377	130	5.8	582	5	5	BP362126	BP362126	BP362126
1304	136.2	6.1	584	6	CB191526	CB191526	py33d04.y	1378	130	5.8	660	2	2	BF829814	MR3-HN006	BF829814
1305	136.2	6.1	584	6	CB192413	CB192413	py28h04.y	C1378	130	5.8	849	4	4	BI086565	BI086565	BI086565
1306	136.2	6.1	942	5	BQ422828	BQ422828	AGENCOURT	1379	129.8	5.8	602	4	4	BJ808404	BJ808404	BJ808404
1307	136	6.1	144	5	BQ338465	BQ338465	QV2-NN005	1380	129.8	5.8	702	7	7	CN552223	tae20h08.	CN552223
1308	135.8	6.1	471	4	BI500526	BI500526	rs74a06.y	C1381	129.8	5.8	426	1	1	AA126163	AA126163	AA126163
1309	135.8	6.1	499	7	CN690046	CN690046	E0287G05-	1382	129.6	5.8	790	5	5	BX673318	BX673318	BX673318
1310	135.8	6.1	884	5	BQ212423	BQ212423	AGENCOURT	1383	129.6	5.8	1047	1	1	AV000937	AV000937	AV000937
1311	135.6	6.0	383	5	BX710760	BX710760	daf67a01.	1384	129.4	5.8	643	6	6	CD629086	CD629086	CD629086
C1312	135.6	6.0	394	4	BG812179	BG812179		1385	129.2	5.8	650	7	7	CN563561	tae68h10.	CN563561
1313	135.6	6.0	446	2	BB849632	BB849632		C1386	129	5.8	650	7	7	AL363847	AL363847	AL363847
1314	135.6	6.0	566	6	CB190890	CB190890	py37c12.y	1387	128.8	5.7	400	1	1	CB743579	AMGNNUC:N	CB743579
1315	135.4	6.0	385	7	CK654777	CK654777	AGENCOURT	1388	128.6	5.7	448	6	6	CD629092	CD629092	CD629092
1316	135.4	6.0	881	6	CB994014	CB994014	AGENCOURT	1389	128.6	5.7	573	6	6	CD629092	CD629092	CD629092
1317	135.2	6.0	386	5	BY076799	BY076799	BY076799	C1390	128.6	5.7	610	5	5	BX554919	BX554919	BX554919
1318	135.2	6.0	388	5	BY097674	BY097674		1391	128.4	5.7	518	7	7	R55887	Yg92b05.r1	R55887
1319	134.8	6.0	581	6	CB191755	CB191755	py36d04.y	1392	128.4	5.7	528	4	4	BG666342	DRACHC02	BG666342
1320	134.8	6.0	666	2	BE795285	BE795285	601592379	C1393	128.4	5.7	555	4	4	BI444237	dai96e07.	BI444237
1321	134.6	6.0	487	7	CO284934	CO284934	EK167619.	C1394	128.4	5.7	632	1	1	AI641228	fc21b09.x	AI641228
1322	134.6	6.0	599	7	CN361487	CN361487	170006001	1395	128.4	5.7	635	7	7	CK655138	CK655138	CK655138
1323	134.6	6.0	618	4	BM590001	BM590001	170006873	1396	128.2	5.7	389	1	1	AJ660637	AJ660637	AJ660637
C1324	134.6	6.0	681	4	BJ506367	BJ506367		1397	128.2	5.7	450	5	5	BY051372	BY051372	BY051372
1325	134.6	6.0	775	1	AV399520	AV399520		C1398	128.2	5.7	464	1	1	AI270136	qt63h04.x	AI270136
1326	134.4	6.0	420	2	BB850312	BB850312		C1399	128.2	5.7	687	6	6	CB492211	omykbra00	CB492211
1327	134.2	6.0	584	5	BP276662	BP276662		1400	128	5.7	426	5	5	BY292255	BY292255	BY292255
C1328	134.2	6.0	639	7	CF688412	CF688412	CCAFJ81TO	1401	127.8	5.7	495	7	7	CR775391	CR775391	CR775391
C1329	134	6.0	385	7	CN319080	CN319080	AGENCOURT	C1402	127.6	5.7	464	5	5	BX721391	BX721391	BX721391
1330	134	6.0	536	6	CB192021	CB192021	py23h01.y	1403	127.6	5.7	496	4	4	BG971174	602839718	BG971174
1331	134	6.0	546	6	CB192383	CB192383	py28e07.y	1404	127.6	5.7	496	4	4	CN361481	170006002	CN361481
1332	134	6.0	548	6	CA958083	CA958083	px18b09.y	1405	127.2	5.7	597	1	1	AJ273786	AJ273786	AJ273786
1333	134	6.0	560	6	CB099687	CB099687	py15f09.y	C1406	126.8	5.7	475	6	6	CB405000	OSTR034H3	CB405000
1334	134	6.0	566	6	CA868609	CA868609	pw83b03.y	1407	126.6	5.6	370	4	4	BI036336	BI036336	BI036336
1335	134	6.0	566	6	CA958062	CA958062	px17906.y	1408	126.6	5.6	508	4	4	BM291344	BM291344	BM291344
1336	134	6.0	566	6	CA958214	CA958214	px19h06.y	C1409	126.6	5.6	682	7	7	CN625746	tae54f10.	CN625746
1337	134	6.0	578	6	CB191356	CB191356	py31c04.y	1410	126.4	5.6	516	1	1	AL673605	AL673605	AL673605
1338	134	6.0	582	6	CB099751	CB099751	py16e08.y	1411	126.4	5.6	569	2	2	BE867633	601443149	BE867633

1412 126.4 5.6 578 4 BI001302
1413 126.4 5.6 591 1 AU204895
c1414 126.4 5.6 610 7 CR449132
1415 126.4 5.6 612 6 CD706654
1416 126.2 5.6 646 6 CB505265
1417 126.2 5.6 784 2 BE395863
1418 126 5.6 536 4 BM838128
1419 125.8 5.6 394 5 BY087309
1420 125.8 5.6 445 6 CA869207
1421 125.4 5.6 433 7 CF644863
1422 125.4 5.6 574 6 CB933182
c1423 125.2 5.6 536 2 AW027963
1424 125.2 5.6 580 1 AJ442838
c1425 125.2 5.6 639 7 CV514427
1426 125 5.6 528 5 BW541942
c1427 125 5.6 605 5 BX563220
c1428 125 5.6 680 7 CN622379
1429 124.8 5.6 1304 4 BM807817
1430 124.6 5.6 470 4 BG893341
1431 124.6 5.6 578 6 CA034135
1432 124.4 5.5 366 2 AW402004
1433 124.4 5.5 420 5 BY295267
1434 124.4 5.5 537 6 CB099701
1435 124.2 5.5 592 5 BP247171
1436 124 5.5 415 2 BB845506
1437 123.6 5.5 582 5 BP357837
c1438 123.6 5.5 685 7 CN622280
1439 123.4 5.5 378 2 BB843788
1440 123.4 5.5 582 7 CR762563
1441 123.4 5.5 690 7 CN361484
1442 123.2 5.5 352 7 CF732400
1443 123.2 5.5 389 2 BB846498
1444 123.2 5.5 410 2 BB845649
c1445 123.2 5.5 755 5 BX737649
1446 123.2 5.5 773 7 CR629731
1447 123 5.5 986 4 BF973920
1448 122.8 5.5 386 5 BY079567
1449 122.6 5.5 569 6 CB267995
1450 122.2 5.5 519 7 CF141464
1451 122.2 5.5 672 7 CF688418
1452 122 5.4 458 1 AA590890
1453 122 5.4 582 5 BP360416
1454 122 5.4 745 1 AU004195
1455 122 5.4 1318 7 CF784910
1456 121.8 5.4 493 7 CR536868
1457 121.8 5.4 512 2 AW966517
1458 121.8 5.4 521 6 CB154729
1459 121.8 5.4 537 7 CF140203
1460 121.6 5.4 482 7 CR534333
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1462 121.4 5.4 415 5 BY218179
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1464 121 5.4 410 2 BB846508
1465 121 5.4 582 5 BP320056
1466 120.8 5.4 462 2 BB745052
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1469 120.6 5.4 606 7 CF237840
1470 120.6 5.4 1286 4 BM804222
1471 120.4 5.4 343 2 BB843678
1472 120.4 5.4 354 2 BB847708
1473 120.4 5.4 460 5 BX625832
c1474 120.4 5.4 481 5 BQ389136
1475 120.4 5.4 526 4 BM866749
1476 120.4 5.4 539 7 W82610
c1477 120.4 5.4 643 5 BQ398331
1478 120.2 5.4 319 4 BJ707460
1479 120.2 5.4 402 2 BE279973
1480 120.2 5.4 403 5 BY264462
1481 120.2 5.4 595 7 CN622576
1482 120.2 5.4 735 4 BG668093
1483 120 5.4 374 5 BY160251
1484 120 5.4 378 5 BY047456

BI001302 MR2-HN006
AU204895 AU204895
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CD706654 EST23181
CB505265 ssalplnb5
BE395863 601312909
BM838128 K-EST0114
BY087309 BY087309
CA869207 pw99e01.Y
CF644863 K26 D02 F
CB933182 ri26g07.Y
AW027963 wv25e07.x
AJ442838 AJ442838
CV514427 taj60e01.
BW541942 BW541942
BX563220 BX563220
CN622379 tad90d02.
BM807817 AGENCOURT
BG893341 kt10h06.Y
CA034135 pw36a07.Y
AW402004 UI-HF-BK0
BY295267 BY295267
CB099701 py15h04.Y
BP247171 BP247171
BB845506 BB845506
BP357837 BP357837
CN622280 tad88h05.
BB843788 BB843788
CR762563 DKFZp469L
CN361484 170006000
CF732400 UI-M-HA0-
BB846498 BB846498
BB845649 BB845649
BX737649 BX737649
CR629731 DKFZp469N
BF973920 602242064
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CB267995 1006901 H
CF141464 UI-HF-CB0
CF688418 CCAFJ81TR
AA590890 vm17f08.r
BP360416 BP360416
AU004195 AU004195
CF784910 AGENCOURT
CR536868 DKFZp459L
AW966517 EST378591
CB154729 K-EST0212
CF140203 UI-HF-CB0
CR534333 CR534333
CK181921 EST771241
BY218179 BY218179
CV528496 dba55f10.
BB846508 BB846508
BP320056 BP320056
BB745052 BB745052
AW335275 S45C8 AGS
BF048496 dc29d01.x
CF237840 AGENCOURT
BM804222 AGENCOURT
BB843678 BB843678
BB847708 BB847708
BX625832 BX625832
BQ389136 NISC_mq05
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W82610 mf05h12.r1
BQ398331 NISC mo06
BJ707460 BJ707460
BE279973 601156986
BY264462 BY264462
CN622576 tad88h05.
BG668093 DRABVD02
BY160251 BY160251
BY047456 BY047456

1485 120 5.4 555 5 BW335441 BW335441
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1487 119.8 5.3 597 4 BG774564 BG774564
c1488 119.8 5.3 599 5 BQ396655 BQ396655
1489 119.6 5.3 339 7 W77356 W77356
1490 119.6 5.3 345 2 AW606681 AW606681
1491 119.6 5.3 380 1 AA350924 AA350924
1492 119.6 5.3 419 6 CA869441 CA869441
1493 119.6 5.3 424 6 CA033921 CA033921
1494 119.6 5.3 427 6 CA869764 CA869764
1495 119.6 5.3 429 6 CB064112 CB064112
1496 119.6 5.3 561 4 BI215486 BI215486
1497 119.6 5.3 605 3 CR649055 CR649055
1498 119.6 5.3 631 1 AL959947 AL959947
c1499 119.6 5.3 711 5 BX753337 BX753337
1500 119.6 5.3 958 7 W12093 W12093

ALIGNMENTS

RESULT 1
CR610360
LOCUS CR610360 2105 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSODN001YK12 of Adult brain of Homo sapiens (human).
ACCESSION CR610360
VERSION CR610360.1 GI:50491167
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2105)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope.
2 (bases 1 to 2105)
Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES
Location/Qualifiers
1..2105
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/mol_type="mRNA"
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/clone="CSODN001YK12"
/tissue_type="Adult brain"
/plasmid="pCMVSPORT_6"

Query Match 93.6%; Score 2098.6; DB 3; Length 2105;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2101; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 40 AATAGCTCCACTATACCAGCCTCGTCTTCTTCCTCCGGGGACAAACGTGGTCCAGGCACAG 99
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Db 1 AATAGCTCCACTATACCAGCCTCGTCTTCTTCCTCCGGGGACAAACGTGGTCCAGGCACAG 60
QY 100 AGAGATATTTAATGTACCCCTCTTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTGTG 159
|||||
Db 61 AGAGATATTTAATGTACCCCTCTTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTGTG 120

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1528)
REFERENCE AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL PUBMED	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932
REFERENCE AUTHORS	2 (bases 1 to 1528) Strausberg,R. Direct Submission
TITLE JOURNAL	Submitted (01-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC/DCTD/DRP CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacqueie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
FEATURES source	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 13 Row: f Column: 3 This clone has the following problem: retained intron. Location/Qualifiers 1..1528 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3614507" /tissue type="Skin, melanotic melanoma." /clone_lib="NIH MGC 20" /lab_host="DH10B-R" /note="Vector: pOTB7"
ORIGIN	Query Match 64.5%; Score 1445.2; DB 3; Length 1528; Best Local Similarity 99.7%; Pred. NO. 0; Matches 1447; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy	754 AAGATCTTCCTGTGAATATCAAATTCATCATTTGAGGGGATGGAAGAGCGTGCTCTGTTG 813

QY 1894 GCACAGATGTTGGAATGTTTAAGGTCCTCCCACTGCACACCTTCTCTCAAGTCATAGCTG 1953
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Db 1218 GCACAGATGTTGGAATGTTTAAGGTCCTCCCACTGCACACCTTCTCTCAAGTCATAGCTG 1277
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QY 1954 CTTGCAGCAACTTGATTTCCTCCCAAGTCCTGTGCAATAGCCCCAGGATTGGATTCTCTTCCA 2013
|||||
Db 1278 CTTGCAGCAACTTGATTTCCTCCCAAGTCCTGTGCAATAGCCCCAGGATTGGATTCTCTTCCA 1337
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QY 2014 ACCTTTTAGCATATCTCCAACCTTGCAATTTGATTGGCATAATCACTCCGGTTTGCTTTC 2073
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Db 1338 ACCTTTTAGCATATCTCCAACCTTGCAATTTGATTGGCATAATCACTCCGGTTTGCTTTC 1397
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QY 2074 TAGTCTCTCAAGTGTCTCGTGACACATAATCATTCCTCAATGATCGCCTTTGCTTTACC 2133
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Db 1398 TAGTCTCTCAAGTGTCTCGTGACACATAATCATTCCTCAATGATCGCCTTTGCTTTACC 1457
|||||
QY 2134 ACTCTTTCTTTTATCTTATTATAAAAAATGTTGGTCTCCACCACCTGNCCTCCCAAAAAA 2193
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Db 1458 ACTCTTTCTTTTATCTTATTATAAAAAATGTTGGTCTCCACCACCTGACTACAAAAAAA 1517
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QY 2194 AAAAAAAAAA 2204
|||||
Db 1518 AAAAAAAAAA 1528
|||||
RESULT 3
AK085308
LOCUS
DEFINITION
AK085308 2814 bp mRNA linear HTC 03-APR-2004
Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched
library, clone:D630009N02 product:similar to GLUTAMATE
CARBOXYPEPTIDASE-LIKE PROTEIN 2 [Homo sapiens], full insert
sequence.
ACCESSION
AK085308
VERSION
AK085308.1 GI:26351560
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5

AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL
Nature 420, 563-573 (2002)
REFERENCE
6 (bases 1 to 2814)
AUTHORS
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
TITLE
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="PANTOM DB:D630009N02"
/db_xref="taxon:10090"
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/tissue_type="kidney"
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similar to GLUTAMATE CARBOXYPEPTIDASE-LIKE PROTEIN 2 [Homo
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GTKTVIPGRVLGKFSIRLPTMSPSVVEKQVTOHLEAVFSKRNSFNKMAVSMVLGLHP
WTANVNDTQYLAARQRTIKTVFGVNPDMIRDGSTPIAKIFQAITQKSVMMPLGAVDD
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polyA_signal
polyA_site
ORIGIN
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Best Local Similarity 78.9%; Pred. No. 2.6e-229;
Matches 1214; Conservative 0; Mismatches 322; Indels 3; Gaps 1;
QY 283 CCTCCCCCGCCCGCGCTGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATG 342

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Matches 1024; Conservative 10; Mismatches 18; Indels 4; Gaps 4;									
QY	1076	CCCTGGAATCTATGATGAAGTGGTTCCTCTTACAGAAGAGGAAATAAATACATACAAAAGC	1135						
Db	1067	CCCCTGRATCTATGATGAAGT-GTTCCTYTAACAGRAGAGGAAATAAAMACATACAARCC	1009						
QY	1136	CATCCATCTAGACCTAGAGAATACCGGAATAGCGCGGTTGAGAAATTTCTGTTCTGA	1195						
Db	1008	CATCCATCTAGACCTAGAGAATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTCTGA	949						
QY	1196	TACTAAGGAGGAGATTCTAATGCACCTCTGGAGGTACCATCTCTTTCTATTATGGGAT	1255						
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QY	1256	CGAGGGCGGTTTGATGAGCCTGGAACTAAA-ACAGTCATACCTGGCCGAGTTATAGGAA	1314						
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QY	1315	AATTTCAATCCGTCTAGTCCCTCACATGAATGTCTGCGGTGGAATAACAGGTGACAC	1374						
Db	829	AATTTCAATCCGTCTAGTCCCTCACATGAATGTCTGCGGTGGAATAACAGKTGACAC	770						
QY	1375	GACATCTTGAAGATGTGTTCTCAAAGAAATAGTTCCAAAGATGGTTGTTTCCATGA	1434						
Db	769	GACATCTTGAAGATGTGTTCTCAAAGAAATAGTTCCAAAGATGGTTGTTTCCATAA	710						
QY	1435	CTCTAGACTACACCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAA	1494						
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Db	409	CTTCTAGTCTGATCTGATCCACTGACAGATTACCTCCCCCACAATCCCTAACAGGGATG	350						
QY	1795	GAATGTAAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAAT	1854						
Db	349	GAATGTAAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAAT	290						
QY	1855	GTCTTGGGATATCTGGATCAGTAATAAAATATTCAAAGGCACAGATGTTGGAATGGTT	1914						
Db	289	GTCTTGGGATATCTGGATCAGTAATAAAATATTCAAAGGCACAGATGTTGGAATGGTT	230						
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Db	229	TAAGGTCCCCCACTGCACACCTTCCTCAAGTCATAGCTGCTTGCAAGCAACTTGATTTCCC	170						
QY	1975	CAAGTCCTGTGCAATAGCCCCCAGGATTGGATTTCCTTCCAACCTTTTAGCATATCTCCAAC	2034						
Db	169	CAAGTCCTGTGCAATAGCCCCCAGGATTGGATTTCCTTCCAACCTTTTAGCATATCTCCAAC	110						
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vector. Library was not normalized."									
ORIGIN									
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Best Local Similarity 98.6%; Pred. No. 4.3e-216;									
Matches 984; Conservative 7; Mismatches 2; Indels 5; Gaps 3;									
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QY	100	AGAGATATTTAATGTCAACCTCTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTT	159						
Db	61	AGAGATATTTAATGTCAACCTCTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTT	120						
QY	160	GAGGTTGGGAAAAGTTGCTAGAGGCTTCAGAACTCCAGCCTAATGGATCCCAAACCTCGGA	219						
Db	121	GAGGTTGGGAAAAGTTGCTAGAGGCTTCAGAACTCCAGCCTAATGGATCCCAAACCTCGGA	180						
QY	220	GAATGGTCCGTCCCTGCTGGCTG--TGCTGCTGCTGCTGCTGGAGCGGCGCATGTTCT	276						
Db	181	GAATGGTCCGTCCCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	240						
QY	277	CCTCACCTTCCCCCCCCCGCGCTGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATC	336						
vector. Library was not normalized."									
ORIGIN									
Query Match 42.5%; Score 952; DB 5; Length 1006;									
Best Local Similarity 98.6%; Pred. No. 4.3e-216;									
Matches 984; Conservative 7; Mismatches 2; Indels 5; Gaps 3;									
QY	40	AATAGCTCCACTATACCAAGCTCGTCTTCCCTCCGGGGGACAACGTGGTCAGGGCACAG	99						
Db	1	AATAGCTCCACTATACCAAGCTCGTCTTCCCTCCGGGGGACAACGTGGTCAGGGCACAG	60						
QY	100	AGAGATATTTAATGTCAACCTCTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTT	159						
Db	61	AGAGATATTTAATGTCAACCTCTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTT	120						
QY	160	GAGGTTGGGAAAAGTTGCTAGAGGCTTCAGAACTCCAGCCTAATGGATCCCAAACCTCGGA	219						
Db	121	GAGGTTGGGAAAAGTTGCTAGAGGCTTCAGAACTCCAGCCTAATGGATCCCAAACCTCGGA	180						
QY	220	GAATGGTCCGTCCCTGCTGGCTG--TGCTGCTGCTGCTGCTGGAGCGGCGCATGTTCT	276						
Db	181	GAATGGTCCGTCCCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	240						
QY	277	CCTCACCTTCCCCCCCCCGCGCTGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATC	336						


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Db      |||||||
241 CCTACCCCTCCCGCCCGCGCGTGTAGAGAAAGTCTTCAGTACATTGACCTCCATC 300
Qy      |||||||
337 AGGATGAATTTGTGCAGACGCTGAAGGAGTGGTGCCATCGAGAGCGACTCTGTCCAGC 396
Db      |||||||
301 AGGATGAATTTGTGCAGACGCTGAAGGAGTGGTGCCATCGAGAGCGACTCTGTCCAGC 360
Qy      |||||||
397 CTGTGCCTCGCTTCAGACAAAGAGCTCTTCAGAAATGATGSCCGTGGCTGCCGACACGCTGC 456
Db      |||||||
361 CTGTGCCTCGCTTCAGACAAAGAGCTCTTCAGAAATGATGSCCGTGGCTGCCGACACGCTGC 420
Qy      |||||||
457 AGCGCCTGGGGCCCGTGTGSCCTCGGTGGACATGGGTCTTCAGCAGCTGCCCGATGGTC 516
Db      |||||||
421 AGCGCCTGGGGCCCGTGTGSCCTCGGTGGACATGGGTCTTCAGCAGCTGCCCGATGGTC 480
Qy      |||||||
517 AGAGTCTTCCAATACCTCCGTCATCCTGGCCGAACTTGTATGGAGCGGATCCCACGAAGGCA 576
Db      |||||||
481 AGAGTCTTCCAATACCTCCGTCATCCTGGCCGAACTTGTATGGAGCGGATCCCACGAAGGCA 540
Qy      |||||||
577 CCGTGTGCTTACGGCCACTTGGACGTGCAGCCTGTGACCGGCGGATGGGTGGCTCA 636
Db      |||||||
541 CCGTGTGCTTACGGCCACTTGGACGTGCAGCCTGTGACCGGCGGATGGGTGGCTCA 600
Qy      |||||||
637 CGGACCCCTATGTGCTGACGAGGTAGACGGGAACTTATGGACGAGGAGCGACCGGACA 696
Db      |||||||
601 CGGACCCCTATGTGCTGACGAGGTAGACGGGAACTTATGGACGAGGAGCGACCGGACA 660
Qy      |||||||
697 ACAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCGCCTTCAGAGCCCTGGAGCAAG 756
Db      |||||||
661 ACAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCGCCTTCAGAGCCCTGGAGCAAG 720
Qy      |||||||
757 ATCTTCCTGTGAATATCAAAATTCATCATTTGAGGGATGGAAGAGGCTGGCTCTGTGCCC 816
Db      |||||||
721 ATCTTCCTGTGAATATCAAAATTCATCATTTGAGGGATGGAAGAGGCTGGCTCTGTGCCC 780
Qy      |||||||
817 TGGAGGAACCTTGTGGAAGAAAGAACCGGATCTTCTCTGGTGTGGACTACATGTAA 876
Db      |||||||
781 TGGAGGAACCTTGTGGAAGAAAGAACCGGATCTTCTCTGGTGTGGACTACATGTAA 840
Qy      |||||||
877 TTTCAGATAACCTGTGGATCAGCCAAAGGAAGCCAGCAATCACTTATGGA-CCCGGGG 935
Db      |||||||
841 TTTCAGATAACCTGTGGATCAGCCAAAGGAAGCCAGCMATCACTTACGGAACCCCGGG 900
Qy      |||||||
936 AACAGCTACTTTCATGTTGAGGTGAAATGCAGAGACAGGATTTTCACTCAGGAACCTTT 995
Db      |||||||
901 AACAGCTACTTTCATGTTGAGGTGAAATGCAGAGACAGGATTTTCACTCAGGRACCTTT 960
Qy      |||||||
996 GGTGGCATCCTTTCATGAACCAATGGCTGATCTGGTGC 1033
Db      |||||||
961 KGTGGCMTCCYTTCATGAA-CAATGGCTGATCTGGTTSY 997
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RESULT 6
BX432016
LOCUS
DEFINITION BX432016 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
ACCESSION BX432016
VERSION BX432016.1 GI:30789074
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 928)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
```

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9111.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0BAG069ZA11_CS06609_1&c=9111.f

FEATURES
source Location/Qualifiers
1..928
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN001YK12"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 38.9%; Score 872.4; DB 5; Length 928;
Best Local Similarity 98.8%; Pred. No. 4.4e-197;
Matches 920; Conservative 0; Mismatches 7; Indels 4; Gaps 4;

QY 847 GATTCTTCTCTGGTGGACTACATTGTAATTTAGATAAACCCTGTGGATCAGCCAAAGGA 906
Db 1 GATTCTTCTCTGGTGGACT-CATTGTAATTT-AGATAAACCCTGTGGATCAGCCAAAGGA 58
QY 907 AGCCAGCAATCACTTATGGAACCCCGGGGAACAGCTACTTTCATGGTGGAGGTGAAATGCA 966
Db 59 AGCCAGCAATCACTTATGGAACCCCGGGGAACAGCTACTTTCATGGTGGAGGTGAAATGCA 118
QY 967 GAGACCAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGGTGTATC 1026
Db 119 GAGACCAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGGTGTATC 178
QY 1027 TGGTGTCTCTTCGGTAGCCTGGTAGACTCGTGGTGCATATCCTGGTCCCTGGAATCT 1086
Db 179 TGGTGTCTCTTCGGTAGCCTGGTAGACTCGTGGTGCATATCCTGGTCCCTGGAATCT 238
QY 1087 ATGATGAAGTGGTTCCTCTTACAGAAGAGGAAATAAATACATACAAAGCCATCCATCTAG 1146
Db 239 ATGATGAAGTGGTTCCTCTTACAGAAGAGGAAATAAATACATACAAAGCCATCCATCTAG 298
QY 1147 ACCTAGAAGATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTTTCGATACTAAGGAGG 1206
Db 299 ACCTAGAAGATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTTTCGATACTAAGGAGG 358
QY 1207 AGATTCTAATGCACTCTGGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGGCGCGT 1266
Db 359 AGATTCTAATGCACTCTGGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGGCGCGT 418
QY 1267 TTGATGAGCCTGGAACTAAACAGTCATACCTGGCCGAGTTATAGGAAAATTTCAATCC 1326
Db 419 TTGATGAGCCTGGAACTAAACAGTCATACCTGGCCGAGTTATAGGAAAATTTTCAATCC 478
QY 1327 GTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAATAAACAGGTGACACGACATCTTGAAG 1386
Db 479 GTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAATAAACAGGTGACACGACATCTTGAAG 538
QY 1387 ATGTGTTCTCCAAAAGAAATAGTTCCAAACAGATGGTTGTTTCCATGACTCTAGGACTAC 1446
Db 539 ATGTGTTCTCCAAAAGAAATAGTTCCAAACAGATGGTTGTTTCCATGACTCTAGGACTAC 598
QY 1447 ACCCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGACCGATCAGAA 1506
Db 599 ACCCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGACCGATCAGAA 658
QY 1507 CAGTGTGTTGGAAACAGAACCCAGATATGATCCGGGATGGATCCACCATTCCCAATTGCCAAA 1566

REFERENCE 1 (bases 1 to 882)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM11430 row: k column: 13
High quality sequence stop: 857.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5172996"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 35.1%; Score 786.2; DB 4; Length 882;
Best Local Similarity 96.1%; Pred. No. 1.7e-176;
Matches 849; Conservative 0; Mismatches 28; Indels 6; Gaps 4;

QY 84 GTGGGTCAGGGCACAGAGATATTAAATGTCACCCCTCTGGGGCTTTTCATGGGACTCCC 143
|||||
Db 1 GTGGGTCAGGGCACAGAGATATTAAATGTCACCCCTCTGGGGCTTTTCATGGGACTCCC 60
|||||

QY 144 TCTGCCACATTTTTTGGAGTTGGGAAAGTTGCTAGAGGCTTCAGAACTCCAGCCTAATG 203
|||||
Db 61 TCTGCCACATTTTTCGGAGGTTGGGAAAGTTGCTAGAGGCTTCAGAACTCCAGCCTAATG 120
|||||

QY 204 GATCCCAAACCTCGGAGAAATGGCTGCGTCCCTGCTGGGTG---TGCTGCTGCTGCTGCTG 260
|||||
Db 121 GATCCCAAACCTCGGAGAAATGGCTGCGTCCCTGCTGGGTGCTGCTGCTGCTGCTGCTG 180
|||||

QY 261 GAGCGCGGCATGTTCTCCTCACCCCTCCCGCCCCCGGGCGCTGTTAGAGAAAGTCTTCCAG 320
|||||
Db 181 GAGCGCGGCATGTTCTCCTCACCCCTCCCGCCCCCGGGCGCTGTTAGAGAAAGTCTTCCAG 240
|||||

QY 321 TACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGGAGTGGTGCCCATCGAG 380
|||||
Db 241 TACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGGAGTGGTGCCCATCGAG 300
|||||

QY 381 ACGGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAAGAGCTCTTCAGAATGATGGCCCGTG 440
|||||
Db 301 ACGGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAAGAGCTCTTCAGAATGATGGCCCGTG 360
|||||

QY 441 GCTGCGGACACGCTGCAGCGCTGGGGCCCCGTGTGGCCTCGGTGGACATGGTCTCTCAG 500
|||||
Db 361 GCTGCGGACACGCTGCAGCGCTGGGGCCCCGTGTGGCCTCGGTGGACATGGTCTCTCAG 420
|||||

QY 501 CAGCTGCCGATGGTCAGAGTCTTCCAATACCTCCCGTCATCCTGGCCGGAAGTGGGGAGC 560
|||||
Db 421 CAGCTGCCGATGGTCAGAGTCTTCCAATACCTCCCGTCATCCTGGCCGGAAGTGGGGAGC 480
|||||

QY 561 GATCCACGAAAGCACCGTGCTTCTACGGCCACTTGGACGTGCAGCCTGCTGACCCGG 620
|||||

Db 481 GATCCACGAAAGGACCCGTGTGCTTCTACGGCCACTTGGACGTGCAGCCTGCTGACCGG 540

QY 621 GCGGATGGTGGCTCAGGACCCCTATGTGCTGACGAGGTAGACGGGAAACTTTTATGGA 680
|||||
Db 541 GCGGATGGTGGCTCAGGACCCCTATGTGCTGACGAGGTAGACGGGAAACTTTTATGGA 600
|||||

QY 681 CGAGGAGCGACCGACAAAGAGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCGCCTTC 740
|||||
Db 601 CGAGGAGCGACCGACAAAGAGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCGCCTTC 660
|||||

QY 741 AGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATTCATTCATTGAGGGGATGGAGAG 800
|||||
Db 661 AGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATTCATTCATTGAGGGGATGGAGAG 720
|||||

QY 801 GCTGGCTCTGTTGCCCTGGAGAACTTGTGGAAGAAAGA-AAAGGACCGATTCTTCTCT-G 858
|||||
Db 721 GCTGGCTCTGTTGCCCTGGAGAACTTGTGGAAGAAAG-TACGTATCGGACCGATACTCTGG 780
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QY 859 GTGTGGACTACATTGTAATTTAGATAAACCTGTGGATCAGCCAAAGGAAAGCCAGCAATCA 918
|||||
Db 781 GTGTGGACTACATTGTAATTTAGATAAACCTGTGGATCAGCAAAAGGAAAGCGCAATCA 840
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QY 919 CTTATGGAACCCGGGGAAACAGCTACTTTCATGTTGGAGGTGAA 961
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Db 841 CTTATGGAACCCGGGGAAAG-TACGTATCGGACAGTGAA 882
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RESULT 9
BG715910
LOCUS 602676657F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4799126 5',
DEFINITION mRNA sequence.
ACCESSION BG715910
VERSION BG715910.1 GI:13995097
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 884)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM10688 row: a column: 15
High quality sequence stop: 883.
Location/Qualifiers
1. .884
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4799126"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_96"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is

QY 572 AGGCACCGTGTGCTTCTACGGCCACTTGGACGCTGCAGCCTGCTGACCGGGCGATGGGTG 631
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 422 AGGCACCGTGTGCTTCTACGGCCACTTGGACGCTGCAGCCTGCTGACCGGGCGATGGGTG 481
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 632 GCTCAGCAGCCCTATGTGCTGACGGAGGTAGACGGGAACCTTATGGACGAGGACGAC 691
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 482 GCTCAGCAGCCCTATGTGCTGACGGAGGTAGACGGGAACCTTATGGACGAGGACGAC 541
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 692 CGACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCGCTTCAGAGCCCTGGA 751
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 542 CGACAAAGAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCGCTTCAGAGCCCTGGA 601
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 752 GCAAGATCTTCTGTGAATATCAAAATTCATATTGAGGGGATGGAAGGCTGGCTCTGT 811
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 602 GCAAGATCTTCTGTGAATATCAAAATTCATATTGAGGGGATGGAAGGCTGGCTCTGT 661
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QY 812 TGCCCTGAGGAACTTGTGGAAGAAAGAACCGGATCTTCTTGTGTGGACTACAT 871
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 662 TGCCCTGAGGAACTTGTGGAAGAAAGAACCGGATCTTCTTGTGTGGACTACAT 721
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QY 872 TGTAAATTCAGATAACCTGTGGATCAGCCAAAGGAAGCCAGCAATCACTTATGGAACCG 931
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 722 TGTAAATTCAGATAACCTGTGGATCAGCCAAAGGAAGCCAGCAATCACTTACGGAACCG 781
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 932 GGGAAACAGCTACTTCAT 949
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 782 GGGAAACAGCTACTTCAT 799
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 11
BM920701
LOCUS
DEFINITION
BM920701.1 GI:19371080 1054 bp mRNA linear EST 12-MAR-2002
AGENCOURT_6706186 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5751910
5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1054)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12785 row: d column: 23
High quality sequence stop: 583.
Location/Qualifiers
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/lab_host="DH10B"
/clone_lib="NIH MGC 115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code

ORIGIN
Query Match 34.0%; Score 761.2; DB 5; Length 1054;
Best Local Similarity 96.0%; Pred. No. 1.6e-170;
Matches 835; Conservative 0; Mismatches 28; Indels 7; Gaps 5;
QY 2 AATGAATACCTCCGAAGCCGCTTGTCTCCAGATGTGAATAGCTCCACTATACCAGCCT 61
Db 1 AATGAATACCTCCGAAGCCGCTTGTCTCCAGATGTGAATAGCTCCACTATACCAGCCT 60
QY 62 CGTCTTCTTCCGGGGACAACGTTGGGTCAAGGCACAGAGAGATATTAAATGTCAACCCTC 121
Db 61 CGTCTTCTTCCGGGGACAACGTTGGGTCAAGGCACAGAGAGATATTAAATGTCAACCCTC 120
QY 122 TTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTTCGAGGTTGGAAAGTTGCTAGAG 181
Db 121 TTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTTCGAGGTTGGAAAGTTGCTAGAG 180
QY 182 GCTTCAGAACTCCAGCCCTAATGGATCCCAAACTCGGAGAAATGGCTGCCCTCCCTGCTGC 241
Db 181 GCTTCAGAACTCCAGCCCTAATGGATCCCAAACTCGGAGAAATGGCTGCCCTCCCTGCTGC 240
QY 242 TG--TGCTGCTGCTGCTGGAGCGCGCATGTTCTCCTCACCTCCCGCCCCCGGC 298
Db 241 TGTGCTGCTGCTGCTGCTGGAGCGCGCATGTTCTCCTCACCTCCCGCCCCCGGC 300
QY 299 GCTGTTAGAGAAAGTCTTCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCT 358
Db 301 GCTGTTAGAGAAAGTCTTCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCT 360
QY 359 GAAGGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTCCCTCGCTTCAGACAAGA 418
Db 361 GAAGGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTCCCTCGCTTCAGACAAGA 420
QY 419 GCTCTTCAGAAATGATGCGCGTGGTGGGACACGCTGCAGCGCCTGGGGGCCCCGTGGC 478
Db 421 GCTCTTCAGAAATGATGCGCGTGGTGGGACACGCTGCAGCGCCTGGGGGCCCCGTGGC 480
QY 479 CTCGGTGGACATGGGTCTCAGCAGCTGCCCGATGGTTCAGAGTCTTCCAATACCTCCCGT 538
Db 481 CTCGGTGGACATGGGTCTCAGCAGCTGCCCGATGGTTCAGAGTCTTCCAATACCTCCCGT 540
QY 539 CATCCTGGCCGAATGGGGAGCGATCCCACGAAGGCACCGTGTGCTTCTACGGCCACTT 598
Db 541 CATCCTGGCCGAATGGGGAGCGATCCCACGAAGGCACCGTGTGCTTCTACGGCCACTT 600
QY 599 GGACGTGCAGCCTGCTGACC-GGGGCGATGGGTGGCTCAGGACCCCTATGTGCTGACGG 657
Db 601 GGACGTGCAGCCTGCTGACC-GGGGCGATGGGTGGCTCAGGACCCCTATGTGCTGACGG 660
QY 658 AGGTAGACGGGAACTTTATGGACGAGGACGCGACGCAACAAGGCCCTGCTTGGCTT 717
Db 661 GAGTAAACGGGAACTTTATGGACGAGGACGCGACCAACAAGGCCCTGCTTGGCT 720
QY 718 GGATCAATGCTGTGAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAT 777
Db 721 GGATCCATGCTGTGAGCGCCTTCAAAGCCCTGGAGCAAGATCTTCCGTGGAATATCAAT 780
QY 778 TCATCA-TTGAGGGGATGGAAGAGGCTGGCTCTG-TTGGCCCTGGAGGAACCTGTGG-AAA 834
Db 781 TCATCATTTGAAGGGATGGAAAAGGCTGGTTCTGTTTGGCCCTGAAGGAACCTGTGGAAAA 840
QY 835 AAGAAAAGGACCGAATCTTCTCTGGTGTGG 864
Db 841 AAGAAAAGGACCGAATCTTCTTCTGGGGGG 870

RESULT 12
BI600248
LOCUS
DEFINITION
BI600248 BI600248 887 bp mRNA linear EST 07-SEP-2001
603245955F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5288268 5',
mRNA sequence.

Db	366	CCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCATCTCGCCGAACTG	425	
QY	555	GGGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGGACGTCGACGCTGCT	614	
Db	426	GGGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGGACGTCGACGCTGCT	485	
QY	615	GACCGGGCGATGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACGGGAAACTT	674	
Db	486	GACCGGGCGATGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACGGGAAACTT	545	
QY	675	TATGGACGAGGACCGACCAACAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGC	734	
Db	546	TATGGACGAGGACCGACCAACAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGC	605	
QY	735	GCCTTCAGAGCCCTGGAGCAAGATCTTCTCTGTG-AAATCAAAATTCATCATTTAGGGGAT	793	
Db	606	GCCTTCAGAGCCCTGGAGCAAGATCTTCTCTGTGNAATATCAAATTCATCATTTAGGGGAT	665	
QY	794	GGAAGA-GGCTGGCTCTGTTGCCCTGGAGGAACCTTGTTGAAAAAGAAAGACCGATTCT	852	
Db	666	GGAAGACGGCTGGCTCTGTTGCCCTGGAGGAACCTTGTTGACAAAAG-ACAGGACCGATTCT	724	
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QY	911	AGC-AATCACTTATGGAACCCGGGGGAACAGCTACTTTCATGTTGGAGTGAATGCAGAG	969	
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LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
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BG708811				
602673107F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4795945 5', mRNA 807 bp linear EST 07-MAY-2000				
mRNA sequence.				
BG708811				
BG708811.1 GI:13986523				
EST.				
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Homo sapiens				
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1 (bases 1 to 807)				
NIH-MGC http://mgc.nci.nih.gov/ .				
National Institutes of Health, Mammalian Gene Collection (MGC)				
Unpublished (1999)				
Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10679 row: m column: 02 High quality sequence stop: 757.				
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	1 (bases 1 to 887)				
NIH-MGC	http://mgc.nci.nih.gov/ .				
	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11728 row: n column: 13 High quality sequence stop: 819.				
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	Query Match 33.1%; Score 741.8; DB 4; Length 887;				
	Best Local Similarity 96.4%; Pred. No. 6.7e-166;				
	Matches 845; Conservative 0; Mismatches 22; Indels 10; Gaps 8;				
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Db			66	AGCCTAATGGATCCCAAACTCAGG	AGATGGCTGCTGCTCCCTGCTGGCTGTGCTGCTG
	QY		255	CTGCTGGAGCGGGCATGTTCTCT	CACCTCCCGCCCCCGCGCTGTTAGAGAAAGTC
		Db	126	CTGCTGGAGCGGGCATGTTCTCT	CACCTCCCGCCCCCGCGCTGTTAGAGAAAGTC
QY			315	TTCCAGTACATTGACCTCCATCAG	GATGAATTTGTGCACAGCTGAAGGATGGGTGGCC
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		QY	375	ATCGAGAGCGACTCTGTCCAGCCT	GTGCCTCGTTTCAGACAAGAGCTCTTCAGATGATG
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	QY		435	GCCGTGGCTGCGGACACGCTGCAG	CGCTGGGGGCCCCGTGTGGCCCTCGGTGGACATGGGT
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ORIGIN		Query Match	Score	DB 4;	Length	807;
		Best Local Similarity	97.1%;	Pred. No. 1.6e-164;		
		Matches	781;	Conservative	0;	Mismatches 20; Indels 3; Gaps 3;
QY	569	GAAGGCACCGTGTGCTTCTACGGCCACTTGGACGTGCAGCCTGCTGACCGGGCGGATGG	628			
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QY	629	GTGGCTACGGACCCCTATGTCTGACGGAGGTAGACGGGAACTTTATGGACGAGGAGC	688			
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QY	689	GACCGACAACAAAGGCCCTGTCTGGCTTGGATCAATGCTGTGAGCGCCTTCAGAGCCCT	748			
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QY	869	CATTGTAATTTACGATAAACCCTGTGGATCAGCCAAAGGAAGCCAGCAATCACTTATGGAAC	928			
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QY	929	CCGGGGGAACAGCTACTTCATGGTGGAGGTGAA-ATGCAGAGACCAGGATTTTCACTCAG	987			
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QY	1108	CAGAAGAGGAATAAATACATACAAAGCCATCCATCTAGACCTAGAAGAATACCGGAATA	1167			
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Db	723	GAGTCATACCTGGCCGAGTTATAGGAAAATGTTTCAATCCGTCTAGTCCCTCAATGAATG	782			
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Db	783	TGTCTGAGGTGGAACAAAGGTTGA	806			

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LOCUS
DEFINITION
BI545916 804 bp mRNA linear EST 05-SEP-2001
603188315F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5259843 5', mRNA sequence.
BI545916
VERSION BI545916.1 GI:15433228
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 804)
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11654 row: n column: 04
High quality sequence stop: 801.
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ORIGIN

		Query Match	32.8%;	Score	735.4;	DB 4;	Length	804;
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Db	6	GGGATTCCCTCTGCCACATTTTGGAGGTTGGGAAAGTTGCTAGAGGCTTCAGAACTCC	65					
QY	195	AGCCTAATGGATCCCAAACTCGGGAGATGGCTGCGTCCCTGCTGGCTGTGCTGCTG	254					
Db	66	AGCCTAATGGATCCCAAACTCAGGAGATGGCTGCGTCCCTGCTGGCTGTGCTGCTG	125					
QY	255	CTGCTGGAGCGCGCATGTTCTCCTCACCTCCCGCCCCCGCGCTGTTAGAGAAAGTC	314					
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QY	315	TTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGGAGTGGTGCC	374					
Db	186	TTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGGAGTGGTGCC	245					
QY	375	ATCGAGAGCGACTCTGTCCAGCCTGTGCCTTCAGTTCAGTTCAGTTCAGTTCAGTTC	434					
Db	246	ATCGAGAGCGACTCTGTCAAGCCTGTGCCTTCAGTTCAGTTCAGTTCAGTTCAGTTC	305					

QY 435 GCCGTGGCTGGGACACGCTGCAGCGCCTGGGGCCCGTGTGGCCTCGGTGGACATGGGT 494
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Db 426 GGGAGCATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGGACGTGCAGCCTGCT 485
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Db 606 GCCTTCAGAGCCCTGGAGCAAGATCTTCCTGTGAATATCAAAATTCATTCAGGGGATT 665
QY 794 GGAAGAGCTGGCTCTGTTGCCCTGGAGGAACCTTGTGGAA-AAAGAAAAGGACCGATTCT 852
Db 666 GGAAGAGCTGGCTCTGTTGCCCTGGAGGAACCTTGTGGAAACAAAGGACCGATTCT 725
QY 853 TCTCTGGTGTGACTACATTGTAATTTTCAGATAAACCTGTGGATCAGCCAAAGGCCAG 912
Db 726 TCTCTGGTGTGACTACATTGTAATTTTCAGATAAACCTGTGGATCAGCAAAGG-AGCCAG 784
QY 913 CAATCACTTATGGAACC 929
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LOCUS
DEFINITION
tm64d04.x5 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2162887 3',
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LIKE ;, mRNA sequence.

AI939620 742 bp mRNA linear EST 13-DEC-1999
AI939620.1 GI:5678490
KEYWORDS
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 742)
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
Unpublished (1998)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: National Cancer Institute / National
Institute of Neurological Disorders and Stroke, Brain Tumor Genome
Anatomy Project (CGAP/BTGP), Tumor Gene Index
This read has been verified (found to hit its original self in the

correct orientation)
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T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN
Query Match 32.4%; Score 726.6; DB 1; Length 742;
Best Local Similarity 98.7%; Pred. No. 2.7e-162;
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Db 742 GAATACCGGATTACAGCGGGGTGAGAAATTTCTGTTTCGATACTAAGGAGGAGATTCTA 683
QY 1215 ATGCACCTCTGGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGGGCGGTTTGATGAG 1274
Db 682 ATGCACCTCTGGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGGGCGGTTTGATGAG 623
QY 1275 CCTGGAACATAAACAGTCATACCTGGCCGAGTTATAGGAAAATTTTCAATCCGTTAGTTC 1334
Db 622 CCTGGAACATAAACAGTCATACCTGGCCGAGTTATAGGAAAATTTTCAATCCGTTAGTTC 563
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Db 562 CCTCACATGAATGTGTCTGGCGGTGAAAAACAGGTGACACGACATCTTGAAGATGTGTTT 503
QY 1395 TCCAAAAAGAAATAGTTCACCAAGAGATGGTTGTTTCCATGACTCTAGGACTACACCCGTGG 1454
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Db 382 GGAACAGAACCATATGATCCGGGATGGATCCACCATTCACAAATGCCAAAATGTTCCAG 323
QY 1575 GAGATCGTCCACAAGAGCGTGGTGTCTAATTCCGCTGGGAGCTGTTGATGATGGAGAACAT 1634
Db 322 GAGATCGTCCACAAGAGCGTGGTGTCTAATTCCGCTGGGAGCTGTTGATGATGGAGAACAT 263
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Db 262 TCGCAGATGAGAAAAATCAACAGGTGGAACTACATAGAGGGAACCAAAATTATTGCTGCC 203
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Db 202 TTTTCTTAGAGATGGCCCGAGCTCCATTAATCAACAAGAACCTTCTAGTCTGATCTGATCC 143
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Db 22 GTAATAAAATATTTCAAAGGCA 1

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2005, 18:57:22 ; Search time 277 Seconds
(without alignments)
13243.799 Million cell updates/sec

Title: US-10-036-342-56
Perfect score: 2242
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	373.2	16.6	1489	4	US-09-270-767-14369
4	292.8	13.1	300	4	US-09-513-999C-13950
5	224.8	10.0	1479	4	US-09-248-796A-652
6	96.4	4.3	273	1	US-08-204-740-5
7	96.4	4.3	273	3	US-09-081-167A-5
8	96.4	4.3	273	3	US-09-081-395-5
9	96.4	4.3	273	3	US-09-416-833-5
10	96.4	4.3	273	5	PCT-US95-02521-5
11	92.2	4.1	334	4	US-09-513-999C-22131
12	85.8	3.8	1374	4	US-09-583-110-2168
13	85.8	3.8	3766	3	US-08-961-527-225
14	80	3.6	1230025	4	US-09-198-452A-1
15	80	3.6	1230230	4	US-09-438-185A-1
16	79.8	3.6	3820	3	US-09-221-017B-839
17	79.4	3.5	912	4	US-09-107-433-1041
18	77.8	3.5	474	4	US-09-621-976-557
19	76.8	3.4	409	4	US-09-513-999C-1625
20	76.8	3.4	464	4	US-09-513-999C-1624
21	72	3.2	2852	3	US-09-027-137-2
22	72	3.2	2852	3	US-09-344-441-2
23	69.4	3.1	1401	4	US-09-902-540-8465
24	69.4	3.1	7012	4	US-09-902-540-890
25	68.4	3.1	396	4	US-09-640-173-16
26	68.4	3.1	396	4	US-09-713-550-16
27	68.4	3.1	396	4	US-09-825-294-16

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	30	68.4	3.1	2239	4	US-09-952-677-1	Sequence 1, Appli
	31	67.2	3.0	1091	4	US-09-328-965-1	Sequence 1, Appli
	32	67	3.0	1925	4	US-09-148-545-128	Sequence 128, App
	33	66.8	3.0	1660	4	US-09-722-971-9	Sequence 9, Appli
	34	66.4	3.0	1781	4	US-09-818-512-1	Sequence 1, Appli
	35	66.4	3.0	1927	3	US-09-336-536-66	Sequence 66, Appl
	36	66.2	3.0	1378	3	US-09-149-476-208	Sequence 208, App
	37	66.2	3.0	2323	3	US-09-149-476-24	Sequence 24, Appl
	38	66	2.9	1181	3	US-09-149-476-310	Sequence 310, App
	39	66	2.9	1212	3	US-09-149-476-186	Sequence 186, App
	40	66	2.9	3116	4	US-09-311-021-187	Sequence 187, App
	41	65.8	2.9	3145	4	US-09-949-016-1149	Sequence 1149, Ap
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	50	64.6	2.9	2246	4	US-09-083-587-3	Sequence 3, Appli
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	58	64.2	2.9	1985	4	US-09-902-775A-212	Sequence 212, App
	59	64.2	2.9	1985	4	US-09-906-700-212	Sequence 212, App
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169 61.4 2.7 3275 4 US-09-854-133-151 Sequence 151, App
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194 61 2.7 1013 4 US-09-451-527-8 Sequence 8, Appli
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238 60.2 2.7 250 4 US-09-621-976-18893 Sequence 18893, A
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243 60.2 2.7 1725 4 US-09-668-097A-21 Sequence 21, Appl
244 60.2 2.7 1897 1 US-08-184-632-1 Sequence 1, Appli
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250	60.2	2.7	6409	4	US-10-159-151-1	Sequence 1, Appli	Sequence 1, Appli	323	59.4	2.6	427	4	US-10-012-542-107	Sequence 107, App
251	60	2.7	146	4	US-09-621-976-8550	Sequence 8550, Ap	Sequence 8550, Ap	324	59.4	2.6	427	4	US-10-115-123-107	Sequence 107, App
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256	60	2.7	960	3	US-09-248-335-57	Sequence 57, Appl	Sequence 57, Appl	329	59.4	2.6	708	4	US-09-270-767-13081	Sequence 13081, A
257	60	2.7	1024	4	US-09-328-475C-50	Sequence 50, Appl	Sequence 50, Appl	330	59.4	2.6	746	3	US-09-013-810-1	Sequence 1, Appli
258	60	2.7	1062	4	US-09-796-766-3	Sequence 3, Appli	Sequence 3, Appli	331	59.4	2.6	949	4	US-09-489-847-35	Sequence 35, Appl
259	60	2.7	1277	4	US-09-461-325-20	Sequence 20, Appl	Sequence 20, Appl	332	59.4	2.6	1486	4	US-09-461-325-73	Sequence 73, Appl
260	60	2.7	1277	4	US-10-012-542-20	Sequence 20, Appl	Sequence 20, Appl	333	59.4	2.6	1486	4	US-10-012-542-73	Sequence 73, Appl
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263	60	2.7	3350	2	US-08-023-610-1	Sequence 1, Appli	Sequence 1, Appli	336	59.4	2.6	1790	4	US-09-866-028-31	Sequence 31, Appl
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266	60	2.7	3350	5	PCT-US95-10245-1	Sequence 1, Appli	Sequence 1, Appli	339	59.4	2.6	1817	2	US-08-474-087-5	Sequence 5, Appli
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271	59.8	2.7	688	6	5498694-3	Patent No. 5498694	Patent No. 5498694	344	59.4	2.6	11517	4	US-09-688-842-1	Sequence 1, Appli
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273	59.8	2.7	748	1	US-08-361-467B-3	Sequence 3, Appli	Sequence 3, Appli	346	59.2	2.6	365	4	US-09-621-976-14699	Sequence 14699, A
274	59.8	2.7	748	1	US-08-484-332C-3	Sequence 3, Appli	Sequence 3, Appli	347	59.2	2.6	399	1	US-07-885-970A-13	Sequence 13, Appl
275	59.8	2.7	903	5	PCT-US95-06406A-21	Sequence 21, Appl	Sequence 21, Appl	348	59.2	2.6	399	1	US-08-298-687A-13	Sequence 13, Appl
276	59.8	2.7	1057	4	US-09-716-129-16	Sequence 16, Appl	Sequence 16, Appl	349	59.2	2.6	399	1	US-08-530-797-12	Sequence 12, Appl
277	59.8	2.7	1308	4	US-10-151-832-1	Sequence 1, Appli	Sequence 1, Appli	c 350	59.2	2.6	399	1	US-08-298-829-13	Sequence 13, Appl
278	59.8	2.7	1414	4	US-09-501-115-5	Sequence 5, Appli	Sequence 5, Appli	c 351	59.2	2.6	399	2	US-08-787-335-12	Sequence 12, Appl
279	59.8	2.7	1872	3	US-09-291-922-27	Sequence 27, Appl	Sequence 27, Appl	c 352	59.2	2.6	756	4	US-09-614-912-93	Sequence 93, Appl
280	59.8	2.7	1998	3	US-09-232-200-68	Sequence 68, Appl	Sequence 68, Appl	353	59.2	2.6	1461	3	US-08-722-126A-4	Sequence 4, Appli
281	59.8	2.7	1998	3	US-09-232-197-68	Sequence 68, Appl	Sequence 68, Appl	354	59.2	2.6	1461	5	PCT-US95-04258-4	Sequence 4, Appli
282	59.8	2.7	1998	3	US-09-232-201-68	Sequence 68, Appl	Sequence 68, Appl	355	59.2	2.6	1662	4	US-09-668-097A-13	Sequence 13, Appl
283	59.8	2.7	1998	4	US-09-232-195-68	Sequence 68, Appl	Sequence 68, Appl	356	59.2	2.6	1882	3	US-09-370-253-1	Sequence 1, Appli
284	59.8	2.7	2087	3	US-09-232-191-6	Sequence 6, Appli	Sequence 6, Appli	357	59	2.6	147	4	US-09-621-976-10254	Sequence 10254, A
285	59.8	2.7	2087	3	US-09-232-200-6	Sequence 6, Appli	Sequence 6, Appli	358	59	2.6	231	4	US-09-621-976-16456	Sequence 16456, A
286	59.8	2.7	2087	3	US-09-232-197-6	Sequence 6, Appli	Sequence 6, Appli	359	59	2.6	299	4	US-09-621-976-10211	Sequence 10211, A
287	59.8	2.7	2087	3	US-09-232-201-6	Sequence 6, Appli	Sequence 6, Appli	360	59	2.6	332	4	US-09-621-976-16050	Sequence 16050, A
288	59.8	2.7	2087	3	US-09-232-195-6	Sequence 6, Appli	Sequence 6, Appli	361	59	2.6	332	4	US-09-621-976-16053	Sequence 16053, A
289	59.8	2.7	2096	3	US-09-008-481A-10	Sequence 10, Appl	Sequence 10, Appl	362	59	2.6	333	4	US-09-621-976-16032	Sequence 16032, A
290	59.8	2.7	2096	3	US-09-195-666A-16	Sequence 16, Appl	Sequence 16, Appl	363	59	2.6	333	4	US-09-621-976-16045	Sequence 16045, A
291	59.8	2.7	2096	3	US-09-309-592-10	Sequence 10, Appl	Sequence 10, Appl	364	59	2.6	334	4	US-09-621-976-16044	Sequence 16044, A
292	59.8	2.7	2096	3	US-09-635-705-16	Sequence 16, Appl	Sequence 16, Appl	365	59	2.6	335	4	US-09-621-976-16061	Sequence 16061, A
293	59.8	2.7	2096	3	US-09-634-858A-16	Sequence 16, Appl	Sequence 16, Appl	366	59	2.6	336	4	US-09-621-976-16013	Sequence 16013, A
294	59.8	2.7	2096	4	US-08-869-927C-16	Sequence 16, Appl	Sequence 16, Appl	367	59	2.6	338	4	US-09-621-976-16041	Sequence 16041, A
295	59.8	2.7	2205	3	US-08-888-077A-41	Sequence 41, Appl	Sequence 41, Appl	368	59	2.6	347	4	US-09-621-976-16026	Sequence 16026, A
296	59.8	2.7	2628	1	US-08-143-219-1	Sequence 1, Appli	Sequence 1, Appli	369	59	2.6	357	4	US-09-621-976-16058	Sequence 16058, A
297	59.8	2.7	2674	3	US-09-817-180-1	Sequence 1, Appli	Sequence 1, Appli	370	59	2.6	359	4	US-09-621-976-16008	Sequence 16008, A
298	59.8	2.7	2674	4	US-10-003-295-1	Sequence 1, Appli	Sequence 1, Appli	371	59	2.6	359	4	US-09-621-976-16019	Sequence 16019, A
299	59.8	2.7	2806	3	US-09-653-839-9	Sequence 9, Appli	Sequence 9, Appli	372	59	2.6	362	4	US-09-621-976-16010	Sequence 16010, A
300	59.8	2.7	2806	4	US-10-202-619-9	Sequence 9, Appli	Sequence 9, Appli	373	59	2.6	365	4	US-09-621-976-16042	Sequence 16042, A
301	59.8	2.7	5173	1	US-08-242-677-1	Sequence 1, Appli	Sequence 1, Appli	374	59	2.6	732	3	US-09-149-476-66	Sequence 66, Appl
302	59.6	2.7	215	4	US-09-621-976-15321	Sequence 15321, A	Sequence 15321, A	375	59	2.6	1129	3	US-09-227-357-40	Sequence 40, Appl
303	59.6	2.7	1023	1	US-08-252-966B-16	Sequence 16, Appl	Sequence 16, Appl	376	59	2.6	1141	4	US-09-800-729-78	Sequence 78, Appl
304	59.6	2.7	1046	1	US-08-361-467B-4	Sequence 4, Appli	Sequence 4, Appli	377	59	2.6	1190	4	US-09-390-207-1	Sequence 1, Appli
305	59.6	2.7	1046	1	US-08-484-332C-4	Sequence 4, Appli	Sequence 4, Appli	378	59	2.6	1297	4	US-09-800-729-80	Sequence 80, Appl
306	59.6	2.7	1406	4	US-10-000-489-81	Sequence 81, Appl	Sequence 81, Appl	379	59	2.6	1359	3	US-09-387-574-11	Sequence 11, Appl
307	59.6	2.7	1509	3	US-09-149-476-179	Sequence 179, App	Sequence 179, App	380	59	2.6	1359	3	US-09-668-096-11	Sequence 11, Appl
308	59.6	2.7	1606	4	US-09-820-004-1	Sequence 1, Appli	Sequence 1, Appli	381	59	2.6	1804	2	US-08-504-459-5	Sequence 5, Appli
309	59.6	2.7	1827	4	US-09-720-318A-9	Sequence 9, Appli	Sequence 9, Appli	382	59	2.6	1858	2	US-08-909-965C-11	Sequence 11, Appl
310	59.6	2.7	1842	4	US-09-482-273-90	Sequence 90, Appl	Sequence 90, Appl	383	59	2.6	1872	3	US-09-801-052-1	Sequence 1, Appli
311	59.6	2.7	2026	2	US-08-993-228-3	Sequence 3, Appli	Sequence 3, Appli	384	59	2.6	1872	4	US-10-020-121-1	Sequence 1, Appli
312	59.6	2.7	2038	4	US-09-885-723-6	Sequence 6, Appli	Sequence 6, Appli	385	59	2.6	4860	4	US-09-949-016-296	Sequence 296, App
313	59.6	2.7	2218	4	US-09-205-258-103	Sequence 103, App	Sequence 103, App	386	58.8	2.6	156	4	US-09-621-976-9095	Sequence 9095, Ap
314	59.6	2.7	4239	4	US-09-815-048-1	Sequence 1, Appli	Sequence 1, Appli	387	58.8	2.6	160	4	US-09-621-976-10335	Sequence 10335, A
315	59.4	2.6	100	4	US-09-621-976-12774	Sequence 12774, A	Sequence 12774, A	388	58.8	2.6	163	4	US-09-621-976-9608	Sequence 9608, Ap
316	59.4	2.6	150	4	US-09-621-976-8656	Sequence 8656, Ap	Sequence 8656, Ap	389	58.8	2.6	183	4	US-09-621-976-13606	Sequence 13606, A
317	59.4	2.6	160	4	US-09-621-976-18066	Sequence 18066, A	Sequence 18066, A	390	58.8	2.6	204	4	US-09-621-976-1323	Sequence 1323, Ap
318	59.4	2.6	165	4	US-09-621-976-8127	Sequence 8127, Ap	Sequence 8127, Ap	c 391	58.8	2.6	227	2	US-08-520-678A-28	Sequence 28, Appl
319	59.4	2.6	196	4	US-09-644-460-40	Sequence 40, Appl	Sequence 40, Appl	c 392	58.8	2.6	227	3	US-08-897-126-28	Sequence 28, Appl

393	58.8	2.6	240	4	US-09-621-976-1324	Sequence 1324, Ap	466	58.6	2.6	991	3	US-09-247-373B-25	Sequence 25, Appl
394	58.8	2.6	249	4	US-09-621-976-1322	Sequence 1322, Ap	467	58.6	2.6	991	3	US-09-296-715-25	Sequence 25, Appl
395	58.8	2.6	263	3	US-09-091-097-26	Sequence 26, Appl	468	58.6	2.6	1411	3	US-08-964-127-5	Sequence 5, Appli
396	58.8	2.6	630	1	US-08-185-414E-1	Sequence 1, Appli	469	58.6	2.6	1411	3	US-09-496-692-5	Sequence 5, Appli
397	58.8	2.6	1069	3	US-09-372-422A-7	Sequence 7, Appli	470	58.6	2.6	1411	4	US-10-000-273-5	Sequence 5, Appli
398	58.8	2.6	1878	3	US-09-465-558-39	Sequence 39, Appl	471	58.6	2.6	1540	4	US-09-560-761B-3	Sequence 3, Appli
399	58.8	2.6	2822	4	US-09-907-794A-48	Sequence 48, Appl	472	58.6	2.6	1558	1	US-08-467-607-2	Sequence 2, Appli
400	58.8	2.6	2822	4	US-09-905-125A-48	Sequence 48, Appl	473	58.6	2.6	1558	2	US-08-469-362-2	Sequence 2, Appli
401	58.8	2.6	2822	4	US-09-902-775A-48	Sequence 48, Appl	474	58.6	2.6	1558	2	US-08-850-392-2	Sequence 2, Appli
402	58.8	2.6	2822	4	US-09-906-700-48	Sequence 48, Appl	475	58.6	2.6	1963	4	US-09-482-273-91	Sequence 91, Appl
403	58.8	2.6	2822	4	US-09-903-603A-48	Sequence 48, Appl	476	58.6	2.6	1965	4	US-09-482-273-27	Sequence 27, Appl
404	58.8	2.6	2822	4	US-09-904-920A-48	Sequence 48, Appl	477	58.6	2.6	2329	4	US-09-800-729-11	Sequence 11, Appl
405	58.8	2.6	2822	4	US-09-909-064-48	Sequence 48, Appl	478	58.6	2.6	2445	6	5215909-9	Patent No. 5215909
406	58.8	2.6	2822	4	US-09-905-381A-48	Sequence 48, Appl	479	58.6	2.6	2445	6	5215909-9	Patent No. 5215909
407	58.8	2.6	2822	4	US-09-906-618-48	Sequence 48, Appl	480	58.6	2.6	2589	3	US-08-569-749-1	Sequence 1, Appli
408	58.8	2.6	3410	3	US-09-020-956-110	Sequence 110, App	481	58.6	2.6	2589	4	US-09-689-366-1	Sequence 1, Appli
409	58.8	2.6	3410	3	US-09-030-607-110	Sequence 110, App	482	58.6	2.6	2589	5	PCT-US96-12860-1	Sequence 1, Appli
410	58.8	2.6	3410	3	US-09-439-313-110	Sequence 110, App	483	58.6	2.6	4880	3	US-09-031-563-1	Sequence 1, Appli
411	58.8	2.6	3410	3	US-09-352-616A-110	Sequence 110, App	484	58.6	2.6	4880	3	US-09-392-277-1	Sequence 1, Appli
412	58.8	2.6	3410	3	US-09-602-877A-100	Sequence 100, App	485	58.6	2.6	4880	4	US-09-258-000-1	Sequence 1, Appli
413	58.8	2.6	3410	3	US-09-232-149A-110	Sequence 110, App	486	58.6	2.6	5125	3	US-09-031-563-4	Sequence 4, Appli
414	58.8	2.6	3410	4	US-09-159-812-110	Sequence 110, App	487	58.6	2.6	5125	3	US-09-392-277-4	Sequence 4, Appli
415	58.8	2.6	3410	4	US-09-636-215-110	Sequence 110, App	488	58.6	2.6	5125	4	US-09-258-000-4	Sequence 4, Appli
416	58.8	2.6	3410	4	US-09-685-166A-110	Sequence 110, App	489	58.6	2.6	6671	1	US-08-280-443-1	Sequence 1, Appli
417	58.8	2.6	3410	4	US-09-115-453-110	Sequence 110, App	490	58.6	2.6	6671	1	US-08-457-459-1	Sequence 1, Appli
418	58.8	2.6	3410	4	US-09-688-489-110	Sequence 110, App	491	58.6	2.6	6671	1	US-08-555-678-1	Sequence 1, Appli
419	58.8	2.6	3410	4	US-09-679-426-110	Sequence 110, App	492	58.6	2.6	6671	5	PCT-US95-02275-1	Sequence 1, Appli
420	58.8	2.6	3410	4	US-09-759-143-110	Sequence 110, App	493	58.4	2.6	75	4	US-09-621-976-12516	Sequence 12516, A
421	58.8	2.6	3410	4	US-09-651-236-110	Sequence 110, App	494	58.4	2.6	80	1	US-07-920-281C-25	Sequence 25, Appl
422	58.6	2.6	300	4	US-09-621-976-16227	Sequence 16227, A	495	58.4	2.6	80	3	US-08-466-277-25	Sequence 25, Appl
423	58.6	2.6	443	4	US-09-936-885A-1	Sequence 1, Appli	496	58.4	2.6	80	4	US-09-688-842-25	Sequence 25, Appl
C 424	58.6	2.6	470	3	US-09-020-956-102	Sequence 102, App	497	58.4	2.6	127	4	US-09-621-976-13933	Sequence 13933, A
C 425	58.6	2.6	470	3	US-09-030-607-102	Sequence 102, App	498	58.4	2.6	159	4	US-09-621-976-17448	Sequence 17448, A
C 426	58.6	2.6	470	3	US-09-439-313-102	Sequence 102, App	499	58.4	2.6	176	4	US-09-621-976-13903	Sequence 13903, A
C 427	58.6	2.6	470	3	US-09-352-616A-102	Sequence 102, App	500	58.4	2.6	253	4	US-09-621-976-12799	Sequence 12799, A
C 428	58.6	2.6	470	3	US-09-232-149A-102	Sequence 102, App	501	58.4	2.6	588	4	US-09-205-258-64	Sequence 64, Appl
C 429	58.6	2.6	470	4	US-09-159-812-102	Sequence 102, App	502	58.4	2.6	687	4	US-09-774-639-106	Sequence 106, App
C 430	58.6	2.6	470	4	US-09-636-215-102	Sequence 102, App	503	58.4	2.6	759	4	US-09-465-559-5	Sequence 5, Appli
C 431	58.6	2.6	470	4	US-09-685-166A-102	Sequence 102, App	504	58.4	2.6	882	4	US-09-311-021-107	Sequence 107, App
C 432	58.6	2.6	470	4	US-09-115-453-102	Sequence 102, App	505	58.4	2.6	890	4	US-09-621-976-2725	Sequence 2725, App
C 433	58.6	2.6	470	4	US-09-688-489-102	Sequence 102, App	506	58.4	2.6	1052	4	US-09-489-847-23	Sequence 23, Appl
C 434	58.6	2.6	470	4	US-09-679-426-102	Sequence 102, App	507	58.4	2.6	1139	4	US-09-690-454-13	Sequence 13, Appl
C 435	58.6	2.6	470	4	US-09-759-143-102	Sequence 102, App	508	58.4	2.6	1405	4	US-09-244-111-9	Sequence 9, Appli
C 436	58.6	2.6	470	4	US-09-651-236-102	Sequence 102, App	509	58.4	2.6	1493	1	US-08-340-820-24	Sequence 24, Appl
C 437	58.6	2.6	509	3	US-09-030-607-202	Sequence 202, App	510	58.4	2.6	1493	1	US-08-593-535-24	Sequence 24, Appl
C 438	58.6	2.6	509	3	US-09-439-313-202	Sequence 202, App	511	58.4	2.6	1746	4	US-09-485-529-57	Sequence 57, Appl
C 439	58.6	2.6	509	3	US-09-352-616A-202	Sequence 202, App	512	58.4	2.6	1768	4	US-09-485-529-13	Sequence 13, Appl
C 440	58.6	2.6	509	3	US-09-232-149A-202	Sequence 202, App	513	58.4	2.6	2186	3	US-09-360-545-66	Sequence 66, Appl
C 441	58.6	2.6	509	4	US-09-159-812-202	Sequence 202, App	514	58.4	2.6	3047	4	US-09-873-737A-1	Sequence 1, Appli
C 442	58.6	2.6	509	4	US-09-636-215-202	Sequence 202, App	515	58.4	2.6	4064	4	US-09-873-737A-3	Sequence 3, Appli
C 443	58.6	2.6	509	4	US-09-685-166A-202	Sequence 202, App	516	58.4	2.6	5554	4	US-09-815-923-1	Sequence 1, Appli
C 444	58.6	2.6	509	4	US-09-115-453-202	Sequence 202, App	517	58.2	2.6	141	4	US-09-621-976-17446	Sequence 17446, A
C 445	58.6	2.6	509	4	US-09-688-489-202	Sequence 202, App	518	58.2	2.6	147	4	US-09-621-976-10383	Sequence 10383, A
C 446	58.6	2.6	509	4	US-09-679-426-202	Sequence 202, App	519	58.2	2.6	148	4	US-09-621-976-17447	Sequence 17447, A
C 447	58.6	2.6	509	4	US-09-679-426-202	Sequence 202, App	520	58.2	2.6	148	4	US-09-621-976-17450	Sequence 17450, A
C 448	58.6	2.6	509	4	US-09-651-236-202	Sequence 202, App	521	58.2	2.6	153	4	US-09-621-976-17451	Sequence 17451, A
449	58.6	2.6	711	4	US-09-621-976-17854	Sequence 17854, A	522	58.2	2.6	182	4	US-09-621-976-16234	Sequence 16234, A
450	58.6	2.6	730	4	US-09-270-767-14600	Sequence 14600, A	523	58.2	2.6	276	4	US-09-621-976-16611	Sequence 16611, A
451	58.6	2.6	760	4	US-09-205-258-232	Sequence 232, App	524	58.2	2.6	371	4	US-09-621-976-16048	Sequence 16048, A
452	58.6	2.6	931	4	US-09-482-273-31	Sequence 31, Appl	525	58.2	2.6	570	1	US-07-885-970A-10	Sequence 10, Appl
453	58.6	2.6	958	2	US-08-757-046A-5	Sequence 5, Appli	526	58.2	2.6	570	1	US-08-298-687A-10	Sequence 10, Appl
454	58.6	2.6	958	3	US-09-447-208-5	Sequence 5, Appli	527	58.2	2.6	570	1	US-08-298-829-10	Sequence 10, Appl
455	58.6	2.6	958	3	US-09-135-988-5	Sequence 5, Appli	C 528	58.2	2.6	609	1	US-08-530-797-9	Sequence 9, Appli
456	58.6	2.6	958	3	US-09-277-716-5	Sequence 5, Appli	C 529	58.2	2.6	609	2	US-08-787-335-9	Sequence 9, Appli
457	58.6	2.6	958	3	US-08-597-274A-5	Sequence 5, Appli	530	58.2	2.6	972	3	US-09-549-831-5	Sequence 5, Appli
458	58.6	2.6	958	3	US-08-908-909-5	Sequence 5, Appli	C 531	58.2	2.6	985	4	US-09-322-409-25	Sequence 25, Appl
459	58.6	2.6	958	3	US-09-609-161B-5	Sequence 5, Appli	532	58.2	2.6	985	4	US-09-322-409-27	Sequence 27, Appl
460	58.6	2.6	958	3	US-08-990-103-5	Sequence 5, Appli	533	58.2	2.6	985	4	US-09-451-527-25	Sequence 25, Appl
461	58.6	2.6	958	4	US-09-746-485A-5	Sequence 5, Appli	C 534	58.2	2.6	985	4	US-09-451-527-27	Sequence 27, Appl
462	58.6	2.6	958	4	US-10-126-139-5	Sequence 5, Appli	535	58.2	2.6	1214	4	US-09-451-527-28	Sequence 28, Appl
463	58.6	2.6	958	4	US-10-126-798-5	Sequence 5, Appli	536	58.2	2.6	1454	4	US-09-614-912-63	Sequence 63, Appl
464	58.6	2.6	958	4	US-10-126-777-5	Sequence 5, Appli	537	58.2	2.6	1485	3	US-09-372-422A-39	Sequence 39, Appl
465	58.6	2.6	991	3	US-08-924-747-25	Sequence 25, Appl	538	58.2	2.6	1534	1	US-08-300-903A-6	Sequence 6, Appli

539	58.2	2.6	1534	4	US-08-988-197-6	Sequence 6, Appli	612	57.8	2.6	339	4	US-09-621-976-16015	Sequence 16015, A
540	58.2	2.6	1534	4	US-10-385-072-6	Sequence 6, Appli	613	57.8	2.6	491	4	US-09-311-021-191	Sequence 191, App
541	58.2	2.6	1578	3	US-09-416-050A-1	Sequence 1, Appli	614	57.8	2.6	1027	3	US-09-465-558-57	Sequence 57, Appl
542	58.2	2.6	1578	3	US-09-664-800-1	Sequence 1, Appli	615	57.8	2.6	1032	3	US-09-257-179-21	Sequence 21, Appl
543	58.2	2.6	1578	3	US-09-665-309-1	Sequence 1, Appli	616	57.8	2.6	1383	4	US-09-735-846-1	Sequence 1, Appli
544	58.2	2.6	1578	3	US-09-661-569-1	Sequence 1, Appli	617	57.8	2.6	1508	3	US-09-039-046-1	Sequence 1, Appli
545	58.2	2.6	1602	1	US-08-530-950-3	Sequence 3, Appli	618	57.8	2.6	1813	3	US-09-071-224-3	Sequence 3, Appli
546	58.2	2.6	1602	3	US-08-888-429A-3	Sequence 3, Appli	619	57.8	2.6	2301	3	US-09-232-191-8	Sequence 8, Appli
547	58.2	2.6	1602	3	US-09-149-879-3	Sequence 3, Appli	620	57.8	2.6	2301	3	US-09-232-200-8	Sequence 8, Appli
548	58.2	2.6	1602	4	US-09-057-009-3	Sequence 3, Appli	621	57.8	2.6	2301	3	US-09-232-197-8	Sequence 8, Appli
549	58.2	2.6	1602	4	US-09-593-653-3	Sequence 3, Appli	622	57.8	2.6	2301	3	US-09-232-201-8	Sequence 8, Appli
550	58.2	2.6	1736	3	US-09-182-816-22	Sequence 22, Appl	623	57.8	2.6	2301	4	US-09-232-195-8	Sequence 8, Appli
C 551	58.2	2.6	1736	3	US-09-182-816-24	Sequence 24, Appl	624	57.8	2.6	2381	1	US-08-021-608D-9	Sequence 9, Appli
552	58.2	2.6	1736	3	US-09-471-528-22	Sequence 22, Appl	625	57.8	2.6	2381	1	US-08-726-160-9	Sequence 9, Appli
C 553	58.2	2.6	1736	3	US-09-471-528-24	Sequence 24, Appl	626	57.8	2.6	2381	5	PCT-US94-01782-9	Sequence 9, Appli
554	58.2	2.6	1736	3	US-09-634-530-22	Sequence 22, Appl	627	57.8	2.6	2384	1	US-08-021-608D-1	Sequence 1, Appli
C 555	58.2	2.6	1736	3	US-09-634-530-24	Sequence 24, Appl	628	57.8	2.6	2384	1	US-08-726-160-1	Sequence 1, Appli
556	58.2	2.6	1882	4	US-09-419-679-3	Sequence 3, Appli	629	57.8	2.6	2384	5	PCT-US94-01782-1	Sequence 1, Appli
557	58.2	2.6	2203	4	US-09-801-861-1	Sequence 1, Appli	630	57.8	2.6	2625	4	US-09-270-767-10080	Sequence 10080, A
558	58.2	2.6	2203	4	US-10-224-562-1	Sequence 1, Appli	631	57.8	2.6	2710	3	US-09-232-200-44	Sequence 44, Appl
559	58.2	2.6	2431	1	US-07-847-743B-25	Sequence 25, Appl	632	57.8	2.6	2710	3	US-09-232-200-70	Sequence 70, Appl
560	58.2	2.6	2431	1	US-08-456-201-25	Sequence 25, Appl	633	57.8	2.6	2710	3	US-09-232-197-44	Sequence 44, Appl
561	58.2	2.6	2431	2	US-08-456-241-25	Sequence 25, Appl	634	57.8	2.6	2710	3	US-09-232-197-70	Sequence 70, Appl
562	58.2	2.6	2431	5	PCT-US92-04295A-25	Sequence 25, Appl	635	57.8	2.6	2710	3	US-09-232-201-44	Sequence 44, Appl
563	58.2	2.6	2718	4	US-09-667-135-1	Sequence 1, Appli	636	57.8	2.6	2710	3	US-09-232-195-44	Sequence 44, Appl
564	58.2	2.6	3238	3	US-08-123-934A-5	Sequence 5, Appli	637	57.8	2.6	2710	4	US-09-232-195-70	Sequence 70, Appl
565	58.2	2.6	3238	4	US-09-874-628-5	Sequence 5, Appli	638	57.8	2.6	2710	4	US-09-232-195-70	Sequence 70, Appl
566	58.2	2.6	3238	5	PCT-US94-10080-5	Sequence 5, Appli	639	57.8	2.6	2908	4	US-09-904-615-35	Sequence 35, Appl
567	58.2	2.6	3994	4	US-09-738-946-7	Sequence 7, Appli	640	57.6	2.6	137	4	US-09-621-976-18434	Sequence 18434, A
568	58	2.6	146	4	US-09-621-976-16115	Sequence 16115, A	641	57.6	2.6	138	4	US-09-621-976-9595	Sequence 9595, Ap
569	58	2.6	351	4	US-09-621-976-15134	Sequence 15134, A	642	57.6	2.6	208	1	US-08-686-878A-37	Sequence 37, Appl
570	58	2.6	371	4	US-09-621-976-19223	Sequence 19223, A	643	57.6	2.6	208	3	US-09-175-928-37	Sequence 37, Appl
571	58	2.6	593	4	US-09-904-615-59	Sequence 59, Appl	644	57.6	2.6	266	4	US-09-621-976-16813	Sequence 16813, A
572	58	2.6	635	1	US-08-455-633A-35	Sequence 35, Appl	645	57.6	2.6	272	4	US-09-621-976-16932	Sequence 16932, A
573	58	2.6	635	1	US-08-416-336-5	Sequence 5, Appli	646	57.6	2.6	283	4	US-09-621-976-16989	Sequence 16989, A
574	58	2.6	635	2	US-08-456-460C-35	Sequence 35, Appl	647	57.6	2.6	316	4	US-09-513-993C-838	Sequence 838, App
575	58	2.6	635	5	PCT-US94-05354-35	Sequence 35, Appl	648	57.6	2.6	550	4	US-09-010-147B-5	Sequence 5, Appli
576	58	2.6	664	4	US-09-904-615-66	Sequence 66, Appl	649	57.6	2.6	812	3	US-09-091-097-7	Sequence 7, Appli
C 577	58	2.6	1020	4	US-09-328-475C-43	Sequence 43, Appl	650	57.6	2.6	1075	3	US-08-400-006B-6	Sequence 6, Appli
578	58	2.6	1039	4	US-09-464-535-23	Sequence 23, Appl	651	57.6	2.6	1193	3	US-09-372-422A-23	Sequence 23, Appl
579	58	2.6	1069	4	US-09-205-258-74	Sequence 74, Appl	652	57.6	2.6	1201	4	US-09-461-325-36	Sequence 36, Appl
580	58	2.6	1206	3	US-09-465-558-53	Sequence 53, Appl	653	57.6	2.6	1201	4	US-10-012-542-36	Sequence 36, Appl
581	58	2.6	1325	1	US-08-306-691B-51	Sequence 51, Appl	654	57.6	2.6	1201	4	US-10-115-123-36	Sequence 36, Appl
582	58	2.6	1325	2	US-08-464-517-1	Sequence 1, Appli	655	57.6	2.6	1210	4	US-09-244-805-45	Sequence 45, Appl
583	58	2.6	1325	2	US-08-246-361A-1	Sequence 1, Appli	656	57.6	2.6	1230	4	US-09-244-805-6	Sequence 6, Appli
584	58	2.6	1325	3	US-08-463-772-1	Sequence 1, Appli	657	57.6	2.6	2184	3	US-08-955-918C-1	Sequence 1, Appli
585	58	2.6	1325	5	PCT-US93-05000-1	Sequence 1, Appli	658	57.6	2.6	2184	3	US-08-697-766A-1	Sequence 1, Appli
586	58	2.6	1412	4	US-09-614-912-197	Sequence 197, App	659	57.6	2.6	2311	4	US-09-720-317A-19	Sequence 19, Appl
587	58	2.6	1604	1	US-08-665-966-9	Sequence 9, Appli	660	57.6	2.6	2369	4	US-09-057-996-13	Sequence 13, Appl
588	58	2.6	1604	3	US-09-041-780-9	Sequence 9, Appli	661	57.6	2.6	3214	1	US-08-484-105-17	Sequence 17, Appl
589	58	2.6	1738	2	US-08-379-482A-2	Sequence 2, Appli	662	57.6	2.6	3214	1	US-08-484-106-17	Sequence 17, Appl
590	58	2.6	1738	4	US-09-918-909A-27	Sequence 27, Appl	C 663	57.6	2.6	4055	4	US-09-620-312D-706	Sequence 706, App
591	58	2.6	1740	4	US-09-709-103-45	Sequence 45, Appl	664	57.6	2.6	5503	2	US-08-726-012B-1	Sequence 1, Appli
592	58	2.6	1740	4	US-09-439-410A-45	Sequence 45, Appl	665	57.6	2.6	5503	4	US-09-023-655-989	Sequence 4, Appli
593	58	2.6	1798	3	US-09-797-906-1	Sequence 1, Appli	666	57.6	2.6	7859	1	US-07-854-596B-4	Sequence 4, Appli
594	58	2.6	1801	4	US-09-709-103-3	Sequence 3, Appli	667	57.6	2.6	7859	2	US-08-450-905B-15	Sequence 15, Appl
595	58	2.6	1801	4	US-09-439-410A-3	Sequence 3, Appli	668	57.6	2.6	7859	3	US-07-982-759F-15	Sequence 15, Appl
596	58	2.6	3124	3	US-09-734-030-1	Sequence 1, Appli	669	57.6	2.6	670689	4	US-09-949-016-12505	Sequence 12505, A
597	58	2.6	3124	4	US-10-153-921-1	Sequence 1, Appli	670	57.6	2.6	670690	4	US-09-949-016-14207	Sequence 14207, A
598	58	2.6	3124	4	US-10-669-689-1	Sequence 1, Appli	671	57.4	2.6	92	4	US-09-621-976-13620	Sequence 13620, A
599	58	2.6	3200	1	US-08-444-405-1	Sequence 1, Appli	672	57.4	2.6	102	4	US-09-621-976-11436	Sequence 11436, A
600	58	2.6	3200	1	US-08-384-850-1	Sequence 1, Appli	673	57.4	2.6	144	1	US-08-702-344-26	Sequence 26, Appl
601	58	2.6	3207	1	US-07-946-497-1	Sequence 1, Appli	674	57.4	2.6	144	4	US-09-621-976-17452	Sequence 17452, A
602	58	2.6	3207	1	US-08-483-322-1	Sequence 1, Appli	675	57.4	2.6	193	4	US-09-621-976-10543	Sequence 10543, A
603	58	2.6	3207	2	US-08-478-882-1	Sequence 1, Appli	676	57.4	2.6	304	4	US-09-621-976-16099	Sequence 16099, A
604	58	2.6	41736	4	US-09-949-016-17091	Sequence 17091, A	677	57.4	2.6	329	4	US-09-621-976-16012	Sequence 16012, A
605	57.8	2.6	140	4	US-09-621-976-17449	Sequence 17449, A	678	57.4	2.6	336	4	US-09-621-976-16051	Sequence 16051, A
606	57.8	2.6	195	4	US-09-621-976-18062	Sequence 18062, A	C 679	57.4	2.6	396	4	US-09-640-173-42	Sequence 42, Appl
607	57.8	2.6	213	4	US-09-621-976-16536	Sequence 16536, A	C 680	57.4	2.6	396	4	US-09-713-550-42	Sequence 42, Appl
608	57.8	2.6	222	3	US-08-481-190-15	Sequence 15, Appl	C 681	57.4	2.6	396	4	US-09-825-294-42	Sequence 42, Appl
609	57.8	2.6	222	5	PCT-US93-00869-15	Sequence 15, Appl	C 682	57.4	2.6	396	4	US-09-970-966-42	Sequence 42, Appl
610	57.8	2.6	246	4	US-09-621-976-13617	Sequence 13617, A	683	57.4	2.6	536	1	US-08-341-568-1	Sequence 1, Appli
611	57.8	2.6	332	4	US-09-621-976-16031	Sequence 16031, A	684	57.4	2.6	536	2	US-08-911-020-1	Sequence 1, Appli

685	57.4	2.6	742	1	US-07-847-010-12	Sequence 12, Appl	758	57	2.5	1696	4	US-09-835-811-1	Sequence 1, Appli
686	57.4	2.6	1034	4	US-09-311-021-105	Sequence 105, App	759	57	2.5	2158	1	US-07-602-608-1	Sequence 1, Appli
687	57.4	2.6	1273	4	US-09-270-767-14731	Sequence 14731, A	760	57	2.5	2158	1	US-08-261-578-1	Sequence 1, Appli
688	57.4	2.6	1708	4	US-09-859-053-31	Sequence 31, Appl	761	57	2.5	2187	3	US-09-127-219B-2	Sequence 2, Appli
689	57.4	2.6	2269	3	US-09-394-645-1	Sequence 1, Appli	762	57	2.5	2218	4	US-09-016-434-1157	Sequence 1157, Ap
690	57.4	2.6	2269	3	US-09-243-560B-1	Sequence 1, Appli	763	57	2.5	2218	4	US-10-329-668-7	Sequence 7, Appli
691	57.4	2.6	2271	4	US-09-205-258-243	Sequence 243, App	764	57	2.5	2233	1	US-08-496-631-1	Sequence 1, Appli
692	57.4	2.6	2276	4	US-09-205-258-183	Sequence 183, App	765	57	2.5	2262	4	US-09-311-021-171	Sequence 171, App
693	57.4	2.6	2481	2	US-08-630-118A-1	Sequence 1, Appli	766	57	2.5	2516	4	US-09-949-016-766	Sequence 766, App
694	57.4	2.6	2481	2	US-08-838-399-1	Sequence 1, Appli	767	57	2.5	2882	4	US-09-949-016-724	Sequence 724, App
695	57.4	2.6	2481	3	US-09-235-839-1	Sequence 1, Appli	768	57	2.5	2964	4	US-09-578-063-25	Sequence 25, Appl
696	57.4	2.6	2481	3	US-09-327-035-1	Sequence 1, Appli	769	57	2.5	3300	3	US-09-336-643A-82	Sequence 82, Appl
697	57.4	2.6	2604	2	US-08-630-118A-3	Sequence 3, Appli	770	57	2.5	3848	3	US-09-112-096-28	Sequence 28, Appl
698	57.4	2.6	2604	2	US-08-838-399-3	Sequence 3, Appli	771	57	2.5	5668	3	US-09-112-096-14	Sequence 14, Appl
699	57.4	2.6	2604	3	US-09-235-839-3	Sequence 3, Appli	772	57	2.5	5668	4	US-09-636-215-777	Sequence 777, App
700	57.4	2.6	2604	3	US-09-327-035-3	Sequence 3, Appli	773	57	2.5	5668	4	US-09-685-166A-777	Sequence 777, App
701	57.4	2.6	2665	3	US-08-971-089-5	Sequence 5, Appli	774	57	2.5	5668	4	US-09-679-426-777	Sequence 777, App
702	57.4	2.6	4895	3	US-09-053-866-1	Sequence 1, Appli	775	57	2.5	5668	4	US-09-759-143-777	Sequence 777, App
703	57.4	2.6	4895	3	US-09-479-130-1	Sequence 1, Appli	776	57	2.5	5668	4	US-09-651-236-777	Sequence 777, App
704	57.4	2.6	4895	4	US-09-472-130A-1	Sequence 1, Appli	777	57	2.5	7286	3	US-09-331-581-3	Sequence 3, Appli
705	57.2	2.6	97	4	US-09-621-976-9086	Sequence 9086, Ap	778	57	2.5	7938	3	US-09-331-581-14	Sequence 14, Appl
706	57.2	2.6	105	4	US-09-621-976-13820	Sequence 13820, A	779	57	2.5	10660	2	US-08-267-803B-8	Sequence 8, Appli
707	57.2	2.6	153	4	US-09-621-976-18058	Sequence 18058, A	780	57	2.5	10660	3	US-09-041-886-16	Sequence 16, Appl
708	57.2	2.6	204	4	US-09-621-976-16458	Sequence 16458, A	c	781	2.5	192506	4	US-09-949-016-15830	Sequence 15830, A
709	57.2	2.6	342	3	US-09-385-982-342	Sequence 342, App		782	2.5	184	4	US-09-513-999C-36135	Sequence 36135, A
710	57.2	2.6	508	4	US-09-621-976-17886	Sequence 17886, A	783	56.8	2.5	212	4	US-09-621-976-1325	Sequence 1325, Ap
711	57.2	2.6	790	3	US-09-363-970-4	Sequence 4, Appli	784	56.8	2.5	255	4	US-09-621-976-9406	Sequence 9406, Ap
712	57.2	2.6	844	4	US-09-690-942-3	Sequence 3, Appli	785	56.8	2.5	270	2	US-08-520-678A-30	Sequence 30, Appl
713	57.2	2.6	1023	4	US-09-229-947-38	Sequence 38, Appl	786	56.8	2.5	270	3	US-08-897-126-30	Sequence 30, Appl
714	57.2	2.6	1153	3	US-09-149-476-41	Sequence 41, Appl	787	56.8	2.5	554	4	US-09-696-169A-14	Sequence 14, Appl
715	57.2	2.6	1210	3	US-09-443-041A-29	Sequence 29, Appl	788	56.8	2.5	789	3	US-09-020-956-32	Sequence 32, Appl
716	57.2	2.6	1503	4	US-09-907-794A-220	Sequence 220, App	789	56.8	2.5	789	3	US-09-030-607-32	Sequence 32, Appl
717	57.2	2.6	1503	4	US-09-905-125A-220	Sequence 220, App	789	56.8	2.5	789	3	US-09-439-313-32	Sequence 32, Appl
718	57.2	2.6	1503	4	US-09-902-775A-220	Sequence 220, App	791	56.8	2.5	789	3	US-09-352-616A-32	Sequence 32, Appl
719	57.2	2.6	1503	4	US-09-906-700-220	Sequence 220, App	792	56.8	2.5	789	3	US-09-232-149A-32	Sequence 32, Appl
720	57.2	2.6	1503	4	US-09-903-603A-220	Sequence 220, App	793	56.8	2.5	789	4	US-09-159-812-32	Sequence 32, Appl
721	57.2	2.6	1503	4	US-09-904-920A-220	Sequence 220, App	794	56.8	2.5	789	4	US-09-636-215-32	Sequence 32, Appl
722	57.2	2.6	1503	4	US-09-909-064-220	Sequence 220, App	795	56.8	2.5	789	4	US-09-685-166A-32	Sequence 32, Appl
723	57.2	2.6	1503	4	US-09-905-381A-220	Sequence 220, App	796	56.8	2.5	789	4	US-09-115-453-32	Sequence 32, Appl
724	57.2	2.6	1503	4	US-09-906-618-220	Sequence 220, App	797	56.8	2.5	789	4	US-09-688-489-32	Sequence 32, Appl
725	57.2	2.6	2146	4	US-10-003-392-3	Sequence 3, Appli	798	56.8	2.5	789	4	US-09-679-426-32	Sequence 32, Appl
726	57.2	2.6	4419	4	US-09-620-312D-187	Sequence 187, App	799	56.8	2.5	789	4	US-09-759-143-32	Sequence 32, Appl
727	57.2	2.6	4874	4	US-09-187-330-2	Sequence 2, Appli	800	56.8	2.5	882	2	US-09-651-236-32	Sequence 32, Appl
728	57.2	2.6	6065	4	US-09-800-729-35	Sequence 35, Appl	801	56.8	2.5	1051	3	US-08-909-965C-9	Sequence 9, Appli
729	57.2	2.6	7724	4	US-08-486-049-1	Sequence 1, Appli	802	56.8	2.5	1051	3	US-09-245-041-10	Sequence 10, Appl
730	57	2.5	134	4	US-09-621-976-18433	Sequence 18433, A	803	56.8	2.5	1051	4	US-09-358-055B-10	Sequence 10, Appl
731	57	2.5	140	1	US-08-628-417-5	Sequence 5, Appli	804	56.8	2.5	1051	4	US-09-893-238-10	Sequence 10, Appl
732	57	2.5	142	4	US-09-621-976-10801	Sequence 10801, A	805	56.8	2.5	1074	3	US-09-357-251-23	Sequence 23, Appl
733	57	2.5	169	4	US-09-621-976-11249	Sequence 11249, A	806	56.8	2.5	1540	3	US-08-977-001-2	Sequence 2, Appli
734	57	2.5	179	4	US-09-621-976-9575	Sequence 9575, Ap	807	56.8	2.5	1653	3	US-09-345-469-2	Sequence 2, Appli
735	57	2.5	240	1	US-08-628-417-6	Sequence 6, Appli	808	56.8	2.5	1771	4	US-09-907-794A-158	Sequence 158, App
736	57	2.5	249	4	US-09-621-976-19144	Sequence 19144, A	809	56.8	2.5	1771	4	US-09-866-028-36	Sequence 36, Appl
737	57	2.5	258	4	US-09-621-976-15353	Sequence 15353, A	810	56.8	2.5	1771	4	US-09-905-125A-158	Sequence 158, App
738	57	2.5	271	4	US-09-621-976-10380	Sequence 10380, A	811	56.8	2.5	1771	4	US-09-902-775A-158	Sequence 158, App
739	57	2.5	326	4	US-09-621-976-16024	Sequence 16024, A	812	56.8	2.5	1771	4	US-09-906-700-158	Sequence 158, App
740	57	2.5	334	4	US-09-621-976-16434	Sequence 16434, A	813	56.8	2.5	1771	4	US-09-944-457-36	Sequence 36, Appl
741	57	2.5	350	4	US-09-621-976-15342	Sequence 15342, A	814	56.8	2.5	1771	4	US-09-903-603A-158	Sequence 158, App
742	57	2.5	674	4	US-09-620-405B-465	Sequence 465, App	815	56.8	2.5	1771	4	US-09-904-920A-158	Sequence 158, App
743	57	2.5	674	4	US-09-433-826B-465	Sequence 465, App	816	56.8	2.5	1771	4	US-09-909-064-158	Sequence 158, App
744	57	2.5	674	4	US-09-604-287A-465	Sequence 465, App	817	56.8	2.5	1771	4	US-09-905-381A-158	Sequence 158, App
745	57	2.5	674	4	US-09-834-759-465	Sequence 465, App	818	56.8	2.5	1771	4	US-09-906-618-158	Sequence 158, App
746	57	2.5	674	4	US-09-590-751A-465	Sequence 465, App	819	56.8	2.5	1835	3	US-09-485-549-1	Sequence 1, Appli
747	57	2.5	674	4	US-09-551-621-465	Sequence 465, App	820	56.8	2.5	2434	4	US-09-489-847-67	Sequence 67, Appl
748	57	2.5	1133	4	US-09-916-204-1	Sequence 1, Appli	821	56.8	2.5	2608	4	US-09-904-615-16	Sequence 16, Appl
749	57	2.5	1133	4	US-10-282-048-1	Sequence 1, Appli	822	56.8	2.5	3975	4	US-09-270-767-3	Sequence 3, Appli
750	57	2.5	1134	3	US-09-248-335-29	Sequence 29, Appl	823	56.8	2.5	139552	4	US-09-949-016-15300	Sequence 15300, A
751	57	2.5	1196	4	US-09-065-040-2	Sequence 2, Appli	824	56.6	2.5	87	4	US-09-621-976-14849	Sequence 14849, A
752	57	2.5	1358	4	US-09-949-016-463	Sequence 463, App	825	56.6	2.5	244	4	US-09-621-976-484	Sequence 484, App
753	57	2.5	1507	3	US-09-453-323-1	Sequence 1, Appli	826	56.6	2.5	269	4	US-09-621-976-16936	Sequence 16936, A
754	57	2.5	1538	4	US-09-205-258-193	Sequence 193, App	827	56.6	2.5	796	1	US-08-104-073-2	Sequence 2, Appli
755	57	2.5	1546	4	US-09-901-151-1	Sequence 1, Appli	828	56.6	2.5	966	1	US-08-514-014-7	Sequence 7, Appli
756	57	2.5	1559	4	US-09-489-847-42	Sequence 42, Appl	829	56.6	2.5	966	2	US-08-833-823-7	Sequence 7, Appli
757	57	2.5	1639	2	US-08-737-524B-1	Sequence 1, Appli	830	56.6	2.5	1048	4	US-09-489-847-38	Sequence 38, Appl

831	56.6	2.5	2065	3	US-09-370-473-5	Sequence 5, Appli	904	56	2.5	66	4	US-09-621-976-14819	Sequence 14819, A
832	56.6	2.5	2790	3	US-08-800-291B-1	Sequence 1, Appli	905	56	2.5	67	4	US-09-621-976-11909	Sequence 11909, A
833	56.4	2.5	132	4	US-09-621-976-13468	Sequence 13468, A	906	56	2.5	67	4	US-09-621-976-13917	Sequence 13917, A
834	56.4	2.5	145	4	US-09-621-976-16688	Sequence 16688, A	907	56	2.5	67	4	US-09-621-976-14753	Sequence 14753, A
835	56.4	2.5	145	4	US-09-621-976-16691	Sequence 16691, A	908	56	2.5	68	4	US-09-621-976-11613	Sequence 11613, A
836	56.4	2.5	146	4	US-09-621-976-16686	Sequence 16686, A	909	56	2.5	68	4	US-09-621-976-11912	Sequence 11912, A
837	56.4	2.5	146	4	US-09-621-976-16695	Sequence 16695, A	910	56	2.5	68	4	US-09-621-976-12005	Sequence 12005, A
838	56.4	2.5	552	4	US-09-461-325-111	Sequence 111, App	911	56	2.5	69	1	US-08-702-344-7	Sequence 7, Appli
839	56.4	2.5	552	4	US-10-012-542-111	Sequence 111, App	912	56	2.5	69	4	US-09-621-976-12006	Sequence 12006, A
840	56.4	2.5	552	4	US-10-115-123-111	Sequence 111, App	913	56	2.5	69	4	US-09-621-976-14105	Sequence 14105, A
841	56.4	2.5	612	4	US-09-902-540-1357	Sequence 1357, Ap	914	56	2.5	69	4	US-09-621-976-14869	Sequence 14869, A
842	56.4	2.5	1118	4	US-08-651-136C-7	Sequence 181, App	915	56	2.5	69	4	US-09-573-080A-447	Sequence 447, App
843	56.4	2.5	1154	3	US-09-229-911A-7	Sequence 7, Appli	916	56	2.5	70	4	US-09-621-976-13579	Sequence 13579, A
844	56.4	2.5	1154	3	US-09-229-911A-7	Sequence 7, Appli	917	56	2.5	70	4	US-09-621-976-14750	Sequence 14750, A
845	56.4	2.5	1279	3	US-09-248-335-25	Sequence 25, Appl	918	56	2.5	71	4	US-09-621-976-14905	Sequence 14905, A
846	56.4	2.5	1296	4	US-09-461-325-29	Sequence 29, Appl	919	56	2.5	72	4	US-09-621-976-10145	Sequence 10145, A
847	56.4	2.5	1296	4	US-10-012-542-29	Sequence 29, Appl	920	56	2.5	72	4	US-09-621-976-14815	Sequence 14815, A
848	56.4	2.5	1296	4	US-10-115-123-29	Sequence 29, Appl	921	56	2.5	72	4	US-09-621-976-14842	Sequence 14842, A
849	56.4	2.5	1958	3	US-08-665-034A-3	Sequence 3, Appli	922	56	2.5	72	4	US-09-621-976-15064	Sequence 15064, A
850	56.4	2.5	2202	3	US-09-465-558-59	Sequence 59, Appl	923	56	2.5	73	4	US-09-621-976-14729	Sequence 14729, A
851	56.4	2.5	2320	3	US-09-202-904A-13	Sequence 13, Appl	924	56	2.5	73	4	US-09-621-976-14963	Sequence 14963, A
852	56.4	2.5	2485	4	US-09-889-463A-9	Sequence 9, Appli	925	56	2.5	75	4	US-09-621-976-14892	Sequence 14892, A
853	56.4	2.5	2744	3	US-09-071-101-1	Sequence 1, Appli	926	56	2.5	76	4	US-09-621-976-12446	Sequence 12446, A
854	56.4	2.5	2744	3	US-09-369-618-1	Sequence 1, Appli	927	56	2.5	76	4	US-09-621-976-14831	Sequence 14831, A
855	56.4	2.5	2744	3	US-09-369-617-1	Sequence 1, Appli	928	56	2.5	76	4	US-09-621-976-14915	Sequence 14915, A
856	56.4	2.5	2797	4	US-09-482-273-74	Sequence 74, Appl	c 929	56	2.5	77	4	US-08-956-171B-2883	Sequence 2883, Ap
857	56.4	2.5	4137	3	US-09-499-964-2	Sequence 2, Appli	c 930	56	2.5	77	4	US-09-621-976-14176	Sequence 14176, A
858	56.4	2.5	5749	4	US-09-949-016-15441	Sequence 15441, A	c 931	56	2.5	77	4	US-08-781-986A-2883	Sequence 2883, Ap
859	56.4	2.5	5749	4	US-09-949-016-15442	Sequence 15442, A	932	56	2.5	78	4	US-09-621-976-14824	Sequence 14824, A
860	56.2	2.5	72	4	US-09-621-976-9837	Sequence 9837, Ap	933	56	2.5	78	4	US-09-621-976-15092	Sequence 15092, A
861	56.2	2.5	166	4	US-09-621-976-18390	Sequence 18390, A	934	56	2.5	79	4	US-09-621-976-15090	Sequence 15090, A
862	56.2	2.5	194	4	US-09-621-976-15317	Sequence 15317, A	935	56	2.5	81	4	US-09-621-976-13152	Sequence 13152, A
863	56.2	2.5	195	4	US-09-621-976-15314	Sequence 15314, A	936	56	2.5	81	4	US-09-513-999C-17324	Sequence 17324, A
864	56.2	2.5	327	4	US-09-621-976-16018	Sequence 16018, A	937	56	2.5	83	4	US-09-621-976-14751	Sequence 14751, A
865	56.2	2.5	341	4	US-09-621-976-16135	Sequence 16135, A	938	56	2.5	83	4	US-09-621-976-14959	Sequence 14959, A
866	56.2	2.5	795	4	US-09-270-767-14068	Sequence 14068, A	939	56	2.5	84	1	US-08-664-596B-3	Sequence 3, Appli
867	56.2	2.5	941	4	US-09-205-258-186	Sequence 186, App	940	56	2.5	84	1	US-08-738-367-3	Sequence 3, Appli
868	56.2	2.5	981	4	US-09-780-717-4	Sequence 4, Appli	941	56	2.5	84	4	US-09-621-976-14571	Sequence 14571, A
869	56.2	2.5	2280	3	US-08-813-150-1	Sequence 1, Appli	942	56	2.5	84	4	US-09-621-976-14577	Sequence 14577, A
870	56.2	2.5	2280	4	US-09-546-553-1	Sequence 1, Appli	943	56	2.5	85	4	US-09-621-976-13395	Sequence 13395, A
871	56.2	2.5	2968	3	US-09-813-819-1	Sequence 1, Appli	944	56	2.5	85	4	US-09-621-976-14949	Sequence 14949, A
872	56.2	2.5	2968	3	US-09-920-048-1	Sequence 1, Appli	945	56	2.5	89	4	US-09-621-976-14749	Sequence 14749, A
873	56.2	2.5	2968	4	US-10-014-501-1	Sequence 1, Appli	946	56	2.5	89	4	US-09-621-976-14974	Sequence 14974, A
874	56.2	2.5	3581	2	US-08-738-349-1	Sequence 1, Appli	c 947	56	2.5	91	3	US-09-404-879A-201	Sequence 201, App
875	56.2	2.5	15450	4	US-09-470-661A-1	Sequence 1, Appli	c 948	56	2.5	91	4	US-09-338-933-201	Sequence 201, App
876	56	2.5	56	4	US-09-621-976-12139	Sequence 12139, A	c 949	56	2.5	91	4	US-09-215-681-201	Sequence 201, App
877	56	2.5	56	4	US-09-621-976-14556	Sequence 14556, A	c 950	56	2.5	91	4	US-09-216-003A-201	Sequence 201, App
878	56	2.5	57	4	US-09-621-976-11970	Sequence 11970, A	c 951	56	2.5	91	4	US-09-667-857-201	Sequence 201, App
879	56	2.5	57	4	US-09-621-976-13937	Sequence 13937, A	c 952	56	2.5	92	4	US-09-621-976-14689	Sequence 14689, A
880	56	2.5	58	4	US-09-621-976-14827	Sequence 14827, A	c 953	56	2.5	94	3	US-09-404-879A-261	Sequence 261, App
881	56	2.5	59	4	US-09-621-976-13084	Sequence 13084, A	c 954	56	2.5	94	4	US-09-338-933-261	Sequence 261, App
882	56	2.5	59	4	US-09-621-976-13752	Sequence 13752, A	c 955	56	2.5	94	4	US-09-215-681-261	Sequence 261, App
883	56	2.5	60	3	US-09-457-959-8	Sequence 8, Appli	c 956	56	2.5	94	4	US-09-216-003A-261	Sequence 261, App
884	56	2.5	60	4	US-09-621-976-12480	Sequence 12480, A	c 957	56	2.5	94	4	US-09-667-857-261	Sequence 261, App
885	56	2.5	60	4	US-09-621-976-13761	Sequence 13761, A	c 958	56	2.5	97	4	US-09-621-976-12430	Sequence 12430, A
886	56	2.5	60	4	US-09-621-976-14742	Sequence 14742, A	959	56	2.5	98	1	US-08-088-658-42	Sequence 42, Appl
887	56	2.5	60	4	US-09-621-976-14884	Sequence 14884, A	960	56	2.5	98	2	US-08-471-907A-42	Sequence 42, Appl
888	56	2.5	60	4	US-10-079-178-8	Sequence 8, Appli	961	56	2.5	98	4	US-09-621-976-11744	Sequence 11744, A
889	56	2.5	61	4	US-09-621-976-14680	Sequence 14680, A	962	56	2.5	98	4	US-09-621-976-12160	Sequence 12160, A
890	56	2.5	61	4	US-09-621-976-14681	Sequence 14681, A	963	56	2.5	98	4	US-09-621-976-15091	Sequence 15091, A
891	56	2.5	61	4	US-09-621-976-14799	Sequence 14799, A	c 964	56	2.5	101	3	US-09-404-879A-293	Sequence 293, App
892	56	2.5	61	4	US-09-621-976-14834	Sequence 14834, A	c 965	56	2.5	101	4	US-09-338-933-293	Sequence 293, App
893	56	2.5	61	4	US-09-621-976-14948	Sequence 14948, A	c 966	56	2.5	101	4	US-09-215-681-293	Sequence 293, App
894	56	2.5	62	4	US-09-621-976-11091	Sequence 11091, A	c 967	56	2.5	101	4	US-09-216-003A-293	Sequence 293, App
895	56	2.5	62	4	US-09-621-976-14130	Sequence 14130, A	c 968	56	2.5	101	4	US-09-667-857-293	Sequence 293, App
896	56	2.5	62	4	US-09-621-976-14936	Sequence 14936, A	969	56	2.5	102	4	US-09-621-976-14804	Sequence 14804, A
897	56	2.5	63	4	US-09-621-976-13480	Sequence 13480, A	c 970	56	2.5	105	3	US-09-284-627-23	Sequence 23, Appl
898	56	2.5	63	4	US-09-621-976-13842	Sequence 13842, A	971	56	2.5	111	3	US-09-297-535-23	Sequence 23, Appl
899	56	2.5	63	4	US-09-621-976-14756	Sequence 14756, A	972	56	2.5	111	4	US-09-621-976-14677	Sequence 14677, A
900	56	2.5	64	4	US-09-621-976-14858	Sequence 14858, A	973	56	2.5	117	1	US-08-702-344-3	Sequence 3, Appli
901	56	2.5	65	4	US-09-621-976-14743	Sequence 14743, A	974	56	2.5	121	3	US-09-297-535-20	Sequence 20, Appl
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903	56	2.5	66	4	US-09-621-976-12404	Sequence 12404, A	976	56	2.5	130	4	US-09-621-976-12892	Sequence 12892, A

c 977	56	2.5	141	3	US-08-737-078A-1	Sequence 1, Appli	1050	55.8	2.5	1249	4	US-09-461-325-128	Sequence 128, App
c 978	56	2.5	141	5	PCT-US94-04706-1	Sequence 1, Appli	1051	55.8	2.5	1249	4	US-10-012-542-128	Sequence 128, App
979	56	2.5	173	4	US-09-621-976-9851	Sequence 9851, Ap	1052	55.8	2.5	1249	4	US-10-115-123-128	Sequence 98, App
980	56	2.5	188	4	US-09-621-976-10364	Sequence 10364, A	c1053	55.8	2.5	1260	4	US-09-461-325-93	Sequence 93, Appl
981	56	2.5	196	4	US-09-442-054A-42	Sequence 42, Appl	c1054	55.8	2.5	1260	4	US-10-012-542-93	Sequence 93, Appl
c 982	56	2.5	196	4	US-09-442-054A-42	Sequence 42, Appl	c1055	55.8	2.5	1260	4	US-10-115-123-93	Sequence 93, Appl
c 983	56	2.5	253	2	US-08-520-678A-25	Sequence 25, Appl	1056	55.8	2.5	1529	4	US-09-523-263B-7	Sequence 7, Appli
c 984	56	2.5	253	3	US-08-897-126-25	Sequence 25, Appl	1057	55.8	2.5	1705	4	US-09-205-258-216	Sequence 216, App
c 985	56	2.5	260	2	US-08-520-678A-29	Sequence 29, Appl	1058	55.8	2.5	2296	3	US-08-496-841C-137	Sequence 137, App
c 986	56	2.5	260	3	US-08-897-126-29	Sequence 29, Appl	1059	55.8	2.5	2695	4	US-09-706-197-3	Sequence 3, Appli
c 987	56	2.5	279	4	US-09-621-976-17626	Sequence 17626, A	1060	55.8	2.5	3623	4	US-09-918-909A-23	Sequence 23, Appl
988	56	2.5	282	4	US-09-621-976-18648	Sequence 18648, A	1061	55.6	2.5	60	4	US-09-513-999C-19779	Sequence 19779, A
989	56	2.5	289	1	US-08-341-568-3	Sequence 3, Appli	1062	55.6	2.5	69	4	US-09-621-976-14838	Sequence 14838, A
990	56	2.5	289	2	US-08-911-020-3	Sequence 3, Appli	1063	55.6	2.5	75	4	US-09-621-976-15073	Sequence 15073, A
991	56	2.5	293	4	US-09-621-976-16965	Sequence 16965, A	1064	55.6	2.5	177	4	US-09-621-976-8073	Sequence 8073, Ap
992	56	2.5	347	4	US-09-621-976-16136	Sequence 16136, A	1065	55.6	2.5	276	4	US-09-621-976-18329	Sequence 18329, A
993	56	2.5	358	4	US-09-621-976-927	Sequence 927, App	1066	55.6	2.5	289	4	US-09-621-976-10009	Sequence 10009, A
994	56	2.5	413	3	US-09-227-357-71	Sequence 71, Appl	1067	55.6	2.5	348	4	US-09-621-976-16137	Sequence 16137, A
995	56	2.5	530	4	US-09-461-325-28	Sequence 28, Appl	c1068	55.6	2.5	612	3	US-09-385-982-280	Sequence 280, App
996	56	2.5	530	4	US-10-012-542-28	Sequence 28, Appl	1069	55.6	2.5	1951	3	US-09-465-558-35	Sequence 35, Appl
997	56	2.5	530	4	US-10-115-123-28	Sequence 28, Appl	1070	55.4	2.5	270	4	US-09-621-976-17927	Sequence 17927, A
998	56	2.5	530	4	US-09-621-976-2461	Sequence 2461, Ap	1071	55.4	2.5	272	4	US-09-621-976-8353	Sequence 8353, Ap
999	56	2.5	773	3	US-09-149-476-20	Sequence 20, Appl	1072	55.4	2.5	298	4	US-09-621-976-3871	Sequence 3871, Ap
1000	56	2.5	1074	3	US-09-248-335-67	Sequence 67, Appl	1073	55.4	2.5	474	3	US-08-516-859A-97	Sequence 97, Appl
1001	56	2.5	1123	3	US-09-152-060-15	Sequence 15, Appl	1074	55.4	2.5	474	3	US-09-586-472-97	Sequence 97, Appl
1002	56	2.5	1147	1	US-08-665-716-1	Sequence 1, Appli	1075	55.4	2.5	474	3	US-09-528-706-97	Sequence 97, Appl
1003	56	2.5	1174	2	US-08-872-437-1	Sequence 1, Appli	1076	55.4	2.5	614	4	US-09-902-540-1318	Sequence 1318, Ap
1004	56	2.5	1174	3	US-08-651-136C-11	Sequence 11, Appl	1077	55.4	2.5	624	4	US-09-270-767-13424	Sequence 13424, A
1005	56	2.5	1174	3	US-09-229-911A-11	Sequence 11, Appl	c1078	55.4	2.5	629	3	US-09-385-982-389	Sequence 389, App
1006	56	2.5	1315	3	US-09-164-193-1	Sequence 1, Appli	1079	55.4	2.5	1375	4	US-09-489-847-120	Sequence 120, App
1007	56	2.5	1315	3	US-09-221-448A-1	Sequence 1, Appli	1080	55.4	2.5	1376	4	US-09-489-847-66	Sequence 66, Appl
1008	56	2.5	1361	4	US-09-489-847-64	Sequence 64, Appl	1081	55.4	2.5	2331	4	US-09-866-028-54	Sequence 54, Appl
1009	56	2.5	1447	3	US-09-443-041A-27	Sequence 27, Appl	1082	55.4	2.5	2331	4	US-09-944-457-54	Sequence 54, Appl
1010	56	2.5	1618	4	US-09-800-729-29	Sequence 29, Appl	1083	55.4	2.5	3136	4	US-09-680-728-1	Sequence 1, Appli
1011	56	2.5	1700	2	US-08-897-340-4	Sequence 4, Appli	1084	55.4	2.5	3136	4	US-10-017-066A-1	Sequence 1, Appli
1012	56	2.5	1700	3	US-09-252-329-4	Sequence 4, Appli	c1085	55.4	2.5	86877	4	US-09-949-016-15491	Sequence 15491, A
1013	56	2.5	1810	4	US-09-800-729-73	Sequence 73, Appl	c1086	55.4	2.5	86877	4	US-09-949-016-15492	Sequence 15492, A
1014	56	2.5	1811	4	US-09-800-729-77	Sequence 77, Appl	1087	55.4	2.5	193303	4	US-09-497-855A-37	Sequence 37, Appl
1015	56	2.5	1813	5	PCT-US94-12883-3	Sequence 3, Appli	1088	55.4	2.5	193303	4	US-09-497-855A-44	Sequence 44, Appl
1016	56	2.5	1898	1	US-08-342-411A-1	Sequence 1, Appli	1089	55.2	2.5	61	4	US-09-513-999C-28913	Sequence 28913, A
1017	56	2.5	1981	4	US-09-720-317A-3	Sequence 3, Appli	1090	55.2	2.5	62	4	US-09-621-976-14825	Sequence 14825, A
1018	56	2.5	2010	1	US-07-864-475A-4	Sequence 4, Appli	1091	55.2	2.5	159	4	US-09-621-976-17182	Sequence 17182, A
1019	56	2.5	2010	2	US-08-468-249A-4	Sequence 4, Appli	1092	55.2	2.5	193	4	US-09-621-976-18588	Sequence 18588, A
1020	56	2.5	2230	3	US-08-378-313-24	Sequence 24, Appl	1093	55.2	2.5	959	4	US-09-578-030-5	Sequence 5, Appli
1021	56	2.5	2389	4	US-09-799-875-7	Sequence 7, Appli	1094	55.2	2.5	1315	3	US-09-721-822A-10	Sequence 10, Appl
1022	56	2.5	2394	4	US-09-800-729-33	Sequence 33, Appl	1095	55.2	2.5	1445	3	US-09-697-367-19	Sequence 19, Appl
1023	56	2.5	2453	4	US-09-455-486-5	Sequence 5, Appli	1096	55.2	2.5	1445	4	US-09-918-909A-19	Sequence 19, Appl
1024	56	2.5	2527	4	US-09-244-805-29	Sequence 29, Appl	1097	55.2	2.5	1933	4	US-09-920-759-3	Sequence 3, Appli
1025	56	2.5	2540	4	US-09-949-016-431	Sequence 431, App	1098	55.2	2.5	118143	4	US-09-949-016-17196	Sequence 17196, A
1026	56	2.5	2808	4	US-09-917-254-27	Sequence 27, Appl	1099	55	2.5	55	4	US-09-621-976-14535	Sequence 14535, A
1027	56	2.5	3871	2	US-08-599-455B-3	Sequence 3, Appli	1100	55	2.5	55	4	US-09-621-976-14800	Sequence 14800, A
1028	56	2.5	3871	3	US-09-069-781B-3	Sequence 3, Appli	1101	55	2.5	69	1	US-08-702-344-22	Sequence 22, Appl
1029	56	2.5	3871	3	US-09-137-132-3	Sequence 3, Appli	1102	55	2.5	135	4	US-09-621-976-11087	Sequence 11087, A
1030	56	2.5	3871	3	US-08-864-564A-3	Sequence 3, Appli	1103	55	2.5	150	4	US-09-621-976-13989	Sequence 13989, A
1031	56	2.5	3871	3	US-09-094-410-3	Sequence 3, Appli	1104	55	2.5	375	3	US-08-946-026-23	Sequence 23, Appl
1032	56	2.5	3871	4	US-08-708-123D-3	Sequence 3, Appli	1105	55	2.5	487	3	US-09-257-179-22	Sequence 22, Appl
1033	56	2.5	3871	4	US-08-583-153A-3	Sequence 3, Appli	1106	55	2.5	563	4	US-09-621-976-19183	Sequence 19183, A
1034	56	2.5	3871	4	US-08-570-142D-3	Sequence 3, Appli	c1107	55	2.5	601	4	US-09-949-016-145251	Sequence 145251, A
1035	56	2.5	3871	4	US-08-638-524B-3	Sequence 3, Appli	c1108	55	2.5	685	3	US-09-227-357-66	Sequence 66, Appl
1036	56	2.5	6200	3	US-09-439-923-1	Sequence 1, Appli	c1109	55	2.5	787	4	US-09-621-976-1878	Sequence 1878, Ap
1037	56	2.5	6200	4	US-09-711-202A-1	Sequence 1, Appli	1110	55	2.5	1151	4	US-09-270-767-12633	Sequence 12633, A
1038	56	2.5	6200	4	US-09-711-205A-1	Sequence 1, Appli	1111	55	2.5	1558	3	US-08-455-550-7	Sequence 7, Appli
c1039	56	2.5	8638	4	US-10-029-907-6	Sequence 6, Appli	1112	55	2.5	1776	3	US-08-655-352-10	Sequence 10, Appl
c1040	56	2.5	8643	4	US-10-029-907-4	Sequence 4, Appli	1113	55	2.5	1776	3	US-09-258-016-10	Sequence 10, Appl
c1041	56	2.5	9472	4	US-08-150-204E-96	Sequence 96, Appl	1114	55	2.5	1776	3	US-09-257-825B-10	Sequence 10, Appl
c1042	56	2.5	9589	1	US-07-925-695-1	Sequence 1, Appli	1115	55	2.5	1886	4	US-09-594-506-31	Sequence 31, Appl
c1043	56	2.5	9589	1	US-07-925-695-2	Sequence 2, Appli	1116	55	2.5	1934	3	US-08-776-844-1	Sequence 1, Appli
1044	55.8	2.5	235	4	US-09-621-976-9455	Sequence 9455, Ap	1117	55	2.5	1934	4	US-09-909-325-1	Sequence 1, Appli
1045	55.8	2.5	235	4	US-09-621-976-18363	Sequence 18363, A	1118	55	2.5	1934	4	US-09-909-326-1	Sequence 1, Appli
1046	55.8	2.5	769	4	US-09-513-775B-5	Sequence 5, Appli	1119	55	2.5	2028	2	US-09-211-930-12	Sequence 12, Appl
1047	55.8	2.5	1013	1	US-07-920-519-30	Sequence 30, Appl	1120	55	2.5	2028	3	US-09-340-993-12	Sequence 12, Appl
1048	55.8	2.5	1013	1	US-08-086-410-23	Sequence 23, Appl	1121	55	2.5	2028	3	US-09-468-442-12	Sequence 12, Appl
1049	55.8	2.5	1013	1	US-08-314-586-30	Sequence 30, Appl	1122	55	2.5	2349	4	US-09-805-455-1	Sequence 1, Appli

1123	55	2.5	2821	4	US-09-702-705-1669	Sequence 1669, Ap	c1196	54.4	2.4	9646	3	US-09-034-756-1	Sequence 1, Appli
1124	55	2.5	2821	4	US-09-736-457-1669	Sequence 1669, Ap	c1197	54.4	2.4	12980	3	US-08-811-566-5	Sequence 5, Appli
1125	55	2.5	2821	4	US-09-671-325-1669	Sequence 1669, Ap	c1198	54.4	2.4	12980	3	US-09-034-756-5	Sequence 5, Appli
1126	55	2.5	2821	4	US-09-658-824-1669	Sequence 1669, Ap	c1199	54.2	2.4	80	3	US-09-284-627-15	Sequence 15, Appl
1127	54.8	2.4	250	4	US-09-621-976-17371	Sequence 17371, A	1200	54.2	2.4	289	4	US-09-621-976-15142	Sequence 15142, A
1128	54.8	2.4	1001	1	US-08-728-259A-10	Sequence 10, Appl	1201	54.2	2.4	611	3	US-09-385-982-376	Sequence 376, App
1129	54.8	2.4	1001	2	US-08-473-486-10	Sequence 10, Appl	1202	54.2	2.4	1049	4	US-09-800-729-67	Sequence 67, Appl
1130	54.8	2.4	1132	3	US-08-894-731-3	Sequence 3, Appli	1203	54.2	2.4	1518	4	US-09-614-912-191	Sequence 191, App
1131	54.8	2.4	2060	4	US-09-345-473E-5	Sequence 5, Appli	1204	54.2	2.4	1810	4	US-09-369-247-11	Sequence 11, Appl
1132	54.8	2.4	2719	3	US-08-706-216-1	Sequence 1, Appli	1205	54.2	2.4	1883	4	US-09-419-679-13	Sequence 13, Appl
1133	54.8	2.4	2719	4	US-09-650-284B-1	Sequence 1, Appli	1206	54.2	2.4	2406	4	US-09-594-506-37	Sequence 37, Appl
c1134	54.8	2.4	64190	4	US-09-949-016-14712	Sequence 14712, A	1207	54.2	2.4	3299	4	US-09-800-729-68	Sequence 68, Appl
c1135	54.8	2.4	64190	4	US-09-949-016-14713	Sequence 14713, A	1208	54	2.4	54	4	US-09-621-976-14994	Sequence 14994, A
1136	54.6	2.4	91	4	US-09-621-976-12161	Sequence 12161, A	1209	54	2.4	56	4	US-09-621-976-13461	Sequence 13461, A
1137	54.6	2.4	105	2	US-08-735-381-2	Sequence 2, Appli	1210	54	2.4	61	4	US-09-621-976-11967	Sequence 11967, A
1138	54.6	2.4	105	3	US-09-183-619-1	Sequence 1, Appli	1211	54	2.4	83	4	US-09-621-976-12195	Sequence 12195, A
1139	54.6	2.4	105	3	US-09-201-674-2	Sequence 2, Appli	1212	54	2.4	166	4	US-09-621-976-8651	Sequence 8651, Ap
1140	54.6	2.4	164	4	US-09-621-976-16692	Sequence 16692, A	1213	54	2.4	324	4	US-09-621-976-16027	Sequence 16027, A
1141	54.6	2.4	472	4	US-09-270-767-12212	Sequence 12212, A	c1214	54	2.4	396	4	US-09-640-173-70	Sequence 70, Appl
1142	54.6	2.4	654	4	US-09-716-129-27	Sequence 27, Appl	c1215	54	2.4	396	4	US-09-713-550-70	Sequence 70, Appl
1143	54.6	2.4	943	3	US-09-149-476-35	Sequence 35, Appl	c1216	54	2.4	396	4	US-09-825-294-70	Sequence 70, Appl
1144	54.6	2.4	1184	4	US-09-489-847-76	Sequence 76, Appl	c1217	54	2.4	396	4	US-09-970-966-70	Sequence 70, Appl
1145	54.6	2.4	1683	3	US-09-347-803-11	Sequence 11, Appl	c1218	54	2.4	873	3	US-09-475-316A-20	Sequence 20, Appl
1146	54.6	2.4	1730	4	US-09-672-785-3	Sequence 3, Appli	1219	54	2.4	873	4	US-09-704-640-20	Sequence 20, Appl
1147	54.6	2.4	1865	3	US-09-370-253-5	Sequence 5, Appli	1220	54	2.4	888	3	US-09-188-930-13	Sequence 13, Appl
1148	54.6	2.4	2625	3	US-09-245-041-18	Sequence 18, Appl	1221	54	2.4	888	4	US-09-312-283C-13	Sequence 13, Appl
1149	54.6	2.4	2625	4	US-09-358-055B-18	Sequence 18, Appl	1222	54	2.4	1707	4	US-09-311-021-51	Sequence 51, Appl
1150	54.6	2.4	2625	4	US-09-893-238-18	Sequence 18, Appl	1223	54	2.4	1728	3	US-08-985-950-7	Sequence 7, Appli
1151	54.6	2.4	2836	3	US-08-747-221B-24	Sequence 24, Appl	1224	54	2.4	1728	4	US-09-546-049-7	Sequence 7, Appli
c1152	54.6	2.4	2836	3	US-08-747-221B-26	Sequence 26, Appl	1225	54	2.4	2013	4	US-09-596-196-3	Sequence 3, Appli
1153	54.6	2.4	2836	3	US-09-005-051-24	Sequence 24, Appl	1226	54	2.4	2311	4	US-09-614-912-91	Sequence 91, Appl
c1154	54.6	2.4	2836	3	US-09-005-051-26	Sequence 26, Appl	1227	54	2.4	2668	3	US-09-370-838-156	Sequence 156, App
1155	54.6	2.4	2836	4	US-09-403-942F-24	Sequence 24, Appl	1228	54	2.4	2668	4	US-09-854-133-156	Sequence 156, App
c1156	54.6	2.4	2836	4	US-09-403-942F-26	Sequence 26, Appl	1229	54	2.4	3242	3	US-09-493-914-2	Sequence 2, Appli
1157	54.6	2.4	3842	3	US-09-115-954-7	Sequence 7, Appli	1230	54	2.4	5878	4	US-09-949-016-939	Sequence 939, App
1158	54.6	2.4	3912	3	US-09-115-954-1	Sequence 1, Appli	c1231	54	2.4	145287	4	US-09-949-016-13530	Sequence 13530, A
1159	54.4	2.4	57	4	US-09-621-976-12150	Sequence 12150, A	c1232	54	2.4	145287	4	US-09-949-016-13531	Sequence 13531, A
1160	54.4	2.4	61	4	US-09-621-976-14754	Sequence 14754, A	c1233	54	2.4	393753	4	US-09-949-016-14573	Sequence 14573, A
1161	54.4	2.4	63	4	US-09-621-976-12231	Sequence 12231, A	c1234	54	2.4	393753	4	US-09-949-016-14574	Sequence 14574, A
1162	54.4	2.4	83	4	US-09-621-976-12087	Sequence 12087, A	c1235	54	2.4	818128	4	US-09-949-016-14546	Sequence 14546, A
1163	54.4	2.4	83	4	US-09-621-976-12175	Sequence 12175, A	c1236	54	2.4	818128	4	US-09-949-016-14547	Sequence 14547, A
1164	54.4	2.4	83	4	US-09-621-976-12429	Sequence 12429, A	c1237	54	2.4	818128	4	US-09-949-016-14548	Sequence 14548, A
1165	54.4	2.4	83	4	US-09-621-976-12450	Sequence 12450, A	c1238	54	2.4	818128	4	US-09-949-016-14549	Sequence 14549, A
c1166	54.4	2.4	90	3	US-09-065-058-16	Sequence 16, Appl	c1239	54	2.4	818128	4	US-09-949-016-14550	Sequence 14550, A
c1167	54.4	2.4	257	2	US-08-520-678A-24	Sequence 24, Appl	c1240	54	2.4	818128	4	US-09-949-016-14551	Sequence 14551, A
c1168	54.4	2.4	257	3	US-08-897-126-24	Sequence 24, Appl	c1241	54	2.4	818128	4	US-09-949-016-14552	Sequence 14552, A
1169	54.4	2.4	270	4	US-09-621-976-17049	Sequence 17049, A	c1242	54	2.4	818128	4	US-09-949-016-14553	Sequence 14553, A
c1170	54.4	2.4	271	2	US-08-731-272A-29	Sequence 29, Appl	c1243	54	2.4	818128	4	US-09-949-016-14554	Sequence 14554, A
1171	54.4	2.4	335	4	US-09-621-976-16038	Sequence 16038, A	c1244	54	2.4	818128	4	US-09-949-016-14555	Sequence 14555, A
c1172	54.4	2.4	356	2	US-08-520-678A-22	Sequence 22, Appl	c1245	54	2.4	818128	4	US-09-949-016-14556	Sequence 14556, A
c1173	54.4	2.4	356	3	US-08-897-126-22	Sequence 22, Appl	c1246	54	2.4	818128	4	US-09-949-016-14557	Sequence 14557, A
c1174	54.4	2.4	537	4	US-09-720-201A-4	Sequence 4, Appli	c1247	54	2.4	818128	4	US-09-949-016-14558	Sequence 14558, A
1175	54.4	2.4	644	4	US-09-720-201A-6	Sequence 6, Appli	c1248	54	2.4	818128	4	US-09-949-016-14559	Sequence 14559, A
1176	54.4	2.4	1277	4	US-09-187-999-30	Sequence 30, Appl	c1249	54	2.4	818128	4	US-09-949-016-14560	Sequence 14560, A
1177	54.4	2.4	1302	4	US-09-322-409-91	Sequence 91, Appl	c1250	54	2.4	818128	4	US-09-949-016-14561	Sequence 14561, A
c1178	54.4	2.4	1302	4	US-09-322-409-93	Sequence 93, Appl	c1251	54	2.4	818128	4	US-09-949-016-14562	Sequence 14562, A
1179	54.4	2.4	1302	4	US-09-451-527-91	Sequence 91, Appl	c1252	54	2.4	818128	4	US-09-949-016-14564	Sequence 14564, A
c1180	54.4	2.4	1302	4	US-09-451-527-93	Sequence 93, Appl	c1253	54	2.4	818128	4	US-09-949-016-14565	Sequence 14565, A
1181	54.4	2.4	1395	2	US-08-553-367A-1	Sequence 1, Appli	c1254	54	2.4	818128	4	US-09-949-016-14566	Sequence 14566, A
1182	54.4	2.4	1395	3	US-09-295-306-1	Sequence 1, Appli	c1255	54	2.4	818128	4	US-09-949-016-14567	Sequence 14567, A
1183	54.4	2.4	1395	3	US-09-734-719-1	Sequence 1, Appli	1256	53.8	2.4	164	4	US-09-621-976-8070	Sequence 8070, Ap
1184	54.4	2.4	1605	3	US-09-149-476-187	Sequence 187, App	1257	53.8	2.4	277	4	US-09-621-976-16983	Sequence 16983, A
1185	54.4	2.4	1921	2	US-08-557-128-11	Sequence 11, Appl	1258	53.8	2.4	351	4	US-09-621-976-16140	Sequence 16140, A
1186	54.4	2.4	2065	2	US-08-968-751-1	Sequence 1, Appli	c1259	53.8	2.4	601	4	US-09-949-016-145250	Sequence 145250, A
1187	54.4	2.4	2327	4	US-10-066-130-20	Sequence 20, Appl	c1260	53.8	2.4	601	4	US-09-949-016-145252	Sequence 145252, A
1188	54.4	2.4	2674	4	US-10-066-130-19	Sequence 19, Appl	1261	53.8	2.4	615	3	US-09-105-542A-2	Sequence 2, Appli
1189	54.4	2.4	2771	4	US-10-066-130-18	Sequence 18, Appl	1262	53.8	2.4	1577	3	US-08-821-994-59	Sequence 59, Appl
1190	54.4	2.4	4072	3	US-09-245-041-16	Sequence 16, Appl	1263	53.8	2.4	1722	4	US-09-482-273-102	Sequence 102, App
1191	54.4	2.4	4072	4	US-09-358-055B-16	Sequence 16, Appl	1264	53.8	2.4	1825	3	US-09-461-697-75	Sequence 75, Appl
1192	54.4	2.4	4072	4	US-09-893-238-16	Sequence 16, Appl	1265	53.8	2.4	1867	4	US-09-482-273-81	Sequence 81, Appl
1193	54.4	2.4	5860	4	US-10-066-130-17	Sequence 17, Appl	1266	53.8	2.4	2311	4	US-09-800-729-66	Sequence 66, Appl
1194	54.4	2.4	7277	4	US-09-795-927-5	Sequence 5, Appli	c1267	53.8	2.4	68580	4	US-09-949-016-15844	Sequence 15844, A
c1195	54.4	2.4	9646	3	US-08-811-566-1	Sequence 1, Appli	c1268	53.8	2.4	92155	4	US-09-949-016-17484	Sequence 17484, A

c1269	53.8	2.4	524032	4	US-09-949-016-16928	Sequence 16928, A	1342	53.2	2.4	1144	4	US-09-904-615-20	Sequence 20, Appl
c1270	53.8	2.4	524032	4	US-09-949-016-16929	Sequence 16929, A	1343	53.2	2.4	1527	4	US-09-244-111-7	Sequence 7, Appli
c1271	53.8	2.4	524032	4	US-09-949-016-16930	Sequence 16930, A	1344	53.2	2.4	1699	3	US-09-152-060-19	Sequence 19, Appl
c1272	53.8	2.4	524032	4	US-09-949-016-16931	Sequence 16931, A	1345	53.2	2.4	1931	3	US-09-019-942-2	Sequence 2, Appli
c1273	53.8	2.4	529885	4	US-09-949-016-14340	Sequence 14340, A	1346	53.2	2.4	1931	3	US-09-099-041A-1	Sequence 1, Appli
c1274	53.8	2.4	529885	4	US-09-949-016-14341	Sequence 14341, A	1347	53.2	2.4	1931	3	US-09-245-281-1	Sequence 1, Appli
c1275	53.8	2.4	529885	4	US-09-949-016-14342	Sequence 14342, A	1348	53.2	2.4	1931	3	US-09-470-271-2	Sequence 2, Appli
c1276	53.8	2.4	529885	4	US-09-949-016-14343	Sequence 14343, A	1349	53.2	2.4	1931	3	US-09-207-359B-1	Sequence 1, Appli
c1277	53.8	2.4	529885	4	US-09-949-016-14344	Sequence 14344, A	1350	53.2	2.4	1931	4	US-09-340-620A-1	Sequence 1, Appli
c1278	53.8	2.4	529885	4	US-09-949-016-14345	Sequence 14345, A	1351	53.2	2.4	1931	4	US-09-865-364-1	Sequence 1, Appli
c1279	53.8	2.4	529885	4	US-09-949-016-14346	Sequence 14346, A	1352	53.2	2.4	1931	4	US-09-748-537-2	Sequence 2, Appli
c1280	53.8	2.4	529885	4	US-09-949-016-14347	Sequence 14347, A	1353	53.2	2.4	1949	4	US-09-461-325-26	Sequence 26, Appl
c1281	53.8	2.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli	1354	53.2	2.4	1949	4	US-10-012-542-26	Sequence 26, Appl
c1282	53.8	2.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli	1355	53.2	2.4	1949	4	US-10-115-123-26	Sequence 26, Appl
1283	53.6	2.4	85	4	US-09-621-976-14741	Sequence 14741, A	1356	53.2	2.4	2103	4	US-09-489-847-40	Sequence 40, Appl
1284	53.6	2.4	443	4	US-09-621-976-17631	Sequence 17631, A	1357	53.2	2.4	2223	1	US-08-296-624-1	Sequence 1, Appli
1285	53.6	2.4	803	4	US-09-800-729-60	Sequence 60, Appl	1358	53.2	2.4	2581	4	US-09-369-247-51	Sequence 51, Appl
1286	53.6	2.4	832	4	US-09-774-639-57	Sequence 57, Appl	1359	53.2	2.4	13584	4	US-09-991-258-17	Sequence 17, Appl
1287	53.6	2.4	1619	4	US-09-522-714-11	Sequence 11, Appl	1360	53.2	2.4	29629	3	US-09-729-995-3	Sequence 3, Appli
1288	53.6	2.4	2288	4	US-09-800-729-24	Sequence 24, Appl	1361	53.2	2.4	29629	4	US-10-135-689-3	Sequence 3, Appli
1289	53.6	2.4	2581	3	US-09-363-708-1	Sequence 1, Appli	1362	53.2	2.4	29629	4	US-10-690-617-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1

US-09-621-976-97
; Sequence 97, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 97
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; LOCATION: 227..307
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 7.09999990463257
; OTHER INFORMATION: seq VLLLLLLERGMFS/SP
; NAME/KEY: misc feature
; LOCATION: 586,602..603
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-97

Query Match 27.3%; Score 612.8; DB 4; Length 672;
Best Local Similarity 98.1%; Pred. No. 7.2e-146;
Matches 635; Conservative 5; Mismatches 3; Indels 4; Gaps 2;

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RESULT 2

US-09-620-312D-931
; Sequence 931, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
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; NAME/KEY: CDS
; LOCATION: (218)..(1645)
US-09-620-312D-931

Query Match 20.8%; Score 467.4; DB 4; Length 2710;
Best Local Similarity 58.5%; Pred. No. 1.5e-108;
Matches 835; Conservative 0; Mismatches 586; Indels 6; Gaps 1;

QY 313 TCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGGAGTGGGTGG 372
|||||

Db 237 TGTTTAAGTACATAGATGAAAAATCAGGATCGCTACATTAAAGAAACTCGCAAAATGGGTGG 296
QY 373 CCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAAGAGCTTTCAGAATGA 432
|||||
Db 297 CTATCCAGAGTGTGTCTCGTGGCCGGAG-----AAGAGAGGCGAAATCAGGAGGATGA 350
|||||
QY 433 TGGCCGTGGCTGCGGACACGCTGCAGCGCCTGGGGGCCCGTGTGGCCTCGGTGGACATGG 492
|||||
Db 351 TGAAGTTGCTGCTGCAGATGTTAAGCAGTTGGGGGGCTCTGTGGAACCTGCTGGATATCG 410
|||||
QY 493 GTCCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCATCTCGGCCGAAC 552
|||||
Db 411 GAAAAACAAAAGCTCCCTGATGGCTCGGAGATCCCGTCCCTCTATTTCTGCTCGCAGGC 470
|||||
QY 553 TGGGGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTTGGACGTGCAGCCTG 612
|||||
Db 471 TGGGCTCTGACCCACAGAAAGACCGTGTGCAATTACGGGCACCTGGATGTGCAGCCTG 530
|||||
QY 613 CTGACCGGGCGGATGGGTGGCTCAGCGACCCCTATGTGTGCTGACGGAGGTAGACGGAAAC 672
|||||
Db 531 CAGCCCTGGAGGACGGCTGGGACAGCGAGCCCTTACCCCTGGTGGAGCGAGACGGCAAGC 590
|||||
QY 673 TTTATGGACGAGGAGCGACCGGACCAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGA 732
|||||
Db 591 TGTATGGGAGAGGTTTCGACTGATGATAAGGGCCCGTGGCTGGCTGATAAACGCCCTGG 650
|||||
QY 733 GCGCCTTCAGAGCCCTGGAGCAAGATCTTCCCTGTGAATATCAAAATTCATATTGAGGGGA 792
|||||
Db 651 AAGCGTATCAGAAAAACAGGCCAGGAGATTCTCTGTCAACGTCGGATTCTGCCCTCGAAGGCA 710
|||||
QY 793 TGAAGAGGCTGGCTCTGTTCCTTGGAGGAACCTTGTGAAAAAGAAAGACCGATTCT 852
|||||
Db 711 TGGAGAGTCAGGCTCTGAGGGCCTAGACGAGCTGATTTTGTCCCGAAAGACACATTCT 770
|||||
QY 853 TCTCTGGTGTGGACTACATTGTAATTTTCAGATAACCTGTGGATCAGCCAAAGGAGCCAG 912
|||||
Db 771 TTAAGGATGTGGACTATGTCTGCATTTTCTGACAATTACTGGCTGGAAAGAAAGCCCT 830
|||||
QY 913 CAATCACTTATGGAACCCGGGGGAACAGTACTTTTCATGGTGGAGGTGAAATGCAGAGACC 972
|||||
Db 831 GCATCACCTACGGCCTCAGGGGCATTTGTACTTTTTTCATCGAGGTGGAGTGCAGGCAACA 890
|||||
QY 973 AGGATTTTCACTCAGGAAACCTTTGGTGGCATCCTTCATGAACCAATGGCTGATCTGGTTG 1032
|||||
Db 891 AAGACCTCCATTCTGGGGTGTACGGGGGCTCGGTGCATGAGGCCATGACTGATCTCATTT 950
|||||
QY 1033 CTCTTCTCGGTAGCCTGTGTAGACTCGTCTGGTCAATCCTGGTCCCTGGAATCTATGATG 1092
|||||
Db 951 TGCTGATGGGCTCTTTGGTGGACAAGAGGGGGAACATCTCTGATCCCCGGCATTAACGAG 1010
|||||
QY 1093 AAGTGGTTCTCTTACAGAAAGAGGAAATAAATACATAACAAAGCCATCTCATAGACCTAG 1152
|||||
Db 1011 CCGTGGCCCGCTCAGCGAAGAGGAGCACAAGCTGTACGACGACATCGACTTTGACATAG 1070
|||||
QY 1153 AAGAATACCGGAATAGCAGCCGGTTGAGAAATTTCTGTTTCGATACTAAGGAGGAGATT 1212
|||||
Db 1071 AGAGTTTGCCAAAGGATGTGGGGGCGCAGATCCTCTGCACAGCCACAAGAAAGACATCC 1130
|||||
QY 1213 TAATGCACCTCTGGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGGGCGCTTTGATG 1272
|||||
Db 1131 TCATGCACCGATGGCGGTACCCGTCCTGTCTCCCTCCATGGCATCGAAGGGCGCTTCTCTG 1190
|||||
QY 1273 AGCCTGGAACATAAAACAGTCATACCTGGCCCGAGTTATAGGAAATTTTCAATCCGCTAG 1332
|||||
Db 1191 GGTCTGGGGCAAGACCGTGATTCCAGGAAGGTGGTTGGCAAGTTCTCCATCAGGCTCG 1250
|||||
QY 1333 TCCCTCACATGAATGTGTCTGCGGTGGAAAAACAGGTGACACGACATCTTGAAGATGTGT 1392
|||||
Db 1251 TGCCGAACATGACTCCTGAAGTCGTGCGGAGCAGGTCAACAAGTACTTAAGAAAGT 1310
|||||
QY 1393 TCTCCAAAAGAAATAGTTCACCAACAAGATGGTTGTTTCCATGACTCTAGGACTACACCCGT 1452
|||||
Db 1311 TTGCTGAACCTACGACGCCCAATGAGTTCAAGGTGTACATGGGCCACGGTGGGAAGCCCT 1370
|||||

; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 13950
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 67
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 68
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 69
; OTHER INFORMATION: m=a or c
; US-09-513-999C-13950

Query Match 13.1%; Score 292.8; DB 4; Length 300;
Best Local Similarity 98.3%; Pred. No. 1.3e-64;
Matches 291; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC 60
Db 5 GARTGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC 64

Qy 61 TCGTCTTCCTCCGGGGGACAAACGTGGGTCAGGGCACAGAGAGATATTAAATGTCACCCCT 120
Db 65 TCRWMTTCCTCCGGGGGACAAACGTGGGTCAGGGCACAGAGAGATATTAAATGTCACCCCT 124

Qy 121 CTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTGGAGGTTGGGAAAGTTGCTAGA 180
Db 125 CTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTGGAGGTTGGGAAAGTTGCTAGA 184

Qy 181 GGCTTCAGAACTCCAGCCCTAATGGATCCCAAACTCGGGAGAAATGGTGGTCCCTGCTGG 240
Db 185 GGCTTCAGAACTCCAGCCCTAATGGATCCCAAACTCAGGAGAAATGGTGGTCCCTGCTGG 244

Qy 241 CTGTGCTGCTGCTGCTGCTGGAGCGCGCATGTTCTCCTCACCCCTCCCCGCCCCCG 296
Db 245 CTGTGCTGCTGCTGCTGCTGGAGCGCGCATGTTCTCCTCACCCCTCCCCGCCCCCG 300

RESULT 5
US-09-248-796A-652
; Sequence 652, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 652
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: unsure

; LOCATION: (1456), (1462)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unknown
; US-09-248-796A-652

Query Match 10.0%; Score 224.8; DB 4; Length 1479;
Best Local Similarity 50.0%; Pred. No. 6e-47;
Matches 593; Conservative 0; Mismatches 588; Indels 6; Gaps 1;

Qy 519 AGTCTTCCAATACCTCCCGTCATCTCTGGCCGAACCTGGGGAGCGATCCCACGAAAGGCACC 578
Db 271 AATTACAATTACCTCCAATTGTTTAGGTCGTTTGGCAATGATCCAGCCCAAGAAAAC 330

Qy 579 GTGTGCTTCTACGGCCACTTGGACGTGCAGCCCTGCTGACCGGGCGGATGGGTGGCTCAGC 638
Db 331 GTTTTAGTTTATGGTCATTATGATGTTCAACCAGCTTTGAAAGATGATGGTTGGAAAAC 390

Qy 639 GACCCCTATGTCTG-----ACGGAGGTAGACGGGAAACTTTTATGGACGAGGAGCGACC 692
Db 391 GAACCATTCACCATGCATTACGATAAGGAAAAAGAAATCTTGTACGGTAGAGGATCTACT 450

Qy 693 GACAAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCGCCTTCAGAGCCCTGGAG 752
Db 451 GATGATAAAGGTCAGTTGTGGGATGGTTGAATGTCAATGAAGCACATAATAAATGGGC 510

Qy 753 CAAGATCTTCTGTGAATATCAAAATTCATCATTTAGGGGATGGAAGAGGCTGGCTCTGTT 812
Db 511 TGGGAATTGCCAGTCAATTAGTTGTTTGTGTTGAGGATGGAAGAAAGTGGATCCTTG 570

Qy 813 GCCCTGGAGGAACCTTGTGAAAAAGAAAGGACCGGATTTCTTCTCTGTTGTGGACTACATT 872
Db 571 GGATGGATGAACCTTGTGCTAAGGAAGCACAAAACCTACTTTAAAAAAGTCGATCAAGTG 630

Qy 873 GTAATTTTCAGATAACCTGTGGATCAGCCAAAGGAAGCCCAACTCACTTATGGAACCCGG 932
Db 631 ACTATTTTCAGATAAATTATTTGGTTAGGTACCCACCAACCTGTTTGACTTATGGGTTAAG 690

Qy 933 GGGAAACAGCTACTTTCATGAGCAATGGCTGATCTGGTTGCTCTTCTCGGTAGCCTGGTA 992
Db 691 GGTTGTAACCTACTATCAAAATTCATTTGAAGGTCCTGGTGTGATTTGCACAGTGGTATC 750

Qy 993 TTTGGTGGCATCCTTTCATGAACCAATGGCTGATCTGGTTGCTCTTCTCGGTAGCCTGGTA 1052
Db 751 TTTGGTGGTATTATTGCTGAACCAATGACAGATTTAATCAAGTGAATGCTACTTTAGTT 810

Qy 1053 GACTCGTCTGCTCATATCCTGTGTCCTTGGAAATCTATGATGAAGTGGTTCCCTTTACAGAA 1112
Db 811 GACGGCAGTGGTAAATCTTGAATTCAGGTGTTTATGATATGGTTGCTCCTTTGACTGAT 870

Qy 1113 GAGGAATAAATACATACAAAGCCATCCATCTAGACCTAGAGAATAACCGGAATAGCAGC 1172
Db 871 AAAGAACATCAATTATATGATAGTATTGATTTTTCAGTTGAAGAATTAATGCTGCTAGT 930

Qy 1173 CGGGTTGAGAAATTTCTGTTCCGATACTAAGGAGGAGATTCTAATGCACCTCTGGAGGTAC 1232
Db 931 GGTTCACCAAACTTCATTACACGACACAAAGAAAGATATTTTGAACACAGATGGAGATTC 990

Qy 1233 CCATCTCTTTTCATTTGCGGATCGAGGGCGGTTTGTATGAGCCTGGAACATAAACAGTC 1292
Db 991 CCATCCCTTTTCATTACATGGTATTGAAGGTGCCTTTTCAGGTGCTGGTCCCAAACTGTT 1050

Qy 1293 ATACCTGGCGAGTTATAGGAAATTTCAATCCGTCTAGTCCCTCACATGAATGTGCT 1352
Db 1051 ATCCCTGCTAAAAGTTGTTGGTAAATTTCTCCATTAGAACTGTCCACAGATATCGAATA 1110

Qy 1353 GCGGTGGAACCAACAGGTGACACGACATCTTGAAGATGTGTTCTCCAAAGAAATAGTTCC 1412
Db 1111 AAATTAGACGATTTGGTATTCCCAACATATAAATCTCTGAATTCAAAAAATTAACCTCACCA 1170

Qy 1413 AACAAAGATGTTGTTTCCATGACTCTAGGACTACACCCGTTGATTGCAAAATATGATGAC 1472
Db 1171 AATAAATTCAAAAGTTGAATTAATTCATGATGGTAATTACTGGGTTTCTGATCCATTAA 1230

Qy 1473 ACCCAGTATCTCGCAGCAAAAAGAGCGCATCAGAACAGTGTGTTGGAACAGAACCATATG 1532

Db 119 GCAAGCTAGGCAGCGACCCAGAGAAACCGTGTGCATTACGGGCACCTGGACGTGC 178
QY 607 AGCCTGCTACCCGGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACG 666
Db 179 AGCCTGC-GCCCTGGAGGACGGGTGGACAGCGAGCCCTTCACCTTGGTGGAGCGGGAAG 237
QY 667 GGAAGCTTTATGGACGAGGAGCGACCGACAACAAAG 702
Db 238 GCAAGCTGTATGGAGAGGCTCCACGGACGATAAGG 273

RESULT 8
US-09-081-395-5
; Sequence 5, Application US/09081395
; Patent No. 6083746
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrei
; APPLICANT: Kazarov, Alexander
; APPLICANT: Mazo, Ilya
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Methods for Identifying Genetic
; TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
; TITLE OF INVENTION: Growth in Cancer Cells
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,395
; FILING DATE: 18-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6083746nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-KK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-09-081-395-5

Query Match 4.3%; Score 96.4; DB 3; Length 273;
Best Local Similarity 64.1%; Pred. No. 1.2e-14;
Matches 177; Conservative 0; Mismatches 96; Indels 3; Gaps 2;
QY 427 GAATGATGGCCGTGGCTGCGGACACGCTGCAGCGCCCTGGGGCCCGTGTGGCCTCGGTGG 486
Db 1 GGATGATGGAGGTGGCAGCTGCCGATGTCCAGAGGCTGGGGGCTCCGTGGAACTGGTGG 60
QY 487 ACATGGGTCTCAGACGATGCCCGATGGTTCAGAGTCTTCCAATACCTCCCGTCATCCTGG 546
Db 61 ATATCGGGAAGCAGAGTCCAGATGGCTCGGAGATACCACCTTCTCCCATC--TGCTGG 118
QY 547 CCGAACTGGGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGGACGTGC 606
Db 119 GCAAGCTAGGCAGCGACCCAGAGAAACCGTGTGCATTTACGGGCACCTGGACGTGC 178

QY 607 AGCCTGCTGACCCGGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACG 666
Db 179 AGCCTGC-GCCCTGGAGGACGGGTGGGACAGCGAGCCCTTCACCTTGGTGGAGCGGGAAG 237
QY 667 GGAAGCTTTATGGACGAGGAGCGACCGACAACAAAG 702
Db 238 GCAAGCTGTATGGAGAGGCTCCACGGACGATAAGG 273

RESULT 9
US-09-416-833-5
; Sequence 5, Application US/09416833
; Patent No. 6197521
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrei
; APPLICANT: Kazarov, Alexander
; APPLICANT: Mazo, Ilya
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Methods for Identifying Genetic
; TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
; TITLE OF INVENTION: Growth in Cancer Cells
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allgretti & Witcoff, Ltd.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,833
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,740
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6197521nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-09-416-833-5

Query Match 4.3%; Score 96.4; DB 3; Length 273;
Best Local Similarity 64.1%; Pred. No. 1.2e-14;
Matches 177; Conservative 0; Mismatches 96; Indels 3; Gaps 2;
QY 427 GAATGATGGCCGTGGCTGCGGACACGCTGCAGCGCCCTGGGGCCCGTGTGGCCTCGGTGG 486
Db 1 GGATGATGGAGGTGGCAGCTGCCGATGTCCAGAGGCTGGGGGCTCCGTGGAACTGGTGG 60
QY 487 ACATGGGTCTCAGACGATGCCCGATGGTTCAGAGTCTTCCAATACCTCCCGTCATCCTGG 546
Db 61 ATATCGGGAAGCAGAGTCCAGATGGCTCGGAGATACCACCTTCTCCCATC--TGCTGG 118
QY 547 CCGAACTGGGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGGACGTGC 606

Db 119 GCAAGCTAGGACGACCCCCAGAGAAAACCGTGTGCTATTACGGGCACCTGGACGTGC 178
QY 607 AGCCTGCTGACCGGGCGGATGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACG 666
Db 179 AGCCTGC-GCCCTGGAGGACGGTGGGACAGCGAGCCCTTCACCTTGGTGGAGCGGGAAG 237
QY 667 GGAACCTTTATGGACGAGGACCGGACCGACAACAAAG 702
Db 238 GCAAGCTGTATGGAGAGGCTCCACGGACGATAAGG 273

RESULT 10
PCT-US95-02521-5
; Sequence 5, Application PC/TUS9502521
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Methods for Identifying Genetic
; TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
; TITLE OF INVENTION: Growth in Cancer Cells
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02521
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US95-02521-5

Query Match 4.3%; Score 96.4; DB 5; Length 273;
Best Local Similarity 64.1%; Pred. No. 1.2e-14;
Matches 177; Conservative 0; Mismatches 96; Indels 3; Gaps 2;
QY 427 GAATGATGGCCGTGGCTCGGACACGCTGCAGCGCCTGGGGCCCGTGTGGCCTCGGTGG 486
Db 1 GGATGATGGAGGTGGCAGCTGCCGATGTCCAGAGGCTGGGGGCTCCGTGGAACTGGTGG 60
QY 487 ACATGGGTCCTCAGCAGCTGCCCGATGGTGCAGAGTCTTCCAATACCTCCCGTCATCCTGG 546
Db 61 ATATCGGGAAGCAGAAAGCTCCAGATGGCTCGGAGATACCACCTTCTCCCATC--TGCTGG 118
QY 547 CCGAACTGGGAGCGATCCACAGAAAGCACCGTGTGCTTCTACGGCCACTTGGACGTGC 606
Db 119 GCAAGCTAGGACGACGCCCCAGAGAAACCGTGTGCATTTACGGGCACCTGGACGTGC 178
QY 607 AGCCTGTGACCGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACG 666
Db 179 AGCCTGC-GCCCTGGAGGACGGTGGGACAGCGAGCCCTTCACCTTGGTGGAGCGGGAAG 237
QY 667 GGAACCTTTATGGACGAGGACCGGACCGACAACAAAG 702
Db 238 GCAAGCTGTATGGAGAGGCTCCACGGACGATAAGG 273

RESULT 11
US-09-513-999C-22131
; Sequence 22131, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG

; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 22131
; LENGTH: 334
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 277
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 303
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 334
; OTHER INFORMATION: s=g or c
US-09-513-999C-22131

Query Match 4.1%; Score 92.2; DB 4; Length 334;
Best Local Similarity 95.9%; Pred. No. 1.6e-13;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2090 CGTGACACATAATCATTCATCCATCAATGATCGCCTTTGCTTTACCACTCTTTCCCTTTATC 2149
Db 1 CGTGACACATAATCATTCATCCATCAATGATCGCCTTTACTTTACCACTCTTTCCCTTTATC 60
QY 2150 TTATTAATAAAAAATGTGGTCTCCACCACCTGNCCTCCCA 2187
Db 61 TTATTAATAAAAAATGTGGTCTCCACCACCTGACTACAA 98

RESULT 12
US-09-583-110-2168
; Sequence 2168, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 2168
; LENGTH: 1374
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2168

Query Match 3.8%; Score 85.8; DB 4; Length 1374;
Best Local Similarity 46.7%; Pred. No. 1.4e-11;
Matches 381; Conservative 0; Mismatches 422; Indels 12; Gaps 3;
QY 576 ACCGTGTGCTTCTACGGCCACTTGGACGTGACGCTGTGACCGGGCGGATGGGTGGCTC 635
Db 250 ACCTTGATTTCTATAAACCACTATGACACTGTGCCAGCGGATGGGATCAGGTCTGGACA 309
QY 636 ACGGACCCCTATGTGCTGACGGAGGTAGACGGGAAACTTTATGGACGAGGACGACCGAC 695
Db 310 GAGGATCCCTTTACGCTTTCGGTCCGCAATGGCTTCATGTATGGCGGTGGGTGTGATGAC 369

Qy 1350 TCTGCGGTGAAAAACAGGTGACACGACATCTTGA 1384
Db 2007 CATGATGTTCTGGAATAATTCGGAACAGCTAGA 2041

RESULT 14

US-09-198-452A-1/c
; Sequence 1, Application US/09198452A
; Patent No. 6559294

; APPLICANT: Grifffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 1

; LENGTH: 1230025

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(15000)

; OTHER INFORMATION: n=a or c or g or t

; NAME/KEY: misc_feature

; LOCATION: (15001)..(30000)

; OTHER INFORMATION: n=a or c or g or t

; NAME/KEY: misc_feature

; LOCATION: (30001)..(45000)

; OTHER INFORMATION: n=a or c or g or t

; NAME/KEY: misc_feature

; LOCATION: (45001)..(60000)

; OTHER INFORMATION: n=a or c or g or t

; NAME/KEY: misc_feature

; LOCATION: (60001)..(75000)

; OTHER INFORMATION: n=a or c or g or t

; NAME/KEY: misc_feature

; LOCATION: (75001)..(90000)

; OTHER INFORMATION: n=a or c or g or t

; NAME/KEY: misc_feature

; LOCATION: (90001)..(105000)

; OTHER INFORMATION: n=a or c or g or t

; NAME/KEY: misc_feature

; LOCATION: (105001)..(120000)

; OTHER INFORMATION: n=a or c or g or t

; NAME/KEY: misc_feature

; LOCATION: (120001)..(135000)

; OTHER INFORMATION: n=a or c or g or t

; NAME/KEY: misc_feature

; LOCATION: (135001)..(150000)

; OTHER INFORMATION: n=a or c or g or t

; NAME/KEY: misc_feature

; LOCATION: (150001)..(165000)

; OTHER INFORMATION: n=a or c or g or t

; NAME/KEY: misc_feature

; LOCATION: (165001)..(180000)

; OTHER INFORMATION: n=a or c or g or t

; NAME/KEY: misc_feature

; LOCATION: (180001)..(195000)

; OTHER INFORMATION: n=a or c or g or t

; NAME/KEY: misc_feature

; LOCATION: (195001)..(210000)

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QY	766	TGAATATCAAAATT	CATCAT	TGAGGGGAT	TGGAAGAGG	CTGGCTCTGTT	CGCCCTGGAGGAAC	825
Db	1126444	TAAATATTAATT	TGGTTAA	TGAGGTTGA	AGAAGAGAGT	GGGAGCTCGC	ATTATTTACTT	1126385
QY	826	TTGTGGA	AAAAAGAACCG	ATTCTTCTCTGGTGTGG	ACTACATTTGTA	ATTTTCAGATA	885	
Db	1126384	GGTTAGAAA	AAAAAAGAACG	CTTT-----ACGCGGG	ACTATCTTCTGATCGT	AGATG	1126331	
QY	886	ACCTGTGGAT	CAGCCAAAGGA	AGCCAGCAATCA	CTTATGGAACCGGGG	AACAGCTACT	945	
Db	1126330	GGGGTTT	CTCTGTGAAAA	ACACCCCTACGTA	AGCATTTGGAGT	CGGGGTATTTGTTCCA	1126271	
QY	946	TCATGGTGGAG	TGAAATGCAGAG	ACCAGGATTTTCA	CTCAGGAACCTTTTGGTGG	CATCC	1005	
Db	1126270	TGAAAATCT	CCCTTGAAGAGGG	GAACAAGGACATG	CACTCAGGAGTTT	TAGGAGGAATTG	1126211	
QY	1006	TTCATGAACCA	ATGGCTGATCTGGT	TGCTTCTCGGTAG	CCTGGTAGACTCGTCTGG	TC	1065	
Db	1126210	CCTACAATA	CGAATCGTGTCTT	TATCAGAAATTTCTG	AGCTCTCTGCATCAC	CCCTGCAATT	1126151	
QY	1066	ATATCCTGGT	CCCTGGAATCTATG	ATGAAGTGGTTT	CTCTTACAGA	1111		
Db	1126150	CTATAGCTAT	TGAAGGATTTTATG	ATGATCTTGTCT	CTCCCTCGGA	1126105		

Search completed: February 13, 2005, 23:21:02
Job time : 318 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2005, 12:41:51 ; Search time 6549 Seconds
(without alignments)
16588.272 Million cell updates/sec

Title: US-10-036-342-56
Perfect score: 2242
Sequence: 1 gaatgaatacctccgaagcc.....aaaaaaaaaaaaaaaaaaaa 2242

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2241	100.0	2242	9	AY358756 Homo sapi
2	2182.8	97.4	2784	6	AX527744 Sequence
3	2147.4	95.8	2235	6	AX059560 Sequence
4	2135.6	95.3	2152	6	BD205653 97 human
5	1877.6	83.7	1970	9	AK098369 Homo sapi
6	1616	72.1	1640	9	HSA417564
7	1531.6	68.3	1587	6	AX231101 Sequence
8	1531.6	68.3	1587	6	AX231560 Sequence
9	1531.6	68.3	1587	6	AX232218 Sequence
10	1531.6	68.3	1587	6	AX233356 Sequence
11	1524	68.0	1524	6	AX319869 Sequence
12	1521	67.8	1521	6	AX527746 Sequence
13	1506.4	67.2	1524	6	AX139747 Sequence
14	1031.2	46.0	2675	10	BC081877 Rattus no
15	1006.2	44.9	2774	10	BC043305 Mus muscu
16	672.6	30.0	1692	5	BX931960 Gallus ga
17	612.8	27.3	672	6	AR412460 Sequence
18	612.8	27.3	672	6	AX969294 Sequence
19	612.8	27.3	672	6	BD108013 EST and e

93	222	9.9	774	6	AX867346	AX867346 Sequence
94	208.4	9.3	40487	3	AY190950	AY190950 Drosophil
95	205.4	9.2	568	6	AX398096	AX398096 Sequence
96	205.4	9.2	594	6	AX398095	AX398095 Sequence
97	204.8	9.1	701	6	AX398092	AX398092 Sequence
98	204.2	9.1	83253	3	AY186999	AY186999 Drosophil
99	203.4	9.1	64201	2	AC117833	AC117833 Homo sapi
c 100	203.4	9.1	64201	2	AC117833	AC117833 Homo sapi
101	191.8	8.6	699	6	AX398102	AX398102 Sequence
102	188.2	8.4	514	6	AX398099	AX398099 Sequence
103	186.8	8.3	554	5	AY260749	AY260749 Oreochrom
104	181.6	8.1	606	6	AX398093	AX398093 Sequence
105	180.8	8.1	623	6	AX398094	AX398094 Sequence
106	178.4	8.0	640	6	AX398097	AX398097 Sequence
107	174.4	7.8	704	6	BD149742	BD149742 Primer fo
108	174.4	7.8	704	6	AX869680	AX869680 Sequence
109	172.6	7.7	613	6	AX398098	AX398098 Sequence
110	169.4	7.6	73476	2	AC123772	AC123772 Homo sapi
c 111	165.6	7.4	19383	3	CER11H6	AX398098 Sequence
112	165.2	7.4	149982	2	AC148745	Z93386 Caenorhabdi
113	165.2	7.4	182565	2	AC148810	AC148745 Bos tauru
c 114	158	7.0	249832	2	AC096927	AC148810 Bos tauru
c 115	157.4	7.0	255946	2	AC126480	AC096927 Rattus no
116	157.4	7.0	754	6	BD148888	AC126480 Rattus no
117	157.4	7.0	754	6	AX868826	BD148888 Primer fo
118	154.8	6.9	148033	2	AC121513	AX868826 Sequence
c 119	154.4	6.9	2006	9	BC047599	BC047599 Homo sapi
120	153.2	6.8	218336	2	AC094007	AC121513 Mus muscu
c 121	153	6.8	73476	2	AC123772	BC047599 Homo sapi
c 122	152.8	6.8	1467	9	BC065925	AC094007 Rattus no
123	150.2	6.7	558	6	AX398100	AC123772 Homo sapi
124	150	6.7	179254	2	AC149168	BC065925 Homo sapi
125	146.4	6.5	128095	2	AC148812	AX398100 Sequence
c 126	145.2	6.5	43541	3	CBRG02A05	AC149168 Carollia
127	143	6.4	665	6	AX398101	AC148812 Dasypus n
128	140	6.2	495	6	AX398103	AC084478 Caenorhab
c 129	134.2	6.0	305153	1	AP001520	AX398101 Sequence
c 130	132.2	5.9	561	11	BV063773	AX398103 Sequence
c 131	130.6	5.8	172828	10	AC124187	AP001520 Bacillus
132	129.6	5.8	886	6	BD134445	BV063773 S212P6035
133	129.6	5.8	886	6	AX017274	AC124187 Mus muscu
134	129.6	5.8	886	6	AX524978	BD134445 Human nuc
135	129.6	5.8	1638	6	BD134485	AX017274 Sequence
136	129.6	5.8	1638	6	AX017385	AX524978 Sequence
137	129.6	5.8	1638	6	AX525089	BD134485 Human nuc
138	128.4	5.7	518	6	AX398108	AX017385 Sequence
c 139	128.2	5.7	464	6	AX398104	AX525089 Sequence
c 140	126	5.6	127	11	G42956	AX398108 Sequence
c 141	125.2	5.6	536	6	AX398112	AX398104 Sequence
142	124.4	5.5	366	6	AX398109	G42956 WtAF-817-ST
143	121.8	5.4	512	6	AX398113	AX398112 Sequence
144	120.2	5.4	402	6	AX398107	AX398109 Sequence
145	119.6	5.3	345	6	AX398111	AX398113 Sequence
146	119.6	5.3	380	6	AX398110	AX398107 Sequence
c 147	119.6	5.3	143786	3	AC024859	AX398111 Sequence
c 148	119.6	5.3	298960	2	AC006896	AX398110 Sequence
149	118.2	5.3	386	6	AX398106	AC024859 Caenorhab
c 150	118	5.3	110000	1	AP006840_13	AC006896 Caenorhab
151	116.2	5.2	12249	1	AE002039	AX398106 Sequence
152	112.6	5.0	387	6	AX398105	Continuation (14 o
153	108.6	4.8	654	6	CQ411141	AE002039 Deinococc
154	108.2	4.8	259335	2	AC126194	AX398105 Sequence
155	103.6	4.6	465	6	CQ398470	CQ411141 Sequence
156	103.6	4.6	465	6	CQ404757	AC126194 Rattus no
c 157	103.6	4.6	301933	1	AE017174	CQ398470 Sequence
158	103	4.6	255446	2	AC095420	CQ404757 Sequence
c 159	100.4	4.5	52514	2	AC149165	AE017174 Porphyrom
c 160	100.4	4.5	70137	2	AC149160	AC095420 Rattus no
c 161	100.4	4.5	90513	2	AC149162	AC149165 Xenopus t
c 162	97.6	4.4	110000	8	CR382132_09	AC149160 Xenopus t
163	96.4	4.3	273	6	AR008079	AC149162 Xenopus t
164	96.4	4.3	273	6	AR102193	Continuation (10 o
165	96.4	4.3	273	6	AR102204	AR008079 Sequence
						AR102193 Sequence
						AR102204 Sequence

166	96.4	4.3	273	6	AR137594	AR137594 Sequence
167	96	4.3	110000	1	AP006841_43	Continuation (44 o
c 168	95.4	4.3	299050	1	BX294154	Continuation (44 o
169	93.8	4.2	168128	5	BX957344	BX294154 Pirellula
170	93.8	4.2	176850	2	BX950869	BX957344 Zebrafish
171	93.8	4.2	215910	2	BX928752	BX950869 Danio rer
c 172	93.2	4.2	136886	2	AC149262	BX928752 Danio rer
173	92.2	4.1	334	6	AX906268	AC149262 Spheeroid
174	92.2	4.1	334	6	BD041801	AX906268 Sequence
c 175	91.4	4.1	134405	2	AC113582	BD041801 Sequence
c 176	91.2	4.1	206423	2	AC148943	AC113582 Tetraodon
177	89.6	4.0	110000	1	BX908798_15	AC148943 Gasterost
c 178	88.8	4.0	11431	1	AE006867	Continuation (16 o
179	88.4	4.0	15085	1	AE002038	AE006867 Sulfolobu
c 180	88.4	3.9	88716	2	AC098644	AE002038 Deinococc
c 181	88.4	3.9	97166	2	AC098643	AC098644 Takifugu
182	86.6	3.9	301731	1	AE016934	AC098643 Takifugu
183	85.8	3.8	1371	6	AX566904	AE016934 Bacteroid
184	85.8	3.8	1374	6	AR481264	AX566904 Sequence
185	85.8	3.8	3766	6	CQ789134	AR481264 Sequence
186	85.8	3.8	3766	6	AR218993	CQ789134 Sequence
187	85.8	3.8	3766	6	BD003905	AR218993 Sequence
188	85.8	3.8	10146	1	AE007331	BD003905 Polynucle
189	85.8	3.8	175936	2	SPNEU1908	AE007331 Streptoco
190	85.8	3.8	349980	6	AX571760	AL449930 Streptoco
191	84.8	3.8	52514	2	AC149165	AX571760 Sequence
192	84.8	3.8	53496	2	AC149150	AC149165 Xenopus t
193	84.2	3.8	11612	1	AE008398	AC149150 Xenopus t
c 194	83	3.7	320150	1	AP005033	AE008398 Streptoco
195	81.8	3.6	311000	1	SCO939122	AP005033 Streptomy
196	81	3.6	110000	1	AP006840_13	AL939122 Streptomy
197	81	3.6	110000	1	AP006840_14	Continuation (14 o
198	80	3.6	10968	1	AE002246	Continuation (15 o
c 199	80	3.6	13485	1	AE001678	AE002246 Chlamydia
c 200	80	3.6	110000	6	AR310754_11	AE001678 Chlamydia
c 201	80	3.6	324746	1	AE017160	Continuation (12 o
c 202	80	3.6	325865	1	AP002548	AE017160 Chlamydia
203	79.8	3.6	3820	6	AR227379	AP002548 Chlamydia
c 204	79.8	3.6	26309	6	CQ363747	AR227379 Sequence
c 205	79.8	3.6	110000	1	AE017283_21	CQ363747 Sequence
c 206	78.8	3.5	110000	8	AE016818_03	Continuation (22 o
207	78.2	3.5	110000	8	CR382137_05	Continuation (4 of
208	78	3.5	2138	10	BC039782	Continuation (6 of
209	77.8	3.5	474	6	AR412920	BC039782 Mus muscu
210	77.8	3.5	474	6	AX969754	AR412920 Sequence
211	77.8	3.5	474	6	BD108473	AX969754 Sequence
212	77.2	3.4	3348	10	BC066211	BD108473 EST and e
213	76.8	3.4	409	6	AX885762	BC066211 Mus muscu
214	76.8	3.4	409	6	AX885762	AX885762 Sequence
215	76.8	3.4	464	6	BD025372	BD025372 Sequence
216	76.8	3.4	464	6	AX885761	AX885761 Sequence
217	75.8	3.4	464	6	BD025371	BD025371 Sequence
218	74.2	3.4	110000	8	CR382128_12	BD025371 Sequence
219	74.2	3.3	1739	8	PCU42442	Continuation (13 o
c 220	73.8	3.3	1826	8	AF196975	U42442 Pneumocysti
221	73.6	3.3	171260	2	CR812474	AF196975 Pneumocys
222	73.4	3.3	110000	2	AC119727_0	CR812474 Danio rer
c 223	72.6	3.3	2382	9	BC050393	AC119727 Homo sapi
c 224	72	3.2	79284	2	BX927314	BC050393 Homo sapi
c 225	72	3.2	467	6	CQ397777	BX927314 Danio rer
226	72	3.2	467	6	CQ404074	CQ397777 Sequence
227	72	3.2	1178	10	BC048734	CQ404074 Sequence
228	72	3.2	2550	9	BSM801250	BC048734 Mus muscu
229	71.8	3.2	2852	6	AR368768	AL122045 Homo sapi
230	71.8	3.2	1993	9	BC063485	AR368768 Sequence
231	71.8	3.2	4396	10	BC058991	AF119337 Macropus
232	71.6	3.2	254733	3	AC117075	BC063485 Homo sapi
233	71.6	3.2	1625	9	BC072433	BC058991 Mus muscu
234	71.4	3.2	760	11	G09488	AC117075 Dictyoste
235	71.4	3.2	110000	8	CR382139_15	BC072433 Homo sapi
236	71.2	3.2	861	9	BC009550	G09488 human STS C
237	71.2	3.2	2580	9	BC062567	Continuation (16 o
238	71	3.2	2087	10	BC054081	BC009550 Homo sapi
						BC062567 Homo sapi
						BC054081 Mus muscu

c 239	70.8	3.2	535	6	CQ524536	CQ524536 Sequence	312	68.2	3.0	2417	9	BC050684	BC050684 Homo sapi
240	70.8	3.2	1461	5	BC064230	BC064230 Xenopus t	313	68.2	3.0	3396	10	BC030323	BC030323 Mus muscu
c 241	70.6	3.1	110000	1	AE016822_15	Continuation (16 o	314	68.2	3.0	4402	10	BC058080	BC058080 Mus muscu
242	70.4	3.1	580	6	CQ526169	CQ526169 Sequence	315	68.2	3.0	4820	10	BC052716	BC052716 Mus muscu
243	70.4	3.1	2228	10	BC023765	BC023765 Mus muscu	c 316	68.2	3.0	85165	8	NC99H12	AL451018 Neurospor
244	70.4	3.1	300050	1	AP004596	AP004596 Oceanobac	317	68.2	3.0	157180	8	NCB18D24	AL513466 Neurospor
245	70.2	3.1	725	5	BC049478	BC049478 Danio rer	c 318	68	3.0	636	6	CQ466958	CQ466958 Sequence
246	70.2	3.1	790	10	BC038163	BC038163 Mus muscu	319	68	3.0	850	6	CQ466958	CQ466958 Sequence
247	70.2	3.1	1527	6	BD227255	BD227255 Secreted	320	68	3.0	850	6	AX478025	AX478025 Sequence
248	70.2	3.1	1580	6	BD231696	BD231696 31 human	321	68	3.0	867	9	BC042105	BC042105 Homo sapi
c 249	70	3.1	381	6	CQ472479	CQ472479 Sequence	322	68	3.0	1009	9	BC065500	BC065500 Homo sapi
250	70	3.1	2690	10	BC058562	BC058562 Mus muscu	323	68	3.0	1240	9	BC073164	BC073164 Homo sapi
c 251	69.8	3.1	425	6	CQ408472	CQ408472 Sequence	324	68	3.0	1690	6	E32442	E32442 Mammal-deri
c 252	69.8	3.1	491	6	CQ397758	CQ397758 Sequence	325	68	3.0	1800	5	BC066699	BC066699 Danio rer
c 253	69.8	3.1	491	6	CQ404055	CQ404055 Sequence	326	68	3.0	2184	5	BC068356	BC068356 Danio rer
254	69.8	3.1	1056	3	AY069036	AY069036 Drosophil	c 327	67.8	3.0	309	6	CQ5113146	CQ5113146 Sequence
255	69.8	3.1	2005	9	HSM803426	AL832119 Homo sapi	328	68	3.0	429	6	CQ525026	CQ525026 Sequence
c 256	69.8	3.1	331039	3	AC116979	AC116979 Dictyoste	329	67.8	3.0	556	6	CQ508215	CQ508215 Sequence
257	69.6	3.1	908	5	BC084191	BC084191 Xenopus t	330	67.8	3.0	556	6	CQ508315	CQ508315 Sequence
258	69.6	3.1	1242	10	BC062228	BC062228 Rattus no	331	67.8	3.0	556	6	CQ510257	CQ510257 Sequence
259	69.6	3.1	1880	9	AB060863	AB060863 Macaca fa	332	67.8	3.0	556	6	CQ511753	CQ511753 Sequence
c 260	69.4	3.1	287	6	CQ422263	CQ422263 Sequence	333	67.8	3.0	809	9	BC063537	BC063537 Homo sapi
261	69.4	3.1	2279	10	BC025490	BC025490 Mus muscu	334	67.8	3.0	834	9	BC063494	BC063494 Homo sapi
262	69.4	3.1	142668	2	CR407568	CR407568 Danio rer	335	67.8	3.0	1018	3	BT003804	BT003804 Drosophil
c 263	69.4	3.1	164335	2	BX950865	BX950865 Danio rer	336	67.8	3.0	1061	8	BT009502	BT009502 Triticum
c 264	69.2	3.1	621	6	AX187131	AX187131 Sequence	337	67.8	3.0	1230	5	BC071358	BC071358 Danio rer
265	69.2	3.1	1374	5	BC053159	BC053159 Danio rer	338	67.8	3.0	1568	10	BC048399	BC048399 Mus muscu
266	69.2	3.1	1946	5	BC077411	BC077411 Xenopus l	339	67.8	3.0	1607	3	AK174679	AK174679 Ciona int
267	69.2	3.1	2534	10	BC066224	BC066224 Mus muscu	340	67.8	3.0	2117	9	BC016320	BC016320 Homo sapi
268	69.2	3.1	4250	9	HSM803434	AL832127 Homo sapi	341	67.8	3.0	5770	5	BC059180	BC059180 Danio rer
269	69	3.1	1095	5	BC066469	BC066469 Danio rer	c 342	67.8	3.0	216474	2	AC139414	AC139414 Rattus no
270	69	3.1	1490	9	BC001236	BC001236 Homo sapi	343	67.6	3.0	575	6	BD269743	BD269743 50 human
271	69	3.1	1619	9	BC032001	BC032001 Homo sapi	344	67.6	3.0	1194	9	BC016139	BC016139 Homo sapi
272	69	3.1	1684	9	BC064148	BC064148 Homo sapi	345	67.6	3.0	1227	10	BC049617	BC049617 Mus muscu
273	69	3.1	2247	8	VFA011303	AJ011303 Vicia fab	346	67.6	3.0	1271	9	BC029647	BC029647 Homo sapi
274	69	3.1	2466	9	HSM802197	AL137712 Homo sapi	347	67.6	3.0	1461	9	BC063130	BC063130 Homo sapi
c 275	68.8	3.1	392	6	CQ395758	CQ395758 Sequence	348	67.6	3.0	1478	5	BC067687	BC067687 Danio rer
c 276	68.8	3.1	392	6	CQ402088	CQ402088 Sequence	349	67.6	3.0	1497	9	AB048888	AB048888 Macaca fa
277	68.8	3.1	708	5	AY190729	AY190729 Pagrus ma	350	67.6	3.0	1638	9	BC034291	BC034291 Homo sapi
278	68.8	3.1	1051	9	AK026408	AK026408 Homo sapi	351	67.6	3.0	1661	9	BC025755	BC025755 Homo sapi
279	68.8	3.1	2325	5	BC065681	BC065681 Danio rer	c 352	67.6	3.0	1912	10	BC027060	BC027060 Mus muscu
280	68.8	3.1	2369	9	AK026627	AK026627 Homo sapi	353	67.6	3.0	1932	9	AK026947	AK026947 Homo sapi
c 281	68.6	3.1	492	6	CQ410352	CQ410352 Sequence	354	67.6	3.0	3899	6	BD191414	BD191414 Secreted
c 282	68.6	3.1	550	6	AX185654	AX185654 Sequence	355	67.6	3.0	4116	5	BC075557	BC075557 Xenopus t
283	68.6	3.1	2055	5	BC008485	BC008485 Homo sapi	356	67.6	3.0	4493	9	BC064843	BC064843 Homo sapi
284	68.6	3.1	2675	9	BC033734	BC033734 Homo sapi	357	67.6	3.0	4519	9	BC055007	BC055007 Homo sapi
c 285	68.4	3.1	396	6	AR391193	AR391193 Sequence	358	67.6	3.0	9330	3	AF466305	AF466305 Dictyoste
c 286	68.4	3.1	396	6	AR392898	AR392898 Sequence	c 359	67.6	3.0	110000	3	AC116957_2	Continuation (3 of
c 287	68.4	3.1	396	6	AR489628	AR489628 Sequence	360	67.4	3.0	453	6	CQ524875	CQ524875 Sequence
c 288	68.4	3.1	396	6	AR493869	AR493869 Sequence	c 361	67.4	3.0	545	6	AX185705	AX185705 Sequence
c 289	68.4	3.1	396	6	AX093198	AX093198 Sequence	362	67.4	3.0	1951	5	BC084252	BC084252 xenopus l
290	68.4	3.1	615	10	BC043668	BC043668 Mus muscu	363	67.4	3.0	2607	9	BC024261	BC024261 Homo sapi
c 291	68.4	3.1	627	9	BC023973	BC023973 Homo sapi	364	67.4	3.0	4176	9	BSM807871	BSM807871 Homo sapi
c 292	68.4	3.1	647	6	CQ397898	CQ397898 Sequence	365	67.4	3.0	4397	6	CQ498439	CQ498439 Sequence
c 293	68.4	3.1	647	6	CQ404191	CQ404191 Sequence	366	67.4	3.0	4485	10	BC052459	BC052459 Mus muscu
294	68.4	3.1	1323	6	BD180179	BD180179 Highly th	367	67.4	3.0	4655	10	BC064463	BC064463 Mus muscu
295	68.4	3.1	1993	9	BC013377	BC013377 Homo sapi	368	67.4	3.0	300955	1	AE016996	AE016996 Chlamydog
296	68.4	3.1	2055	8	TAU48227	U48227 Triticum ae	c 369	67.2	3.0	294	6	CQ481603	CQ481603 Sequence
297	68.4	3.1	2161	9	BC034395	BC034395 Homo sapi	c 370	67.2	3.0	376	6	CQ524552	CQ524552 Sequence
298	68.4	3.1	2239	6	A93350	A93350 Sequence 1	371	67.2	3.0	916	5	BC082880	BC082880 xenopus l
299	68.4	3.1	2239	6	AR174875	AR174875 Sequence	372	67.2	3.0	1043	6	AX188197	AX188197 Sequence
300	68.4	3.1	2239	6	AR535116	AR535116 Sequence	373	67.2	3.0	1091	6	AR271010	AR271010 Sequence
301	68.4	3.1	2239	6	BD008446	BD008446 Nucleic a	374	67.2	3.0	1091	6	AX053122	AX053122 Sequence
302	68.4	3.1	2771	6	BD209997	BD209997 Nucleic a	375	67.2	3.0	1101	9	BC050400	BC050400 Homo sapi
303	68.4	3.1	2771	6	AX010492	AX010492 Sequence	376	67.2	3.0	1343	5	BC057508	BC057508 Danio rer
304	68.4	3.1	3232	9	AF090901	AF090901 Homo sapi	377	67.2	3.0	1720	5	BC056713	BC056713 Danio rer
c 305	68.4	3.1	110000	3	AC116984_0	AC116984 Dictyoste	378	67.2	3.0	1820	9	BC035606	BC035606 Homo sapi
306	68.4	3.1	202089	2	CR382364	CR382364 Danio rer	379	67.2	3.0	1883	10	BC022165	BC022165 Mus muscu
c 307	68.2	3.0	327	6	CQ395651	CQ395651 Sequence	380	67.2	3.0	2207	10	BC066857	BC066857 Mus muscu
c 308	68.2	3.0	327	6	CQ401984	CQ401984 Sequence	381	67.2	3.0	2356	10	BC061208	BC061208 Mus muscu
309	68.2	3.0	420	8	CNS01B5E	AL113802 Botrytis	382	67.2	3.0	2465	9	BC040164	BC040164 Homo sapi
310	68.2	3.0	1069	10	BC008653	BC008653 Mus muscu	383	67.2	3.0	2672	9	BC035512	BC035512 Homo sapi
311	68.2	3.0	2258	5	BC054598	BC054598 Danio rer	384	67.2	3.0	2684	9	HSM805935	EX537504 Homo sapi

385	2923	3.0	67.2	385	Z70314 A.thaliana
386	3047	3.0	67.2	458	BC056574 Danio rer
387	3585	3.0	67.2	459	BC063072 Mus muscu
388	4041	3.0	67.2	460	BC080392 Xenopus l
C 389	346	3.0	67	461	CQ398070 Sequence
C 390	346	3.0	67	462	CQ404361 Sequence
C 391	404	3.0	67	463	CQ524546 Sequence
C 392	461	3.0	67	464	CQ410708 Sequence
C 393	768	3.0	67	465	CQ415516 Sequence
394	1006	3.0	67	466	AF111112 Homo sapi
395	1169	3.0	67	C 468	BC055454 Mus muscu
396	1309	3.0	67	469	BC009884 Homo sapi
397	1674	3.0	67	C 470	BC050418 Homo sapi
398	1709	3.0	67	C 471	AK174392 Ciona int
399	1709	3.0	67	C 472	BC032784 Homo sapi
400	1925	3.0	67	C 473	BD195666 70 human
401	1925	3.0	67	C 474	CQ775711 Sequence
402	1925	3.0	67	475	AR352721 Sequence
403	2554	3.0	67	C 476	BC022172 Mus muscu
404	2635	3.0	67	C 477	BC032204 Mus muscu
405	3447	3.0	67	478	BC052983 Homo sapi
406	3700	3.0	67	479	BC084282 Xenopus l
407	3964	3.0	67	480	BC077739 Xenopus l
408	54441	3.0	67	481	AC115584 Dictyoste
C 409	330	3.0	66.8	482	CQ410575 Sequence
C 410	445	3.0	66.8	483	CQ395672 Sequence
C 411	445	3.0	66.8	484	CQ402005 Sequence
C 412	610	3.0	66.8	485	CQ398031 Sequence
C 413	610	3.0	66.8	486	CQ404323 Sequence
414	693	3.0	66.8	487	BC042451 Homo sapi
415	1564	3.0	66.8	488	AB125186 Macaca fa
416	1660	3.0	66.8	489	AR361032 Sequence
417	1689	3.0	66.8	490	BC044066 Xenopus l
418	1693	3.0	66.8	491	BC051454 Mus muscu
419	1742	3.0	66.8	492	BC074598 Xenopus t
420	1844	3.0	66.8	493	BC007718 Homo sapi
421	4438	3.0	66.8	494	BC067016 Mus muscu
C 422	6155	3.0	66.8	495	AX323748 Sequence
423	183648	3.0	66.8	496	AC117081 Dictyoste
424	196	3.0	66.6	497	AL389939 Homo sapi
C 425	291	3.0	66.6	498	CQ399019 Sequence
C 426	291	3.0	66.6	499	CQ405298 Sequence
427	310	3.0	66.6	C 500	AX440309 Sequence
C 428	390	3.0	66.6	C 501	CQ410737 Sequence
C 429	445	3.0	66.6	C 502	CQ410337 Sequence
430	601	3.0	66.6	C 503	AJ245866 Arabidops
C 431	688	3.0	66.6	504	CQ422987 Sequence
432	936	3.0	66.6	505	BD107846 36 human
433	2150	3.0	66.6	506	BC080776 Mus muscu
434	2326	3.0	66.6	507	BC073076 Xenopus l
435	2350	3.0	66.6	508	BC038457 Homo sapi
436	2768	3.0	66.6	509	AL832391 Homo sapi
437	2826	3.0	66.6	510	BC040919 Homo sapi
438	2846	3.0	66.6	511	AR252533 Sequence
439	2846	3.0	66.6	512	AX092306 Sequence
440	2846	3.0	66.6	513	AX376102 Sequence
441	2846	3.0	66.6	514	AX403343 Sequence
442	2846	3.0	66.6	515	AY358346 Homo sapi
443	2933	3.0	66.6	516	BC063258 Mus muscu
444	3666	3.0	66.6	517	AL833816 Homo sapi
445	5149	3.0	66.6	518	BC050918 Mus muscu
C 446	228	3.0	66.4	519	CQ410517 Sequence
C 447	255	3.0	66.4	520	AX211073 Sequence
C 448	266	3.0	66.4	521	CQ475720 Sequence
C 449	300	3.0	66.4	522	CQ472434 Sequence
C 450	522	3.0	66.4	523	CQ507363 Sequence
451	556	3.0	66.4	524	BC027917 Homo sapi
452	728	3.0	66.4	525	BC032976 Mus muscu
453	1059	3.0	66.4	526	BC039808 Mus muscu
454	1159	3.0	66.4	527	AK074398 Homo sapi
455	1339	3.0	66.4	528	BC030149 Homo sapi
456	1781	3.0	66.4	529	AR300434 Sequence
457	1874	3.0	66.4	530	CQ769657 Sequence

1906	3.0	66.4	458	BC007169 Mus muscu
1927	3.0	66.4	459	AR214141 Sequence
1960	3.0	66.4	460	BC064376 Homo sapi
2034	3.0	66.4	461	BC037974 Homo sapi
2438	3.0	66.4	462	BC075617 Mus muscu
2703	3.0	66.4	463	BC084491 Xenopus t
3183	3.0	66.4	464	BC037327 Homo sapi
4515	3.0	66.4	465	AB047853 Gallus ga
4587	3.0	66.4	466	AB047852 Gallus ga
8177	3.0	66.4	467	BX537861 Homo sapi
379	3.0	66.2	C 468	CQ427910 Sequence
470	3.0	66.2	469	CQ523311 Sequence
476	3.0	66.2	C 470	CQ397629 Sequence
476	3.0	66.2	C 471	CQ403928 Sequence
693	3.0	66.2	C 472	CQ422235 Sequence
723	3.0	66.2	C 473	CQ397655 Sequence
723	3.0	66.2	C 474	CQ403953 Sequence
724	3.0	66.2	475	BC082953 Xenopus l
810	3.0	66.2	C 476	CQ398775 Sequence
810	3.0	66.2	C 477	CQ405056 Sequence
1152	3.0	66.2	478	BC015991 Homo sapi
1152	3.0	66.2	479	BC021621 Homo sapi
1378	3.0	66.2	480	BD191241 186 human
1378	3.0	66.2	481	AX924751 Sequence
1487	3.0	66.2	482	BC079692 Xenopus l
1674	3.0	66.2	483	AY070845 Drosophil
1869	3.0	66.2	484	BC028200 Homo sapi
2323	3.0	66.2	485	BD191059 186 human
2323	3.0	66.2	486	AX924569 Sequence
2335	3.0	66.2	487	BC045171 Homo sapi
2411	3.0	66.2	488	BC071111 Xenopus l
2505	3.0	66.2	489	BC061964 Rattus no
2800	3.0	66.2	490	BC014632 Homo sapi
2911	3.0	66.2	491	BC074650 Xenopus t
3507	3.0	66.2	492	BC047240 Homo sapi
4146	3.0	66.2	493	BC058389 Mus muscu
4336	3.0	66.2	494	BC079878 Mus muscu
4372	3.0	66.2	495	BC054749 Mus muscu
6742	3.0	66.2	496	BC081543 Xenopus t
146570	3.0	66.2	497	AC117076 Dictyoste
164335	3.0	66.2	498	BX950865 Danio rer
309267	3.0	66.2	499	AE017235 Mycobacte
375	2.9	66	C 500	CQ513063 Sequence
384	2.9	66	C 501	CQ395463 Sequence
384	2.9	66	C 502	CQ401799 Sequence
464	2.9	66	C 503	CQ471935 Sequence
656	2.9	66	504	BC081675 Danio rer
656	2.9	66	505	AL834413 Homo sapi
706	2.9	66	506	BC054047 Homo sapi
830	2.9	66	507	BC041445 Homo sapi
890	2.9	66	508	BC014163 Homo sapi
1181	2.9	66	509	BD191338 186 human
1181	2.9	66	510	AX924848 Sequence
1195	2.9	66	511	AL137429 Homo sapi
1212	2.9	66	512	BD191221 186 human
1212	2.9	66	513	AX924731 Sequence
1370	2.9	66	514	BC073975 Homo sapi
1445	2.9	66	515	BC040875 Homo sapi
1447	2.9	66	516	AX086256 Sequence
1464	2.9	66	517	BC021958 Homo sapi
1539	2.9	66	518	BC002373 Homo sapi
1539	2.9	66	519	BC064397 Homo sapi
1739	2.9	66	520	AK026045 Homo sapi
1785	2.9	66	521	BC067644 Danio rer
1906	2.9	66	522	BC063161 Rattus no
1963	2.9	66	523	U86674 Schistosoma
2033	2.9	66	524	BC021915 Mus muscu
2095	2.9	66	525	BC073888 Homo sapi
2166	2.9	66	526	AK025798 Homo sapi
2176	2.9	66	527	BC040224 Homo sapi
2188	2.9	66	528	BC031566 Homo sapi
2291	2.9	66	529	AK000753 Homo sapi
2360	2.9	66	530	BC063595 Homo sapi

531	66	2.9	2410	9	BC036849	BC036849 Homo sapi	604	65.6	2.9	1342	6	AR243851	AR243851 Sequence
532	66	2.9	2769	10	BC058616	BC058616 Mus muscu	605	65.6	2.9	1538	5	BC051777	BC051777 Danio rer
533	66	2.9	2833	9	HSM803718	AL832410 Homo sapi	606	65.6	2.9	1584	5	BC042270	BC042270 Xenopus l
534	66	2.9	2979	9	BC031084	BC031084 Homo sapi	607	65.6	2.9	1619	10	BC057862	BC057862 Mus muscu
535	66	2.9	3012	9	HSM808446	BX648298 Homo sapi	608	65.6	2.9	1720	10	BC058559	BC058559 Mus muscu
536	66	2.9	3116	6	AR487919	AR487919 Sequence	609	65.6	2.9	1737	10	BC081887	BC081887 Rattus no
537	66	2.9	3610	10	BC055012	BC055012 Mus muscu	610	65.6	2.9	1745	9	BC043567	BC043567 Homo sapi
538	66	2.9	3962	9	HSM807528	BX647383 Homo sapi	611	65.6	2.9	1989	10	BC047157	BC047157 Mus muscu
539	66	2.9	4154	9	HSM803629	AL832322 Homo sapi	612	65.6	2.9	2038	9	BC043591	BC043591 Homo sapi
540	66	2.9	4454	9	HSM806344	BX538143 Homo sapi	613	65.6	2.9	2039	9	HSM806781	BX640711 Homo sapi
541	66	2.9	110000	3	AC116984_1	Continuation (2 of	614	65.6	2.9	2041	9	BC065218	BC065218 Homo sapi
c 542	65.8	2.9	216	6	CQ397929	CQ397929 Sequence	615	65.6	2.9	2068	10	BC064122	BC064122 Mus muscu
c 543	65.8	2.9	216	6	CQ404221	CQ404221 Sequence	616	65.6	2.9	2352	9	S69510	S69510 cytokeratin
c 544	65.8	2.9	425	6	AX284646	AX284646 Sequence	617	65.6	2.9	3004	9	BC064983	BC064983 Homo sapi
545	65.8	2.9	522	4	AB063246	AB063246 Sus scrof	618	65.6	2.9	3110	10	BC057617	BC057617 Mus muscu
546	65.8	2.9	522	6	BD142629	BD142629 Use of po	c 619	65.6	2.9	3527	8	SCYBR281C	Z36150 S.cerevisia
547	65.8	2.9	522	6	BD181690	BD181690 Polypepti	620	65.6	2.9	4082	9	HSM805880	BX537790 Homo sapi
548	65.8	2.9	522	6	E49223	E49223 Polypeptide	c 621	65.6	2.9	5216	6	AX281348	AX281348 Sequence
549	65.8	2.9	525	9	BC034020	BC034020 Homo sapi	c 622	65.6	2.9	5216	6	AX345249	AX345249 Sequence
c 550	65.8	2.9	608	6	CQ398119	CQ398119 Sequence	c 623	65.6	2.9	32421	8	SCDPB3	X76053 S.cerevisia
c 551	65.8	2.9	608	6	CQ404407	CQ404407 Sequence	c 624	65.6	2.9	81975	2	AP000450	AP000450 Homo sapi
552	65.8	2.9	617	9	IROEST087	AL357195 Homo sapi	625	65.6	2.9	184182	2	CR352221	CR352221 Danio rer
553	65.8	2.9	638	4	AB063244	AB063244 Sus scrof	626	65.6	2.9	203687	2	BX957279	BX957279 Danio rer
554	65.8	2.9	638	6	BD142627	BD142627 Use of po	627	65.6	2.9	217000	2	AC114158	AC114158 Rattus no
555	65.8	2.9	638	6	BD181688	BD181688 Polypepti	628	65.6	2.9	225294	2	AC105897	AC105897 Rattus no
556	65.8	2.9	638	6	E49221	E49221 Polypeptide	c 629	65.4	2.9	330	6	AX185119	AX185119 Sequence
557	65.8	2.9	1065	10	BC026521	BC026521 Mus muscu	c 630	65.4	2.9	413	6	CQ427117	CQ427117 Sequence
558	65.8	2.9	1139	9	HSM807844	BX647698 Homo sapi	c 631	65.4	2.9	578	6	AX282981	AX282981 Sequence
559	65.8	2.9	1474	9	BC039576	BC039576 Homo sapi	632	65.4	2.9	578	6	AX429956	AX429956 Sequence
560	65.8	2.9	1883	6	AR528702	AR528702 Sequence	633	65.4	2.9	690	8	ATH245631	AJ245631 Arabidops
561	65.8	2.9	1883	6	AX464368	AX464368 Sequence	c 634	65.4	2.9	752	6	CQ430891	CQ430891 Sequence
562	65.8	2.9	1883	6	AX697077	AX697077 Sequence	635	65.4	2.9	753	10	BC049652	BC049652 Mus muscu
563	65.8	2.9	1883	9	AY358954	AY358954 Homo sapi	636	65.4	2.9	905	3	AF081800	AF081800 Dictyoste
564	65.8	2.9	1903	9	BC031676	BC031676 Homo sapi	637	65.4	2.9	1119	9	BC071717	BC071717 Homo sapi
565	65.8	2.9	1966	9	HSM808069	BX647923 Homo sapi	638	65.4	2.9	1311	3	BT011164	BT011164 Drosophil
566	65.8	2.9	2073	9	HSM802983	AL713655 Homo sapi	639	65.4	2.9	1312	6	AX306543	AX306543 Sequence
567	65.8	2.9	2172	9	AB096991	AB096991 Macaca fa	640	65.4	2.9	1340	9	BC064379	BC064379 Homo sapi
568	65.8	2.9	2195	5	BC079680	BC079680 Xenopus l	641	65.4	2.9	1426	3	AY069730	AY069730 Drosophil
569	65.8	2.9	2440	8	AB021862	AB021862 Cucumis m	642	65.4	2.9	1493	9	HSM805897	BX538346 Homo sapi
570	65.8	2.9	2529	10	BC054360	BC054360 Mus muscu	643	65.4	2.9	1567	9	BC058074	BC058074 Homo sapi
571	65.8	2.9	2647	9	BC043484	BC043484 Homo sapi	644	65.4	2.9	1619	10	RATWHCTMRA	L40363 Rattus norv
572	65.8	2.9	2938	5	BC057479	BC057479 Danio rer	645	65.4	2.9	1626	6	AX090420	AX090420 Sequence
573	65.8	2.9	2940	9	BC037172	BC037172 Homo sapi	646	65.4	2.9	1626	8	AY150283	AY150283 Eucalyptu
574	65.8	2.9	3145	6	CQ870633	CQ870633 Sequence	647	65.4	2.9	1663	6	BD260635	BD260635 49 human
575	65.8	2.9	3345	9	BC041132	BC041132 Homo sapi	648	65.4	2.9	1803	9	HSM807650	BX647504 Homo sapi
576	65.8	2.9	3380	9	AB062978	AB062978 Macaca fa	649	65.4	2.9	1848	9	BC053543	BC053543 Homo sapi
577	65.8	2.9	6347	10	AY035343	AY035343 Rattus no	650	65.4	2.9	1974	10	BC064004	BC064004 Mus muscu
c 578	65.8	2.9	17534	6	AX348413	AX348413 Sequence	651	65.4	2.9	2069	6	CQ845785	CQ845785 Sequence
c 579	65.8	2.9	25136	2	AC099801	AC099801 Trypanoso	652	65.4	2.9	2069	9	AK131389	AK131389 Homo sapi
c 580	65.8	2.9	219941	2	AC099717	AC099717 Mus muscu	653	65.4	2.9	2115	5	BC051611	BC051611 Danio rer
581	65.6	2.9	249	6	AR424795	AR424795 Sequence	654	65.4	2.9	2533	9	HSM803787	AL8332479 Homo sapi
582	65.6	2.9	249	6	AX985489	AX985489 Sequence	655	65.4	2.9	2608	6	BD250066	BD250066 48 human
583	65.6	2.9	249	6	BD120348	BD120348 EST and e	656	65.4	2.9	2735	9	BC046366	BC046366 Homo sapi
c 584	65.6	2.9	319	6	CQ399044	CQ399044 Sequence	657	65.4	2.9	2817	9	BC000556	BC000556 Homo sapi
c 585	65.6	2.9	319	6	CQ405323	CQ405323 Sequence	658	65.4	2.9	3200	10	BC049178	BC049178 Mus muscu
c 586	65.6	2.9	372	6	CQ505680	CQ505680 Sequence	659	65.4	2.9	3295	10	BC005469	BC005469 Mus muscu
c 587	65.6	2.9	394	6	CQ410884	CQ410884 Sequence	660	65.4	2.9	3301	10	BC029098	BC029098 Mus muscu
588	65.6	2.9	429	6	CQ526617	CQ526617 Sequence	661	65.4	2.9	3490	10	BC028819	BC028819 Mus muscu
589	65.6	2.9	442	6	CQ522574	CQ522574 Sequence	662	65.4	2.9	3682	10	BC052169	BC052169 Mus muscu
590	65.6	2.9	572	5	AY612425	AY612425 Rhinobato	663	65.4	2.9	3826	5	BC060479	BC060479 Xenopus l
591	65.6	2.9	599	9	BC035333	BC035333 Homo sapi	664	65.4	2.9	3826	9	BC051756	BC051756 Homo sapi
592	65.6	2.9	604	6	BD270370	BD270370 50 human	665	65.4	2.9	4726	9	HSM808819	BX648668 Homo sapi
593	65.6	2.9	673	5	BC055524	BC055524 Danio rer	666	65.4	2.9	5143	10	BC035523	BC035523 Mus muscu
594	65.6	2.9	720	10	BC083088	BC083088 Mus muscu	667	65.4	2.9	145032	2	BX890579	BX890579 Danio rer
595	65.6	2.9	942	5	BC057474	BC057474 Danio rer	c 668	65.4	2.9	158504	2	AC107810	AC107810 Mus muscu
596	65.6	2.9	961	9	AK000718	AK000718 Homo sapi	c 669	65.2	2.9	318	6	CQ399318	CQ399318 Sequence
597	65.6	2.9	989	5	BC083533	BC083533 Danio rer	c 670	65.2	2.9	318	6	CQ405595	CQ405595 Sequence
598	65.6	2.9	1084	9	BC026265	BC026265 Homo sapi	c 671	65.2	2.9	327	6	CQ474244	CQ474244 Sequence
599	65.6	2.9	1180	6	BD132791	BD132791 Apo-2Dcr.	c 672	65.2	2.9	337	6	CQ529058	CQ529058 Sequence
600	65.6	2.9	1180	6	BD132792	BD132792 Apo-2Dcr.	c 673	65.2	2.9	368	6	CQ422024	CQ422024 Sequence
601	65.6	2.9	1180	9	AF012536	AF012536 Homo sapi	c 674	65.2	2.9	566	6	CQ410439	CQ410439 Sequence
602	65.6	2.9	1330	10	BC064023	BC064023 Mus muscu	c 675	65.2	2.9	643	6	AX186197	AX186197 Sequence
603	65.6	2.9	1342	6	BD223153	BD223153 98 human	676	65.2	2.9	773	6	BD072968	BD072968 70 human

677	65.2	2.9	776	8	AB007819	AB007819 Citrus un	750	65	2.9	2924	9	BC063554	BC063554 Homo sapi
678	65.2	2.9	931	9	BC010286	BC010286 Homo sapi	751	65	2.9	2970	9	BC064624	BC064624 Homo sapi
679	65.2	2.9	933	10	BC048388	BC048388 Mus muscu	752	65	2.9	3124	10	BC052923	BC052923 Mus muscu
680	65.2	2.9	987	8	CLJACOIV	X57832 C.lacryma-j	753	65	2.9	3250	5	BC068779	BC068779 Xenopus l
681	65.2	2.9	1064	9	BC047708	BC047708 Homo sapi	754	65	2.9	3250	9	BC063474	BC063474 Homo sapi
682	65.2	2.9	1250	9	BC033385	BC033385 Homo sapi	755	65	2.9	3660	10	BC051069	BC051069 Mus muscu
683	65.2	2.9	1344	8	BT009299	BT009299 Triticum	756	65	2.9	3916	10	BC018439	BC018439 Mus muscu
684	65.2	2.9	1360	10	BC010258	BC010258 Mus muscu	757	65	2.9	4223	10	BC058958	BC058958 Mus muscu
685	65.2	2.9	1375	3	AK115965	AK115965 Ciona int	758	65	2.9	4236	5	BC071048	BC071048 Xenopus l
686	65.2	2.9	1480	9	BC032007	BC032007 Homo sapi	759	65	2.9	4260	9	BC033735	BC033735 Homo sapi
687	65.2	2.9	1513	6	AX320874	AX320874 Sequence	c 760	65	2.9	4990	6	CQ493127	CQ493127 Sequence
688	65.2	2.9	1600	10	BC042579	BC042579 Mus muscu	c 761	65	2.9	4990	6	CQ493522	CQ493522 Sequence
689	65.2	2.9	1720	9	BC053999	BC053999 Homo sapi	762	64.8	2.9	201	11	BV200403	BV200403 sqnm20407
690	65.2	2.9	1734	6	AX092320	AX092320 Sequence	763	64.8	2.9	214	6	CQ487824	CQ487824 Sequence
691	65.2	2.9	1734	6	AX358902	AX358902 Sequence	764	64.8	2.9	247	6	CQ524135	CQ524135 Sequence
692	65.2	2.9	1734	6	AX362395	AX362395 Sequence	765	64.8	2.9	249	6	AR424794	AR424794 Sequence
693	65.2	2.9	1734	6	AX376134	AX376134 Sequence	766	64.8	2.9	249	6	AX985488	AX985488 Sequence
694	65.2	2.9	1734	6	AX403750	AX403750 Sequence	767	64.8	2.9	249	6	BD120347	BD120347 EST and e
695	65.2	2.9	1734	6	AX454564	AX454564 Sequence	768	64.8	2.9	278	6	CQ517619	CQ517619 Sequence
696	65.2	2.9	1734	6	AX491042	AX491042 Sequence	769	64.8	2.9	296	6	CQ466754	CQ466754 Sequence
697	65.2	2.9	1734	6	AX696983	AX696983 Sequence	c 770	64.8	2.9	474	6	AX284811	AX284811 Sequence
698	65.2	2.9	1734	9	AY358412	AY358412 Homo sapi	c 771	64.8	2.9	533	6	CQ410881	CQ410881 Sequence
699	65.2	2.9	1821	9	BC004951	BC004951 Homo sapi	772	64.8	2.9	538	9	BC071930	BC071930 Homo sapi
700	65.2	2.9	1845	9	HSM800467	AL050172 Homo sapi	c 773	64.8	2.9	539	6	CQ398781	CQ398781 Sequence
701	65.2	2.9	1944	5	BC068212	BC068212 Xenopus t	c 774	64.8	2.9	539	6	CQ405062	CQ405062 Sequence
702	65.2	2.9	2208	9	BC016137	BC016137 Homo sapi	c 775	64.8	2.9	539	6	CQ410791	CQ410791 Sequence
703	65.2	2.9	2347	10	BC055476	BC055476 Mus muscu	c 776	64.8	2.9	703	6	BD276320	BD276320 MOLECULES
704	65.2	2.9	2469	3	AK116766	AK116766 Ciona int	c 777	64.8	2.9	703	6	AX049467	AX049467 Sequence
705	65.2	2.9	2489	5	BC068397	BC068397 Danio rer	778	64.8	2.9	770	3	AK174296	AK174296 Ciona int
706	65.2	2.9	2490	5	BC066711	BC066711 Danio rer	779	64.8	2.9	836	5	BC075785	BC075785 Danio rer
707	65.2	2.9	2846	9	HSM802834	AL442082 Homo sapi	780	64.8	2.9	935	10	BC049727	BC049727 Mus muscu
708	65.2	2.9	2930	9	BC037961	BC037961 Homo sapi	781	64.8	2.9	935	10	BC049693	BC049693 Mus muscu
709	65.2	2.9	3000	9	BC040558	BC040558 Homo sapi	782	64.8	2.9	946	3	AY089358	AY089358 Drosophil
710	65.2	2.9	3340	5	AF364811	AF364811 Danio rer	783	64.8	2.9	998	8	AB079024	AB079024 Nicotiana
711	65.2	2.9	3399	9	BC063840	BC063840 Homo sapi	784	64.8	2.9	1374	3	AK173685	AK173685 Ciona int
712	65.2	2.9	3796	5	BC066783	BC066783 Xenopus t	785	64.8	2.9	1479	9	BC018977	BC018977 Homo sapi
713	65.2	2.9	4091	9	HSM803794	AL8322486 Homo sapi	786	64.8	2.9	1500	9	BC036767	BC036767 Homo sapi
714	65.2	2.9	4504	9	HSM803661	AL832353 Homo sapi	787	64.8	2.9	1551	9	AK027104	AK027104 Homo sapi
715	65.2	2.9	5929	9	HSM806922	BX640814 Homo sapi	788	64.8	2.9	1597	5	BC055126	BC055126 Danio rer
c 716	65	2.9	281	6	CQ410312	CQ410312 Sequence	789	64.8	2.9	1761	9	BC006103	BC006103 Homo sapi
717	65	2.9	298	6	CQ527058	CQ527058 Sequence	790	64.8	2.9	1815	9	BC028038	BC028038 Homo sapi
c 718	65	2.9	336	6	CQ397671	CQ397671 Sequence	791	64.8	2.9	1836	5	BC054588	BC054588 Danio rer
c 719	65	2.9	336	6	CQ403968	CQ403968 Sequence	792	64.8	2.9	1839	8	D14059	D14059 Ananas como
c 720	65	2.9	346	6	CQ410605	CQ410605 Sequence	793	64.8	2.9	2156	6	AX098198	AX098198 Sequence
c 721	65	2.9	388	6	AX070834	AX070834 Sequence	794	64.8	2.9	2170	10	BC052486	BC052486 Mus muscu
722	65	2.9	514	9	AK000450	AK000450 Homo sapi	795	64.8	2.9	2181	9	BC037561	BC037561 Homo sapi
c 723	65	2.9	565	6	CQ410458	CQ410458 Sequence	796	64.8	2.9	2190	9	BC063454	BC063454 Homo sapi
c 724	65	2.9	599	6	BD210257	BD210257 Human gen	797	64.8	2.9	2194	5	BC072042	BC072042 Xenopus l
725	65	2.9	749	9	BC008417	BC008417 Homo sapi	798	64.8	2.9	2203	9	BC020540	BC020540 Homo sapi
726	65	2.9	762	5	BC062844	BC062844 Danio rer	799	64.8	2.9	2305	10	BC005428	BC005428 Mus muscu
727	65	2.9	828	10	BC049756	BC049756 Mus muscu	800	64.8	2.9	2332	6	CQ414481	CQ414481 Sequence
728	65	2.9	912	10	RNY17327	Y17327 Rattus norv	801	64.8	2.9	2370	10	BC029024	BC029024 Mus muscu
729	65	2.9	1037	8	AY046929	AY046929 Oryza sat	802	64.8	2.9	2407	10	BC058192	BC058192 Mus muscu
730	65	2.9	1095	9	HSM801185	AL117648 Homo sapi	803	64.8	2.9	2410	5	BC077410	BC077410 Xenopus l
731	65	2.9	1154	9	HSM808002	BX647856 Homo sapi	804	64.8	2.9	2590	9	BC073988	BC073988 Homo sapi
732	65	2.9	1290	5	BC065608	BC065608 Danio rer	805	64.8	2.9	2658	9	BC027867	BC027867 Homo sapi
733	65	2.9	1308	9	BC021569	BC021569 Homo sapi	806	64.8	2.9	2870	9	HSM800882	AL110225 Homo sapi
734	65	2.9	1316	10	BC018263	BC018263 Mus muscu	807	64.8	2.9	2888	3	DMGELS	X75630 D.melanogas
735	65	2.9	1366	9	BC043379	BC043379 Homo sapi	808	64.8	2.9	3061	9	BC008751	BC008751 Homo sapi
736	65	2.9	1383	5	BC053308	BC053308 Danio rer	809	64.8	2.9	3080	10	BC052728	BC052728 Mus muscu
737	65	2.9	1403	9	BC005858	BC005858 Homo sapi	810	64.8	2.9	3080	10	BC064444	BC064444 Mus muscu
738	65	2.9	1447	9	BC020589	BC020589 Homo sapi	811	64.8	2.9	3114	5	BC080333	BC080333 Xenopus t
739	65	2.9	1455	5	BC053247	BC053247 Danio rer	812	64.8	2.9	3269	5	BC073066	BC073066 Xenopus l
740	65	2.9	1500	5	BC065586	BC065586 Danio rer	813	64.8	2.9	3309	10	BC051423	BC051423 Mus muscu
741	65	2.9	1560	8	BT009323	BT009323 Triticum	814	64.8	2.9	3473	9	BC030601	BC030601 Homo sapi
742	65	2.9	1605	9	BC065230	BC065230 Homo sapi	815	64.8	2.9	3513	6	AX277590	AX277590 Sequence
743	65	2.9	1637	5	BC067576	BC067576 Danio rer	816	64.8	2.9	4265	9	HSM806990	BX640873 Homo sapi
744	65	2.9	1695	3	AK112719	AK112719 Ciona int	817	64.8	2.9	4710	10	BC060613	BC060613 Mus muscu
745	65	2.9	1748	9	BC027853	BC027853 Homo sapi	818	64.8	2.9	302156	3	AC116977	AC116977 Dictyoste
746	65	2.9	2101	5	BC067661	BC067661 Danio rer	819	64.6	2.9	198	6	CQ487384	CQ487384 Sequence
747	65	2.9	2231	5	BC081288	BC081288 Xenopus t	820	64.6	2.9	201	11	BV207631	BV207631 sqnm22410
748	65	2.9	2486	3	CEU23830	U23830 Caenorhabdi	821	64.6	2.9	212	6	CQ677317	CQ677317 Sequence
749	65	2.9	2833	9	HSM802926	AL512765 Homo sapi	c 822	64.6	2.9	267	6	CQ410745	CQ410745 Sequence

823	64.6	2.9	285	6	AX284863	AX284863 Sequence	896	64.6	2.9	33899	2	AC149412	AC149412 Phakopsor
C 824	64.6	2.9	309	6	CQ398213	CQ398213 Sequence	C 897	64.6	2.9	36188	3	AC116922	AC116922 Dictyoste
C 825	64.6	2.9	309	6	CQ404500	CQ404500 Sequence	C 898	64.6	2.9	194593	2	AC139989	AC139989 Rattus no
826	64.6	2.9	358	6	CQ671266	CQ671266 Sequence	899	64.6	2.9	271546	3	AE014843	AE014843 Plasmodiu
827	64.6	2.9	384	6	BD275366	BD275366 49 Human	C 900	64.6	2.9	349980	6	AX344558	AX344558 Sequence
828	64.6	2.9	414	9	BC061644	BC061644 Homo sapi	901	64.4	2.9	177	6	AR413410	AR413410 Sequence
829	64.6	2.9	550	6	CQ525224	CQ525224 Sequence	902	64.4	2.9	177	6	AX970244	AX970244 Sequence
C 830	64.6	2.9	556	6	CQ508215	CQ508215 Sequence	903	64.4	2.9	177	6	BD108963	BD108963 EST and e
C 831	64.6	2.9	556	6	CQ508315	CQ508315 Sequence	904	64.4	2.9	268	6	AR412436	AR412436 Sequence
C 832	64.6	2.9	556	6	CQ510257	CQ510257 Sequence	905	64.4	2.9	268	6	AX969270	AX969270 Sequence
C 833	64.6	2.9	556	6	CQ511753	CQ511753 Sequence	906	64.4	2.9	268	6	BD107989	BD107989 EST and e
C 834	64.6	2.9	695	6	CQ423017	CQ423017 Sequence	907	64.4	2.9	300	3	AF153692	AF153692 Mesobuthu
835	64.6	2.9	794	9	BC058920	BC058920 Homo sapi	C 908	64.4	2.9	393	6	CQ408183	CQ408183 Sequence
836	64.6	2.9	860	6	BD260192	BD260192 50 human	909	64.4	2.9	395	3	AF151795	AF151795 Butthus ma
837	64.6	2.9	913	5	BC041718	BC041718 Xenopus l	C 910	64.4	2.9	402	6	CQ411023	CQ411023 Sequence
838	64.6	2.9	920	10	BC027780	BC027780 Mus muscu	911	64.4	2.9	444	6	CQ524602	CQ524602 Sequence
839	64.6	2.9	931	10	BC049725	BC049725 Mus muscu	C 912	64.4	2.9	673	6	CQ397868	CQ397868 Sequence
840	64.6	2.9	935	5	BC071066	BC071066 Xenopus l	C 913	64.4	2.9	673	6	CQ404162	CQ404162 Sequence
841	64.6	2.9	1024	3	AK174562	AK174562 Ciona int	914	64.4	2.9	691	5	BC071138	BC071138 Xenopus l
842	64.6	2.9	1032	10	BC002285	BC002285 Mus muscu	915	64.4	2.9	738	9	HSM806309	BX538116 Homo sapi
843	64.6	2.9	1044	10	BC049565	BC049565 Mus muscu	916	64.4	2.9	805	10	BC063183	BC063183 Rattus no
844	64.6	2.9	1058	9	BC053997	BC053997 Homo sapi	917	64.4	2.9	916	3	RPU61144	U61144 Rhodnius pr
845	64.6	2.9	1108	8	AF378131	AF378131 Zantedesc	918	64.4	2.9	916	6	E12747	E12747 Rhodnius pr
846	64.6	2.9	1118	9	AK000652	AK000652 Homo sapi	919	64.4	2.9	916	6	E17385	E17385 cDNA encodi
847	64.6	2.9	1162	8	AF275315	AF275315 Lotus jap	920	64.4	2.9	1022	8	AY044236	AY044236 Lycopersi
848	64.6	2.9	1180	5	BC066714	BC066714 Danio rer	921	64.4	2.9	1138	9	HSM802391	AL137627 Homo sapi
849	64.6	2.9	1254	6	BD276346	BD276346 143 Human	922	64.4	2.9	1372	8	ATCOQ3	Y15055 Arabidopsis
850	64.6	2.9	1260	9	BC042335	BC042335 Homo sapi	923	64.4	2.9	1410	10	BC061781	BC061781 Rattus no
851	64.6	2.9	1341	9	BC043518	BC043518 Homo sapi	924	64.4	2.9	1436	5	BC074511	BC074511 Xenopus t
852	64.6	2.9	1359	5	BC053194	BC053194 Danio rer	925	64.4	2.9	1500	9	BC056861	BC056861 Homo sapi
853	64.6	2.9	1457	9	BC056863	BC056863 Homo sapi	926	64.4	2.9	1560	3	AF061281	AF061281 Dictyoste
854	64.6	2.9	1521	10	BC083563	BC083563 Rattus no	927	64.4	2.9	1567	9	AB047887	AB047887 Macaca fa
855	64.6	2.9	1545	10	BC067396	BC067396 Mus muscu	928	64.4	2.9	1616	10	BC010209	BC010209 Mus muscu
856	64.6	2.9	1569	10	HSM83659	BC083659 Rattus no	929	64.4	2.9	1700	9	BC072389	BC072389 Homo sapi
857	64.6	2.9	1572	9	BC0808149	BX648003 Homo sapi	930	64.4	2.9	1731	9	BC012800	BC012800 Homo sapi
858	64.6	2.9	1706	5	BC082351	BC082351 Xenopus l	931	64.4	2.9	1775	9	BC039831	BC039831 Homo sapi
859	64.6	2.9	1769	9	BC025749	BC025749 Homo sapi	932	64.4	2.9	1776	10	BC024054	BC024054 Mus muscu
860	64.6	2.9	1793	3	AK112657	AK112657 Ciona int	933	64.4	2.9	1780	3	AK115159	AK115159 Ciona int
861	64.6	2.9	1903	10	BC023012	BC023012 Mus muscu	934	64.4	2.9	1808	6	AX535019	AX535019 Sequence
862	64.6	2.9	1925	9	BC050524	BC050524 Homo sapi	935	64.4	2.9	1865	10	BC054438	BC054438 Mus muscu
863	64.6	2.9	1950	9	BC028206	BC028206 Homo sapi	936	64.4	2.9	1899	6	AX055388	AX055388 Sequence
864	64.6	2.9	2079	5	BC084664	BC084664 Xenopus l	937	64.4	2.9	1899	6	AX077025	AX077025 Sequence
865	64.6	2.9	2122	9	BC037277	BC037277 Homo sapi	938	64.4	2.9	1899	6	AX080781	AX080781 Sequence
866	64.6	2.9	2131	5	BC047846	BC047846 Danio rer	939	64.4	2.9	1899	6	AX574484	AX574484 Sequence
867	64.6	2.9	2207	9	BC043549	BC043549 Homo sapi	940	64.4	2.9	1899	9	AY358921	AY358921 Homo sapi
868	64.6	2.9	2234	5	BC053153	BC053153 Danio rer	941	64.4	2.9	1920	10	BC061765	BC061765 Rattus no
869	64.6	2.9	2246	6	AR212256	AR212256 Sequence	C 942	64.4	2.9	1946	3	DDIRRS	LJ36941 Dictyosteli
870	64.6	2.9	2246	6	AR265251	AR265251 Sequence	943	64.4	2.9	1982	3	CEL427855	AJ427855 Caenorhab
871	64.6	2.9	2246	10	AF017152	AF017152 Mus muscu	944	64.4	2.9	2062	8	WHTTEFLX	M90077 Wheat trans
872	64.6	2.9	2307	5	BC070730	BC070730 Xenopus l	945	64.4	2.9	2085	5	BC077186	BC077186 Xenopus l
873	64.6	2.9	2330	5	BC064863	BC064863 Xenopus t	946	64.4	2.9	2085	9	BC029120	BC029120 Homo sapi
874	64.6	2.9	2345	10	BC052187	BC052187 Mus muscu	947	64.4	2.9	2106	9	BC027948	BC027948 Homo sapi
875	64.6	2.9	2390	9	AF090900	AF090900 Homo sapi	948	64.4	2.9	2143	9	BC023358	BC023358 Homo sapi
876	64.6	2.9	2445	10	BC005514	BC005514 Mus muscu	949	64.4	2.9	2219	4	AB044390	AB044390 Sus scrof
877	64.6	2.9	2524	5	BC045217	BC045217 Xenopus l	950	64.4	2.9	2291	6	AR274977	AR274977 Sequence
878	64.6	2.9	2576	5	BC057416	BC057416 Danio rer	951	64.4	2.9	2291	6	AR559328	AR559328 Sequence
879	64.6	2.9	2677	9	BC050385	BC050385 Homo sapi	952	64.4	2.9	2291	9	HSU42031	U42031 Human 54 kD
880	64.6	2.9	2730	9	BC053349	BC053349 Homo sapi	953	64.4	2.9	2363	9	AB056372	AB056372 Macaca fa
881	64.6	2.9	2754	10	BC066817	BC066817 Mus muscu	954	64.4	2.9	2371	9	HSM805927	BX537833 Homo sapi
882	64.6	2.9	3092	9	BC043441	BC043441 Homo sapi	955	64.4	2.9	2604	9	BC032396	BC032396 Homo sapi
883	64.6	2.9	3413	9	BC064848	BC064848 Homo sapi	956	64.4	2.9	2621	10	BC052772	BC052772 Mus muscu
884	64.6	2.9	4299	9	HSM807262	BX647118 Homo sapi	957	64.4	2.9	2626	9	BC036765	BC036765 Homo sapi
885	64.6	2.9	4362	9	HSM805498	AL834414 Homo sapi	958	64.4	2.9	2703	9	BC063394	BC063394 Homo sapi
886	64.6	2.9	4438	9	HSM807504	BX647360 Homo sapi	959	64.4	2.9	2832	9	BC041896	BC041896 Homo sapi
887	64.6	2.9	4508	10	BC053013	BC053013 Mus muscu	960	64.4	2.9	2875	9	HSM808745	BX648594 Homo sapi
888	64.6	2.9	4640	6	AX376008	AX376008 Sequence	961	64.4	2.9	2914	10	BC050274	BC050274 Mus muscu
889	64.6	2.9	4649	6	CQ767646	CQ767646 Sequence	962	64.4	2.9	3095	9	HSM804691	AL833378 Homo sapi
890	64.6	2.9	4649	9	AY358647	AY358647 Homo sapi	963	64.4	2.9	3218	9	BC050412	BC050412 Homo sapi
891	64.6	2.9	4669	5	BC048022	BC048022 Xenopus l	964	64.4	2.9	3300	9	BC011656	BC011656 Homo sapi
892	64.6	2.9	4727	5	BC070018	BC070018 Danio rer	965	64.4	2.9	3724	5	BC068927	BC068927 Xenopus l
893	64.6	2.9	5000	10	BC058783	BC058783 Mus muscu	966	64.4	2.9	3763	9	BC025767	BC025767 Homo sapi
894	64.6	2.9	12178	10	AF466694	AF466694 Rattus no	967	64.4	2.9	3782	9	HSM804515	AL833204 Homo sapi
C 895	64.6	2.9	23499	2	AC149322	AC149322 Phakopsor	968	64.4	2.9	3894	10	BC053925	BC053925 Mus muscu

969	64.4	2.9	4381	9	HSM808410	BX648262 Homo sapi	1042	64	2.9	240	6	AX284880	AX284880 Sequence
970	64.4	2.9	4454	3	AY070553	AY070553 Drosophil	c1043	64	2.9	281	6	CQ529993	CQ529993 Sequence
971	64.4	2.9	4753	10	BC058514	BC058514 Mus muscu	c1044	64	2.9	299	6	CQ397773	CQ397773 Sequence
972	64.4	2.9	4981	9	HSM805684	BX537363 Homo sapi	c1045	64	2.9	299	6	CQ404070	CQ404070 Sequence
C 973	64.4	2.9	105320	3	AC116920	AC116920 Dictyoste	c1046	64	2.9	311	3	AF159977	AF159977 Butus ma
C 974	64.4	2.9	110000	3	AC116305	AC116305 Dictyoste	c1047	64	2.9	314	6	CQ472429	CQ472429 Sequence
C 975	64.4	2.9	111079	9	HS419C19	AL035407 Human DNA	c1048	64	2.9	337	6	CQ527057	CQ527057 Sequence
C 976	64.4	2.9	155657	10	AC124454	AC124454 Mus muscu	c1049	64	2.9	388	6	CQ410454	CQ410454 Sequence
977	64.4	2.9	200578	2	AC147296	AC147296 Pan trogl	c1050	64	2.9	398	8	BT008934	BT008934 Triticum
C 978	64.4	2.9	270418	1	AE017303	AE017303 Thermus t	c1051	64	2.9	416	6	CQ484252	CQ484252 Sequence
C 979	64.4	2.9	349980	6	CQ870473	CQ870473 Sequence	c1052	64	2.9	507	6	CQ397890	CQ397890 Sequence
980	64.2	2.9	373	6	CQ526228	CQ526228 Sequence	c1053	64	2.9	507	6	CQ404183	CQ404183 Sequence
981	64.2	2.9	381	3	AF159974	AF159974 Butus ma	c1054	64	2.9	533	6	AX184534	AX184534 Sequence
982	64.2	2.9	523	6	CQ522700	CQ522700 Sequence	c1055	64	2.9	709	8	AB053296	AB053296 Oryza sat
983	64.2	2.9	844	9	BC009571	BC009571 Homo sapi	c1056	64	2.9	790	3	AF040384	AF040384 Schistos
984	64.2	2.9	923	5	BC084674	BC084674 Xenopus l	c1057	64	2.9	845	9	BC044653	BC044653 Homo sapi
985	64.2	2.9	942	5	BC049498	BC049498 Danio rer	c1058	64	2.9	896	3	AY055470	AY055470 Lucilia c
986	64.2	2.9	989	8	CPCR7	Y08243 C.pteroides	c1059	64	2.9	935	10	BC061157	BC061157 Mus muscu
987	64.2	2.9	1108	9	BC018104	BC018104 Homo sapi	c1060	64	2.9	1023	9	BC063642	BC063642 Homo sapi
988	64.2	2.9	1174	9	AF094850	AF094850 Homo sapi	c1061	64	2.9	1098	6	AR105082	AR105082 Sequence
989	64.2	2.9	1267	3	AY122138	AY122138 Drosophil	c1062	64	2.9	1098	8	AF244681	AF244681 Zea mays
990	64.2	2.9	1343	10	S63521	S63521 glucose-reg	c1063	64	2.9	1129	10	BC060535	BC060535 Rattus no
991	64.2	2.9	1349	9	BC065039	BC065039 Homo sapi	c1064	64	2.9	1162	8	AF117707	AF117707 Lycopersi
992	64.2	2.9	1390	3	AK174654	AK174654 Ciona int	c1065	64	2.9	1164	6	AX098194	AX098194 Sequence
993	64.2	2.9	1432	10	BC026548	BC026548 Mus muscu	c1066	64	2.9	1178	10	BC012273	BC012273 Mus muscu
994	64.2	2.9	1441	6	A65340	A65340 Sequence 63	c1067	64	2.9	1221	5	BC082954	BC082954 Xenopus l
995	64.2	2.9	1441	6	AR150478	AR150478 Sequence	c1068	64	2.9	1260	5	BC065590	BC065590 Danio rer
996	64.2	2.9	1451	9	AF028823	AF028823 Homo sapi	c1069	64	2.9	1314	9	BC012733	BC012733 Homo sapi
997	64.2	2.9	1547	10	BC058197	BC058197 Mus muscu	c1070	64	2.9	1318	9	BC002359	BC002359 Homo sapi
998	64.2	2.9	1553	9	BC017440	BC017440 Homo sapi	c1071	64	2.9	1319	9	BC015490	BC015490 Homo sapi
999	64.2	2.9	1673	10	BC010324	BC010324 Mus muscu	c1072	64	2.9	1331	6	CQ776637	CQ776637 Sequence
1000	64.2	2.9	1860	9	BC063016	BC063016 Homo sapi	c1073	64	2.9	1338	5	BC064198	BC064198 Xenopus t
1001	64.2	2.9	1960	10	BC061459	BC061459 Mus muscu	c1074	64	2.9	1387	3	AY069134	AY069134 Drosophil
1002	64.2	2.9	1985	6	BD172402	BD172402 Secreted	c1075	64	2.9	1422	5	BC080890	BC080890 Xenopus t
1003	64.2	2.9	1985	6	BD172721	BD172721 Secreted	c1076	64	2.9	1544	6	AR255999	AR255999 Sequence
1004	64.2	2.9	1985	6	BD173040	BD173040 Secreted	c1077	64	2.9	1555	9	AB063070	AB063070 Macaca fa
1005	64.2	2.9	1985	6	BD173359	BD173359 Secreted	c1078	64	2.9	1568	10	BC003796	BC003796 Mus muscu
1006	64.2	2.9	1985	6	BD175393	BD175393 Secretary	c1079	64	2.9	1570	5	BC074376	BC074376 Xenopus l
1007	64.2	2.9	1985	6	CQ881212	CQ881212 Sequence	c1080	64	2.9	1592	5	BC074590	BC074590 Xenopus t
1008	64.2	2.9	1985	6	AR410771	AR410771 Sequence	c1081	64	2.9	1593	5	BC080114	BC080114 Xenopus l
1009	64.2	2.9	1985	6	AR439135	AR439135 Sequence	c1082	64	2.9	1616	10	BC026899	BC026899 Mus muscu
1010	64.2	2.9	1985	6	AR473155	AR473155 Sequence	c1083	64	2.9	1645	10	BC039761	BC039761 Mus muscu
1011	64.2	2.9	1985	6	AR527141	AR527141 Sequence	c1084	64	2.9	1827	5	AB105880	AB105880 Oryzias l
1012	64.2	2.9	1985	6	AR566174	AR566174 Sequence	c1085	64	2.9	1865	9	BC047609	BC047609 Homo sapi
1013	64.2	2.9	1985	6	AX375960	AX375960 Sequence	c1086	64	2.9	1952	9	BC002343	BC002343 Homo sapi
1014	64.2	2.9	1985	6	AX697621	AX697621 Sequence	c1087	64	2.9	1957	9	BC006494	BC006494 Homo sapi
1015	64.2	2.9	1985	6	BD075542	BD075542 Secretary	c1088	64	2.9	1957	9	BC006516	BC006516 Homo sapi
1016	64.2	2.9	1985	9	AY358500	AY358500 Homo sapi	c1089	64	2.9	1991	9	BC037532	BC037532 Homo sapi
1017	64.2	2.9	2023	9	BC025685	BC025685 Homo sapi	c1090	64	2.9	2066	10	BC046399	BC046399 Mus muscu
1018	64.2	2.9	2138	10	BC035945	BC035945 Mus muscu	c1091	64	2.9	2116	10	BC030862	BC030862 Mus muscu
1019	64.2	2.9	2186	10	BC079471	BC079471 Rattus no	c1092	64	2.9	2137	9	BC033678	BC033678 Homo sapi
1020	64.2	2.9	2348	10	BC057177	BC057177 Mus muscu	c1093	64	2.9	2145	9	BC037968	BC037968 Homo sapi
1021	64.2	2.9	2360	9	BC065193	BC065193 Homo sapi	c1094	64	2.9	2167	10	BC028325	BC028325 Mus muscu
1022	64.2	2.9	2385	6	BD186882	BD186882 Nucleic a	c1095	64	2.9	2223	5	BC067619	BC067619 Danio rer
1023	64.2	2.9	2426	9	BC004874	BC004874 Homo sapi	c1096	64	2.9	2245	9	BC028076	BC028076 Homo sapi
1024	64.2	2.9	2487	6	BD074862	BD074862 Secreted	c1097	64	2.9	2312	9	AK000250	AK000250 Homo sapi
1025	64.2	2.9	2975	9	BC012172	BC012172 Homo sapi	c1098	64	2.9	2420	9	BC072670	BC072670 Homo sapi
1026	64.2	2.9	3309	9	BC017311	BC017311 Homo sapi	c1099	64	2.9	2439	10	BC017643	BC017643 Mus muscu
1027	64.2	2.9	3399	5	BC077830	BC077830 Xenopus l	c1100	64	2.9	2489	10	BC055307	BC055307 Mus muscu
1028	64.2	2.9	3505	9	HSM806327	BX537608 Homo sapi	c1101	64	2.9	2517	5	BC063218	BC063218 Xenopus t
1029	64.2	2.9	3520	9	BC053544	BC053544 Homo sapi	c1102	64	2.9	2533	8	AY161310	AY161310 Pisum sat
1030	64.2	2.9	3544	10	BC042521	BC042521 Mus muscu	c1103	64	2.9	2656	9	BC071753	BC071753 Homo sapi
1031	64.2	2.9	3674	10	BC058943	BC058943 Mus muscu	c1104	64	2.9	2698	5	BC053122	BC053122 Danio rer
1032	64.2	2.9	3992	10	BC062650	BC062650 Mus muscu	c1105	64	2.9	2890	10	BC036168	BC036168 Mus muscu
1033	64.2	2.9	4069	9	BC054003	BC054003 Homo sapi	c1106	64	2.9	3010	9	BC075802	BC075802 Homo sapi
1034	64.2	2.9	4500	9	BC035514	BC035514 Homo sapi	c1107	64	2.9	3094	9	AB047609	AB047609 Macaca fa
C1035	64.2	2.9	14006	6	AX346860	AX346860 Sequence	c1108	64	2.9	3220	9	BC064576	BC064576 Homo sapi
1036	64.2	2.9	110000	3	AC116957	AC116957 Dictyoste	c1109	64	2.9	3315	9	BC037319	BC037319 Homo sapi
1037	64.2	2.9	161200	2	AC109190	AC109190 Mus muscu	c1110	64	2.9	3599	9	BC064543	BC064543 Homo sapi
C1038	64.2	2.9	182870	3	AC116960	AC116960 Dictyoste	c1111	64	2.9	4356	9	BC022792	BC022792 Homo sapi
1039	64.2	2.9	193047	9	AC147069	AC147069 Pan trogl	c1112	64	2.9	4496	9	BC058918	BC058918 Homo sapi
1040	64	2.9	201	6	CQ526416	CQ526416 Sequence	c1113	64	2.9	5739	6	AX345621	AX345621 Sequence
1041	64	2.9	221	6	CQ663915	CQ663915 Sequence	c1114	64	2.9	7240	9	HSM808174	BX648028 Homo sapi

c1115	64	2.9	8305	6	AX346470	AX346470 Sequence	1188	63.8	2.8	2312	6	AR478071	AR478071 Sequence
1116	64	2.9	9699	9	BC066363	BC066363 Homo sapi	1189	63.8	2.8	2312	6	AR535342	AR535342 Sequence
c1117	64	2.9	40611	3	AC116987	AC116987 Dictyoste	1190	63.8	2.8	2312	6	AX045159	AX045159 Sequence
c1118	64	2.9	192187	3	AC117072	AC117072 Dictyoste	1191	63.8	2.8	2317	9	BC027906	BC027906 Homo sapi
1119	63.8	2.8	198	6	CQ488001	CQ488001 Sequence	1192	63.8	2.8	2342	10	BC069844	BC069844 Mus muscu
1120	63.8	2.8	202	6	CQ486699	CQ486699 Sequence	1193	63.8	2.8	2359	9	BSM808756	BSM808756 Homo sapi
1121	63.8	2.8	218	6	CQ517186	CQ517186 Sequence	1194	63.8	2.8	2368	3	AK112620	AK112620 Ciona int
1122	63.8	2.8	241	6	CQ525610	CQ525610 Sequence	1195	63.8	2.8	2442	10	BC020028	BC020028 Mus muscu
1123	63.8	2.8	244	6	AX408053	AX408053 Sequence	1196	63.8	2.8	2610	9	BC038448	BC038448 Homo sapi
1124	63.8	2.8	301	6	CQ516510	CQ516510 Sequence	1197	63.8	2.8	2675	10	BC023831	BC023831 Mus muscu
1125	63.8	2.8	321	6	CQ671494	CQ671494 Sequence	1198	63.8	2.8	2792	10	AF177401	AF177401 Spermophi
1126	63.8	2.8	338	3	AF156596	AF156596 Butthus ma	1199	63.8	2.8	2856	9	BSA508777	BSA508777 Homo sapi
1127	63.8	2.8	359	9	AK026647	AK026647 Homo sapi	1200	63.8	2.8	3040	5	BC056332	BC056332 Danio rer
1128	63.8	2.8	381	6	CQ526814	CQ526814 Sequence	1201	63.8	2.8	3101	10	BC059280	BC059280 Mus muscu
c1129	63.8	2.8	405	6	CQ411907	CQ411907 Sequence	1202	63.8	2.8	3326	9	BSM808512	BSM808512 Homo sapi
1130	63.8	2.8	419	9	BC021680	BC021680 Homo sapi	1203	63.8	2.8	3591	9	BC037320	BC037320 Homo sapi
c1131	63.8	2.8	436	6	AX284728	AX284728 Sequence	1204	63.8	2.8	3715	9	BC054004	BC054004 Homo sapi
c1132	63.8	2.8	445	6	CQ473555	CQ473555 Sequence	1205	63.8	2.8	3884	9	BSM806337	BSM806337 Homo sapi
c1133	63.8	2.8	496	6	CQ397791	CQ397791 Sequence	1206	63.8	2.8	4016	9	BC042556	BC042556 Homo sapi
c1134	63.8	2.8	496	6	CQ404088	CQ404088 Sequence	1207	63.8	2.8	4246	9	BC037888	BC037888 Homo sapi
c1135	63.8	2.8	500	6	CQ408389	CQ408389 Sequence	1208	63.8	2.8	4297	10	BC063098	BC063098 Mus muscu
c1136	63.8	2.8	521	6	CQ418873	CQ418873 Sequence	1209	63.8	2.8	4297	10	BSM807046	BSM807046 Homo sapi
1137	63.8	2.8	559	6	CQ517792	CQ517792 Sequence	1210	63.8	2.8	78402	8	NCB16M17	NCB16M17 Neurospor
c1138	63.8	2.8	585	6	CQ467430	CQ467430 Sequence	1211	63.8	2.8	90373	3	AC115680	AC115680 Dictyoste
1139	63.8	2.8	618	6	BD191023	BD191023 Secreted	1212	63.8	2.8	182871	3	AC117176	AC117176 Dictyoste
1140	63.8	2.8	667	9	BC041440	BC041440 Homo sapi	c1213	63.8	2.8	183648	3	AC117081	AC117081 Dictyoste
1141	63.8	2.8	710	10	BC049608	BC049608 Mus muscu	1214	63.8	2.8	191949	2	AC109158	AC109158 Mus muscu
c1142	63.8	2.8	711	6	CQ422915	CQ422915 Sequence	1215	63.6	2.8	201	11	BSM20821	BSM20821 sqm20999
1143	63.8	2.8	741	6	AR414257	AR414257 Sequence	1216	63.6	2.8	255	6	CQ521197	CQ521197 Sequence
1144	63.8	2.8	741	6	AX971091	AX971091 Sequence	c1217	63.6	2.8	289	6	CQ423504	CQ423504 Sequence
1145	63.8	2.8	741	6	BD109810	BD109810 EST and e	c1218	63.6	2.8	302	6	CQ398264	CQ398264 Sequence
1146	63.8	2.8	883	9	BC015164	BC015164 Homo sapi	c1219	63.6	2.8	302	6	CQ404551	CQ404551 Sequence
1147	63.8	2.8	891	5	BC079953	BC079953 Xenopus t	c1220	63.6	2.8	356	6	CQ471948	CQ471948 Sequence
1148	63.8	2.8	921	5	BC081142	BC081142 Xenopus l	c1221	63.6	2.8	383	6	CQ502211	CQ502211 Sequence
1149	63.8	2.8	972	6	I22272	I22272 Sequence l	c1222	63.6	2.8	383	6	CQ511079	CQ511079 Sequence
1150	63.8	2.8	1058	5	BC064179	BC064179 Xenopus t	1223	63.6	2.8	463	6	CQ526887	CQ526887 Sequence
1151	63.8	2.8	1071	9	AF078844	AF078844 Homo sapi	c1224	63.6	2.8	498	6	CQ481059	CQ481059 Sequence
1152	63.8	2.8	1108	10	BC032259	BC032259 Mus muscu	c1225	63.6	2.8	596	6	CQ477183	CQ477183 Sequence
1153	63.8	2.8	1129	9	BC013587	BC013587 Homo sapi	1226	63.6	2.8	642	10	MMU95114	MMU95114 Mus musculu
1154	63.8	2.8	1217	9	AK026533	AK026533 Homo sapi	1227	63.6	2.8	659	9	AF151109	AF151109 Homo sapi
1155	63.8	2.8	1247	6	BD271574	BD271574 49 human	c1228	63.6	2.8	738	6	CQ431080	CQ431080 Sequence
1156	63.8	2.8	1400	9	BC035287	BC035287 Homo sapi	1229	63.6	2.8	762	9	BC047115	BC047115 Homo sapi
1157	63.8	2.8	1408	10	BC048693	BC048693 Mus muscu	1230	63.6	2.8	871	5	BC061446	BC061446 Xenopus t
1158	63.8	2.8	1414	10	BC049767	BC049767 Mus muscu	1231	63.6	2.8	958	9	BC034296	BC034296 Homo sapi
1159	63.8	2.8	1447	9	BC044232	BC044232 Homo sapi	1232	63.6	2.8	1013	3	AK174215	AK174215 Ciona int
1160	63.8	2.8	1495	5	BC074583	BC074583 Xenopus t	1233	63.6	2.8	1015	5	BC080081	BC080081 Xenopus l
1161	63.8	2.8	1580	10	BC072688	BC072688 Rattus no	1234	63.6	2.8	1073	6	BD190930	BD190930 Secreted
1162	63.8	2.8	1595	9	BC043553	BC043553 Homo sapi	1235	63.6	2.8	1079	5	BC060411	BC060411 Xenopus l
1163	63.8	2.8	1602	5	BC074589	BC074589 Xenopus t	1236	63.6	2.8	1087	5	BC083541	BC083541 Danio rer
1164	63.8	2.8	1610	5	AB075198	AB075198 Oryzias l	1237	63.6	2.8	1130	10	BC061770	BC061770 Rattus no
1165	63.8	2.8	1611	5	BC077257	BC077257 Xenopus l	1238	63.6	2.8	1243	8	AB093028	AB093028 Pyrus com
1166	63.8	2.8	1619	9	BC043510	BC043510 Homo sapi	1239	63.6	2.8	1319	9	BC034528	BC034528 Homo sapi
1167	63.8	2.8	1634	9	BC040915	BC040915 Homo sapi	1240	63.6	2.8	1378	9	BC040939	BC040939 Homo sapi
1168	63.8	2.8	1669	10	BC064715	BC064715 Mus muscu	1241	63.6	2.8	1381	5	BC063358	BC063358 Xenopus t
1169	63.8	2.8	1710	5	BC053110	BC053110 Danio rer	1242	63.6	2.8	1420	5	BC074693	BC074693 Xenopus t
1170	63.8	2.8	1744	9	AB070194	AB070194 Macaca fa	1243	63.6	2.8	1425	3	AK114531	AK114531 Ciona int
1171	63.8	2.8	1785	5	BC055495	BC055495 Danio rer	1244	63.6	2.8	1439	10	BC058686	BC058686 Mus muscu
1172	63.8	2.8	1930	5	BC054953	BC054953 Xenopus l	1245	63.6	2.8	1545	6	AR307542	AR307542 Sequence
1173	63.8	2.8	1946	9	BSM808123	BSM808123 Homo sapi	1246	63.6	2.8	1545	6	AX401915	AX401915 Sequence
1174	63.8	2.8	1995	5	BC082524	BC082524 Xenopus t	1247	63.6	2.8	1545	10	RNU67958	RNU67958 Rattus norv
1175	63.8	2.8	2012	10	BC048918	BC048918 Mus muscu	1248	63.6	2.8	1571	10	BC072658	BC072658 Mus muscu
1176	63.8	2.8	2024	9	BC025694	BC025694 Homo sapi	1249	63.6	2.8	1590	9	BC008284	BC008284 Homo sapi
1177	63.8	2.8	2042	9	BC044947	BC044947 Homo sapi	1250	63.6	2.8	1603	6	CQ490224	CQ490224 Sequence
1178	63.8	2.8	2047	10	BC051189	BC051189 Mus muscu	1251	63.6	2.8	1603	6	CQ491236	CQ491236 Sequence
1179	63.8	2.8	2085	10	BC067207	BC067207 Mus muscu	1252	63.6	2.8	1603	6	CQ496086	CQ496086 Sequence
1180	63.8	2.8	2091	6	AR228745	AR228745 Sequence	1253	63.6	2.8	1603	6	CQ497104	CQ497104 Sequence
1181	63.8	2.8	2094	9	BC044310	BC044310 Homo sapi	1254	63.6	2.8	1628	9	BSM801754	BSM801754 Homo sapi
1182	63.8	2.8	2095	5	BC084410	BC084410 Xenopus l	1255	63.6	2.8	1648	10	BC052159	BC052159 Mus muscu
1183	63.8	2.8	2106	9	BC015775	BC015775 Homo sapi	1256	63.6	2.8	1687	9	BC041166	BC041166 Homo sapi
1184	63.8	2.8	2152	5	BC077173	BC077173 Xenopus l	1257	63.6	2.8	1696	5	BC067590	BC067590 Danio rer
1185	63.8	2.8	2280	10	BC055379	BC055379 Mus muscu	1258	63.6	2.8	1798	9	AB060834	AB060834 Macaca fa
1186	63.8	2.8	2298	6	BD192299	BD192299 Secreted	1259	63.6	2.8	1815	5	BC044453	BC044453 Danio rer
1187	63.8	2.8	2312	3	TGU93689	TGU93689 Toxoplasma	1260	63.6	2.8	1850	10	BC016432	BC016432 Mus muscu

1261	63.6	2.8	1865	9	BC016153	BC016153 Homo sapi
1262	63.6	2.8	1884	10	BC036992	BC036992 Mus muscu
1263	63.6	2.8	1933	6	BD270058	BD270058 Secreted
1264	63.6	2.8	1975	5	BC057415	BC057415 Danio rer
1265	63.6	2.8	1988	3	AY069585	AY069585 Drosophil
1266	63.6	2.8	2068	9	BC016791	BC016791 Homo sapi
1267	63.6	2.8	2090	9	BC071171	BC071171 Homo sapi
1268	63.6	2.8	2118	9	BC073946	BC073946 Homo sapi
1269	63.6	2.8	2176	9	BC051801	BC051801 Homo sapi
1270	63.6	2.8	2214	9	HSM807772	HSM807772 Homo sapi
1271	63.6	2.8	2350	5	BC078091	BC078091 Xenopus l
1272	63.6	2.8	2380	9	HSM808648	HSM808648 Homo sapi
1273	63.6	2.8	2394	9	AF061795	AF061795 Homo sapi
1274	63.6	2.8	2417	10	BC026514	BC026514 Mus muscu
1275	63.6	2.8	2465	5	BC070798	BC070798 Xenopus l
1276	63.6	2.8	2472	9	AF151685	AF151685 Homo sapi
1277	63.6	2.8	2725	5	BC077764	BC077764 Xenopus l
1278	63.6	2.8	2869	9	HSM804689	HSM804689 Homo sapi
1279	63.6	2.8	2874	9	BC037236	BC037236 Homo sapi
1280	63.6	2.8	2993	10	BC050858	BC050858 Mus muscu
1281	63.6	2.8	3484	9	BC018919	BC018919 Homo sapi
1282	63.6	2.8	3556	9	BC033587	BC033587 Homo sapi
1283	63.6	2.8	3676	9	HSM801343	HSM801343 Homo sapi
1284	63.6	2.8	3773	5	BC077375	BC077375 Xenopus l
1285	63.6	2.8	4420	10	BC036971	BC036971 Mus muscu
1286	63.6	2.8	4513	10	BC027791	BC027791 Mus muscu
1287	63.6	2.8	5335	9	HSM803927	HSM803927 Homo sapi
1288	63.6	2.8	5405	10	BC038061	BC038061 Mus muscu
c1289	63.6	2.8	12951	6	AX3348366	AX3348366 Sequence
c1290	63.6	2.8	12951	6	AX3348366	AX3348366 Sequence
1291	63.6	2.8	256602	2	AC137381	AC137381 Rattus no
c1292	63.4	2.8	154	6	AX381214	AX381214 Sequence
c1293	63.4	2.8	161	6	AX381305	AX381305 Sequence
c1294	63.4	2.8	269	6	CQ475616	CQ475616 Sequence
1295	63.4	2.8	301	6	CQ526142	CQ526142 Sequence
1296	63.4	2.8	305	6	CQ487458	CQ487458 Sequence
1297	63.4	2.8	390	6	CQ522607	CQ522607 Sequence
1298	63.4	2.8	420	6	CQ526309	CQ526309 Sequence
1299	63.4	2.8	429	10	AY262005	AY262005 Mus muscu
1300	63.4	2.8	434	6	CQ526683	CQ526683 Sequence
1301	63.4	2.8	456	6	CQ516799	CQ516799 Sequence
1302	63.4	2.8	513	6	CQ524938	CQ524938 Sequence
1303	63.4	2.8	612	10	BC061085	BC061085 Mus muscu
1304	63.4	2.8	639	6	BD218567	BD218567 71 human
1305	63.4	2.8	687	6	BD269361	BD269361 Gene show
1306	63.4	2.8	726	10	BC061530	BC061530 Rattus no
1307	63.4	2.8	824	10	BC038684	BC038684 Mus muscu
1308	63.4	2.8	887	3	AY099474	AY099474 Haematobi
1309	63.4	2.8	969	10	BC025974	BC025974 Mus muscu
1310	63.4	2.8	970	10	BC049752	BC049752 Mus muscu
1311	63.4	2.8	1017	10	BC049561	BC049561 Mus muscu
1312	63.4	2.8	1063	9	BC001418	BC001418 Homo sapi
1313	63.4	2.8	1063	9	BC013953	BC013953 Homo sapi
1314	63.4	2.8	1104	10	BC003429	BC003429 Mus muscu
1315	63.4	2.8	1147	5	BC047838	BC047838 Danio rer
1316	63.4	2.8	1165	5	BC054180	BC054180 Xenopus l
1317	63.4	2.8	1165	5	BC071549	BC071549 Danio rer
1318	63.4	2.8	1198	10	BC033305	BC033305 Mus muscu
1319	63.4	2.8	1376	3	AK174695	AK174695 Ciona int
1320	63.4	2.8	1411	10	BC002101	BC002101 Mus muscu
1321	63.4	2.8	1512	10	BC010278	BC010278 Mus muscu
1322	63.4	2.8	1516	6	E02253	E02253 human 'A my
1323	63.4	2.8	1519	6	AX546769	AX546769 Sequence
1324	63.4	2.8	1523	6	BD270351	BD270351 50 human
1325	63.4	2.8	1566	10	BC079404	BC079404 Rattus no
1326	63.4	2.8	1579	9	BC058934	BC058934 Homo sapi
1327	63.4	2.8	1605	9	BC037234	BC037234 Homo sapi
1328	63.4	2.8	1607	9	BC025369	BC025369 Homo sapi
1329	63.4	2.8	1610	9	BC073973	BC073973 Homo sapi
1330	63.4	2.8	1636	5	BC067630	BC067630 Danio rer
1331	63.4	2.8	1730	6	CQ830452	CQ830452 Sequence
1332	63.4	2.8	1736	5	BC070796	BC070796 Xenopus l
1333	63.4	2.8	1770	9	BC063419	BC063419 Homo sapi
1334	63.4	2.8	1334	9	BC071757	BC071757 Homo sapi
1335	63.4	2.8	1828	9	BC003610	BC003610 Homo sapi
1336	63.4	2.8	1872	10	BC023437	BC023437 Mus muscu
1337	63.4	2.8	1889	6	CQ412127	CQ412127 Sequence
1338	63.4	2.8	1902	9	AB047930	AB047930 Macaca fa
1339	63.4	2.8	1949	9	AB104615	AB104615 Homo sapi
1340	63.4	2.8	1954	9	AK026613	AK026613 Homo sapi
1341	63.4	2.8	1956	10	BC030941	BC030941 Mus muscu
1342	63.4	2.8	1968	10	BC006016	BC006016 Mus muscu
1343	63.4	2.8	1980	6	AX040974	AX040974 Sequence
1344	63.4	2.8	1992	10	RNO301634	AJ301634 Rattus no
1345	63.4	2.8	2054	5	BC063322	BC063322 Danio rer
1346	63.4	2.8	2061	6	CQ489941	CQ489941 Sequence
1347	63.4	2.8	2061	6	CQ495788	CQ495788 Sequence
1348	63.4	2.8	2108	9	AB047801	AB047801 Homo sapi
1349	63.4	2.8	2132	9	BC042102	BC042102 Homo sapi
1350	63.4	2.8	2134	9	BC039050	BC039050 Homo sapi
1351	63.4	2.8	2161	9	AB063084	AB063084 Macaca fa
1352	63.4	2.8	2199	9	BC064841	BC064841 Homo sapi
1353	63.4	2.8	2209	5	BC068394	BC068394 Danio rer
1354	63.4	2.8	2213	9	AB060825	AB060825 Macaca fa
1355	63.4	2.8	2239	5	AF207751	AF207751 Danio rer
1356	63.4	2.8	2310	10	BC080813	BC080813 Mus muscu
1357	63.4	2.8	2358	4	AF254119	AF254119 Ovis arie
1358	63.4	2.8	2360	10	BC008547	BC008547 Mus muscu
1359	63.4	2.8	2446	6	CQ413150	CQ413150 Sequence
1360	63.4	2.8	2458	5	BC076840	BC076840 Xenopus l
1361	63.4	2.8	2507	9	BC006411	BC006411 Homo sapi
1362	63.4	2.8	2563	9	AF125949	AF125949 Homo sapi
1363	63.4	2.8	2569	9	BC081566	BC081566 Homo sapi
1364	63.4	2.8	2635	10	BC066812	BC066812 Mus muscu
1365	63.4	2.8	2688	9	BC021087	BC021087 Homo sapi
1366	63.4	2.8	2699	9	HSM808469	EX648321 Homo sapi
1367	63.4	2.8	2988	9	BC073907	BC073907 Homo sapi
1368	63.4	2.8	2991	9	BC045767	BC045767 Homo sapi
1369	63.4	2.8	3049	9	HSM807028	EX640895 Homo sapi
1370	63.4	2.8	3050	5	BC066571	BC066571 Danio rer
1371	63.4	2.8	3069	9	BC010058	BC010058 Homo sapi
1372	63.4	2.8	3115	10	BC058780	BC058780 Mus muscu
1373	63.4	2.8	3159	10	BC030921	BC030921 Mus muscu
1374	63.4	2.8	3619	9	HSM807853	BC043709 Mus muscu
1375	63.4	2.8	3686	10	BC043709	BC067018 Mus muscu
1376	63.4	2.8	3787	10	BC067018	AL833175 Homo sapi
1377	63.4	2.8	3809	9	HSM804486	BC038481 Mus muscu
1378	63.4	2.8	3820	10	BC038481	BC067005 Mus muscu
1379	63.4	2.8	4057	10	BC067005	BC053753 Mus muscu
1380	63.4	2.8	4283	10	BC053753	BC054123 Mus muscu
1381	63.4	2.8	4486	10	BC054123	CQ493241 Sequence
1382	63.4	2.8	4531	6	CQ493241	BC049781 Mus muscu
1383	63.4	2.8	4593	10	BC049781	Continuation (3 of
1384	63.4	2.8	110000	1	EX897700_02	Continuation (4 of
1385	63.4	2.8	110000	1	EX897700_03	AC115592 Dictyoste
1386	63.4	2.8	125958	3	AC115592	AC124388 Mus muscu
c1387	63.4	2.8	149152	10	AC124388	AC124096 Mus muscu
1388	63.4	2.8	164878	2	AC124096	BX322550 Zebrafish
1389	63.4	2.8	184426	5	EX322550	AE014840 Plasmodiu
c1390	63.4	2.8	249995	3	AE014840	AE014846 Plasmodiu
c1391	63.4	2.8	253132	3	AE014846	AC087146 Mus muscu
1392	63.4	2.8	256673	2	AC087146	AC116986 Dictyoste
1393	63.4	2.8	333321	3	AC116986	BV202819 sqnm20999
1394	63.2	2.8	201	11	BV202819	BV202820 sqnm20999
1395	63.2	2.8	201	11	BV202820	CQ398332 Sequence
c1396	63.2	2.8	300	6	CQ398332	CQ404619 Sequence
c1397	63.2	2.8	300	6	CQ404619	CQ408965 Sequence
c1398	63.2	2.8	316	6	CQ408965	AR418750 Sequence
1399	63.2	2.8	318	6	AR418750	AX979444 Sequence
1400	63.2	2.8	318	6	AX979444	BD114303 EST and e
1401	63.2	2.8	318	6	BD114303	AX184967 Sequence
c1402	63.2	2.8	349	6	AX184967	CQ411533 Sequence
c1403	63.2	2.8	384	6	CQ411533	CQ411979 Sequence
c1404	63.2	2.8	385	6	CQ411979	CQ410120 Sequence
c1405	63.2	2.8	400	6	CQ410120	BC029475 Homo sapi
1406	63.2	2.8	465	9	BC029475	

1407	63.2	2.8	505	6	CQ524936	CQ524936 Sequence
1408	63.2	2.8	511	5	BC078541	BC078541 Xenopus 1
c1409	63.2	2.8	550	6	CQ398027	CQ398027 Sequence
c1410	63.2	2.8	550	6	CQ404319	CQ404319 Sequence
c1411	63.2	2.8	597	6	CQ397801	CQ397801 Sequence
c1412	63.2	2.8	597	6	CQ404098	CQ404098 Sequence
c1413	63.2	2.8	607	5	BC049055	BC049055 Danio rer
c1414	63.2	2.8	631	6	CQ397563	CQ397563 Sequence
c1415	63.2	2.8	631	6	CQ403862	CQ403862 Sequence
c1416	63.2	2.8	669	6	CQ422520	CQ422520 Sequence
1417	63.2	2.8	683	8	AY621633	AY621633 Nicotiana
1418	63.2	2.8	705	9	BSM800237	AL049452 Homo sapi
1419	63.2	2.8	894	5	BC084598	BC084598 Xenopus 1
1420	63.2	2.8	963	10	BC035045	BC035045 Mus muscu
1421	63.2	2.8	997	9	BC047943	BC047943 Homo sapi
1422	63.2	2.8	1080	8	AY190244	AY190244 Coccidioi
1423	63.2	2.8	1155	9	BC036792	BC036792 Homo sapi
1424	63.2	2.8	1172	6	AR013797	AR013797 Sequence
1425	63.2	2.8	1172	6	113099	113099 Sequence 9
1426	63.2	2.8	1172	6	125472	125472 Sequence 9
1427	63.2	2.8	1176	9	BC003410	BC003410 Homo sapi
1428	63.2	2.8	1199	10	BC013338	BC013338 Mus muscu
1429	63.2	2.8	1202	9	BC041171	BC041171 Homo sapi
1430	63.2	2.8	1343	9	BC052989	BC052989 Homo sapi
1431	63.2	2.8	1361	10	BC026510	BC026510 Mus muscu
1432	63.2	2.8	1409	5	BC064261	BC064261 Xenopus t
1433	63.2	2.8	1411	10	BC049571	BC049571 Mus muscu
1434	63.2	2.8	1438	9	BC070233	BC070233 Homo sapi
1435	63.2	2.8	1544	9	AB062942	AB062942 Macaca fa
1436	63.2	2.8	1560	10	BC064655	BC064655 Rattus no
1437	63.2	2.8	1566	9	AF258571	AF258571 Homo sapi
1438	63.2	2.8	1580	9	BC037569	BC037569 Homo sapi
1439	63.2	2.8	1619	10	BC058767	BC058767 Mus muscu
1440	63.2	2.8	1630	5	BC065344	BC065344 Danio rer
1441	63.2	2.8	1635	9	BC017004	BC017004 Homo sapi
1442	63.2	2.8	1666	9	BC001128	BC001128 Homo sapi
1443	63.2	2.8	1679	5	BC048062	BC048062 Danio rer
1444	63.2	2.8	1715	5	BC067176	BC067176 Danio rer
1445	63.2	2.8	1739	5	BC070678	BC070678 Xenopus 1
1446	63.2	2.8	1757	9	BSM802709	AL359600 Homo sapi
1447	63.2	2.8	1884	9	AF086921	AF086921 Homo sapi
1448	63.2	2.8	1900	9	BC025963	BC025963 Homo sapi
1449	63.2	2.8	1922	10	BC080807	BC080807 Mus muscu
1450	63.2	2.8	1946	5	AJ720792	AJ720792 Gallus ga
1451	63.2	2.8	1994	9	AB048974	AB048974 Macaca fa
1452	63.2	2.8	2030	10	BC051019	BC051019 Mus muscu
1453	63.2	2.8	2053	9	BC030196	BC030196 Homo sapi
1454	63.2	2.8	2055	9	BC063413	BC063413 Homo sapi
1455	63.2	2.8	2095	9	BC006472	BC006472 Homo sapi
1456	63.2	2.8	2139	10	BC005458	BC005458 Mus muscu
1457	63.2	2.8	2149	9	BC072428	BC072428 Homo sapi
1458	63.2	2.8	2160	5	BC084345	BC084345 Xenopus 1
c1459	63.2	2.8	2176	6	CQ414271	CQ414271 Sequence
1460	63.2	2.8	2296	5	BC054631	BC054631 Danio rer
1461	63.2	2.8	2300	6	AX020124	AX020124 Sequence
1462	63.2	2.8	2300	6	AX3333053	AX3333053 Sequence
1463	63.2	2.8	2300	6	AX336441	AX336441 Sequence
1464	63.2	2.8	2300	6	AX411235	AX411235 Sequence
1465	63.2	2.8	2300	9	BSMXXR7MR	Z37987 H.sapiens m
1466	63.2	2.8	2305	9	BC038807	BC038807 Homo sapi
1467	63.2	2.8	2328	9	BC007567	BC007567 Homo sapi
1468	63.2	2.8	2497	9	BC042040	BC042040 Homo sapi
1469	63.2	2.8	2533	10	BC006690	BC006690 Mus muscu
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1483	63.2	2.8	2851	9	BC021117	BC021117 Homo sapi
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1491	63.2	2.8	3305	10	BC054378	BC054378 Mus muscu
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ALIGNMENTS

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LOCUS
DEFINITION Homo sapiens clone DNA92234 DPXL1915 (UNQ1915) mRNA, complete cds.
ACCESSION AY358756
VERSION AY358756.1 GI:37182630
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2242)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
TITLE The Secreted Protein Discovery Initiative (SPDI),-a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 2242)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES
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DEFINITION			
Sequence 8 from Patent WO0075298.			
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AX059560			
VERSION			
AX059560.1 GI:12311667			
KEYWORDS			
Homo sapiens (human)			
SOURCE			
ORGANISM			
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REFERENCE			
1			
AUTHORS			
Hodgson,D.M., Lincoln,S.E., Russo,F.D., Spiro,P.A., Banville,S.C.,			
Bratcher,S.R., Dufour,G.E., Cohen,H.J., Rosen,B.H., Chalup,M.S.,			
Hillman,J.L., Jones,A.L., Yu,J.Y., Greenawalt,L.B., Panzer,S.R.,			
Roseberry,A.M., Wright,R.J. and Daniels,S.E.			
Molecules for disease detection and treatment			
Patent: WO 0075298-A 8 14-DEC-2000;			
Incyte Genomics, Inc. (US)			
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DEFINITION 97 human secreted proteins.
ACCESSION BD205653
VERSION BD205653.1 GI:33015423
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2152)
Ruben,S.M., Florence,K., Ni,J., Rosen,C.A., Carter,K.C.,
Moore,P.A., Olsen,H.S., Shi,Y., Young,P.E., Wei,F.F., Brewer,L.A.,
Soppet,D.R., Lafleur,D.W., Endress,G.A. and Ebner,R.
97 human secreted proteins
Patent: JP 2002533058-A 30 08-OCT-2002;
HUMAN GENOME SCIENCES INC
OS Homo sapiens (human)
PN JP 2002533058-A/30
PD 08-OCT-2002
PF 06-MAY-1999 JP 2000548451
PR 12-MAY-1998 US 60/085093,12-MAY-1998 US 60/085094 PR
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PI STEVEN M RUBEN,KIMBERLY FLORENCE,JIAN NI,CRAIG A ROSEN,KENNETH
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PI REINHARD EBNER
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Qy	1216	TGACCTCTGGAGGTACCCATCTTTCTATTATCGGATCGAGGCGCGTTTGTATGAGC	1275
Db	1201	TGACCTCTGGAGGTACCCATCTTTCTATTATCGGATCGAGGCGCGTTTGTATGAGC	1260
Qy	1276	CTGGAATAAAACAGTCATACCTGGCCGAGTTATAGGAAAATTTCAATCCGCTAGTCC	1335
Db	1261	CTGGAATAAAACAGTCATACCTGGCCGAGTTATAGGAAAATTTCAATCCGCTAGTCC	1320
Qy	1336	CTCACAATGAATGTGTCTGGGTGGAAAAACAGGTGACACGACATCTTGAAGATGTGTTCT	1395
Db	1321	CTCACAATGAATGTGTCTGGGTGGAAAAACAGGTGACACGACATCTTGAAGATGTGTTCT	1380
Qy	1396	CCAAAAGAAATAGTTCCAACAAGATGGTTTCCATGACTCTAGGACTACACCCGTGGA	1455
Db	1381	CCAAAAGAAATAGTTCCAACAAGATGGTTTCCATGACTCTAGGACTACACCCGTGGA	1440
Qy	1456	TTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGCGGATCAGAACAGTGTG	1515
Db	1441	TTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGCGGATCAGAACAGTGTG	1500
Qy	1516	GAACAGAACCCAGATATGATCCGGGATGGATCCACCATTTCCAATTGCCAAAATGTTCCAGG	1575
Db	1501	GAACAGAACCCAGATATGATCCGGGATGGATCCACCATTTCCAATTGCCAAAATGTTCCAGG	1560
Qy	1576	AGATCGTCCACAAGAGCGTGTGTAATTCGGTGGAGCTGTGATGGAGAACATT	1635
Db	1561	AGATCGTCCACAAGAGCGTGTGTAATTCGGTGGAGCTGTGATGGAGAACATT	1620
Qy	1636	CGCAGAATGAGAAAATCAACAGGTGGAACTACATAGAGGGAACCAAAATATTGCTGCCT	1695
Db	1621	CGCAGAATGAGAAAATCAACAGGTGGAACTACATAGAGGGAACCAAAATATTGCTGCCT	1680
Qy	1696	TTTTCTTAGAGATGCCCCAGCTCCATTAATCACAAGAACCTTCTAGTCTGATCTGATCCA	1755
Db	1681	TTTTCTTAGAGATGCCCCAGCTCCATTAATCACAAGAACCTTCTAGTCTGATCTGATCCA	1740
Qy	1756	CTGACAGATTCACTCCCCACATCCCTTAGACAGGGATGGAATGTAATATCCAGAGAAT	1815
Db	1741	CTGACAGATTCACTCCCCACATCCCTTAGACAGGGATGGAATGTAATATCCAGAGAAT	1800
Qy	1816	TTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTGGGATATCTGGATCAG	1875
Db	1801	TTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTGGGATATCTGGATCAG	1860
Qy	1876	TAATAAAATATTTCAAAGGCACAGATGTTGGAATGGTTTAAGGTCCCCCACTGCACACC	1935
Db	1861	TAATAAAATATTTCAAAGGCACAGATGTTGGAATGGTTTAAGGTCCCCCACTGCACACC	1920
Qy	1936	TTCTCTCAAGTCATAGCTGCTTGCAGCAACTTGATTTCCCAAGTCTCTGTGCAATAGCCCC	1995
Db	1921	TTCTCTCAAGTCATAGCTGCTTGCAGCAACTTGATTTCCCAAGTCTCTGTGCAATAGCCCC	1980
Qy	1996	AGGATTGGATTCTTCCCAACCTTTTAGCATATCTCCAACCTTGCAATTTGATTGGCATAA	2055
Db	1981	AGGATTGGATTCTTCCCAACCTTTTAGCATATCTCCAACCTTGCAATTTGATTGGCATAA	2040
Qy	2056	TCACCTCCGTTTGTCTTCTAGTCTCTCAAGTCTCGTGACACATAATCATTCATCCAT	2115
Db	2041	TCACCTCCGTTTGTCTTCTAGTCTCTCAAGTCTCGTGACACATAATCATTCATCCAT	2100
Qy	2116	GATCGCCTTTGCTTTACCACTCTTCCCTTTTATCTTATTAATAAAAATGTTG	2167
Db	2101	GATCGCCTTTGCTTTACCACTCTTCCCTTTTATCTTATTAATAAAAATGTTG	2152
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LOCUS	1970 bp mRNA linear PRI 12-SEP-2003		
DEFINITION	Homo sapiens cDNA FLJ25503 fis, clone CBR04457.		
ACCESSION	AK098369		
VERSION	AK098369.1 GI:21758369		
KEYWORDS	oligo capping; fis (full insert sequence).		
SOURCE	Homo sapiens (human)		

Qy	139	CTCCCTCTGCCACATTTTGGAGGTTGGGAAAGTTGCTAGAGGCTTCAGAACTCCAGCC	198
Db	121	CTCCCTCTGCCACATTTTGGAGGTTGGGAAAGTTGCTAGAGGCTTCAGAACTCCAGCC	180
Qy	199	TAATGGATCCAAACTCGGAGAAATGGCTGCGTCCCTGCTGGCTGCTGCTGCTGCTG	255
Db	181	TAATGGATCCAAACTCGGAGAAATGGCTGCGTCCCTGCTGGCTGCTGCTGCTGCTG	240
Qy	256	TGCTGAGCGCGGCATGTTCTCTCACCTCCCGCCCGCGCGCTGTTAGAGAAAGTCT	315
Db	241	TGCTGAGCGCGGCATGTTCTCTCACCTCCCGCCCGCGCGCTGTTAGAGAAAGTCT	300
Qy	316	TCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGGAGTGGTGGCCA	375
Db	301	TCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGGAGTGGTGGCCA	360
Qy	376	TCGAGAGCGACTCTGTCCAGCCTGCTTCAGACAAAGAGCTCTTCAGAAATGATGG	435
Db	361	TCGAGAGCGACTCTGTCCAGCCTGCTTCAGACAAAGAGCTCTTCAGAAATGATGG	420
Qy	436	CCGTGGCTCGGACACGCTGCAGCGCTGGGGCCCGTGTGGCTCGGTGGACATGGTTC	495
Db	421	CCGTGGCTCGGACACGCTGCAGCGCTGGGGCCCGTGTGGCTCGGTGGACATGGTTC	480
Qy	496	CTCAGCAGCTGCGCGATGGTCAGAGTCTTCCAATACCTCCCGTCATCCTGGCCGAACTGG	555
Db	481	CTCAGCAGCTGCGCGATGGTCAGAGTCTTCCAATACCTCCCGTCATCCTGGCCGAACTGG	540
Qy	556	GGAGCGATCCCAAGAAAGGACCGTGTGCTTACCGGCCACTTGGACGTGCAGCCTGCTG	615
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Qy	616	ACCGGGCGATGGGTGGCTCACGGACCCCTATGTCTGACGGAGTAGACGGGAACTTT	675
Db	601	ACCGGGCGATGGGTGGCTCACGGACCCCTATGTCTGACGGAGTAGACGGGAACTTT	660
Qy	676	ATGGACGAGGAGCGACGACAAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTAGCG	735
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Qy	736	CCTTCAGAGCCCTGGAGCAAGATCTTCCCTGTGAATATCAAAATTCATGAGGGATGG	795
Db	721	CCTTCAGAGCCCTGGAGCAAGATCTTCCCTGTGAATATCAAAATTCATGAGGGATGG	780
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Qy	856	CTGGTGTGGAATACTGTAATTTTCAGATAACCTGTGGATCAGCCAAAGGAAGCCAGCAA	915
Db	841	CTGGTGTGGAATACTGTAATTTTCAGATAACCTGTGGATCAGCCAAAGGAAGCCAGCAA	900
Qy	916	TCACTTATGGAACCCGGGGGAAACAGCTACTTTCATGGTGGAGGTGAAATGCAGACCCAGG	975
Db	901	TCACTTATGGAACCCGGGGGAAACAGCTACTTTCATGGTGGAGGTGAAATGCAGACCCAGG	960
Qy	976	ATTTTCACTCAGGAACCTTTGGTGGCATCTTTCATGAACCAATGGCTGATCTGGTTGCTC	1035
Db	961	ATTTTCACTCAGGAACCTTTGGTGGCATCTTTCATGAACCAATGGCTGATCTGGTTGCTC	1020
Qy	1036	TTCTCGSPAGCCTGGTAGACTCGTCTGGTCATATCCTGGTCCCTGGAATCTATGATGAAG	1095
Db	1021	TTCTCGSPAGCCTGGTAGACTCGTCTGGTCATATCCTGGTCCCTGGAATCTATGATGAAG	1080
Qy	1096	TGGTTCCTCTTACAGAAAGAGGAAATAAATACATACAAAGCATCCATCTAGACCTAGAAG	1155
Db	1081	TGGTTCCTCTTACAGAAAGAGGAAATAAATACATACAAAGCATCCATCTAGACCTAGAAG	1140
Qy	1156	AATACCGGAATAGCAGCCGGGTTTGAGAAATTTCTGTTCCGATACATAAGGAGGAGATTCTAA	1215
Db	1141	AATACCGGAATAGCAGCCGGGTTTGAGAAATTTCTGTTCCGATACATAAGGAGGAGATTCTAA	1200

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Tanigami,A., Fujiwara,T., Shibahara,T., Goto,Y., Hirao,M.,
Shimizu,F., Wakebe,H., Ono,T., Hishigaki,H., Watanabe,T., Ozaki,K.,
Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M.,
Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and
Sugano,S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1970)
AUTHORS Sugano,S. and Suzuki,Y.
TITLE Direct Submission
JOURNAL Submitted (08-JUL-2002) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing: Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB; clone selection for
full insert sequencing: RAB and Helix Research Institute.
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QY 135 GGGACTCCCTCTGGCACATTTTGGAGGTTGGGAAAGTTGCTAGAGGCTTCAGAACTCC 194
DB 1 GGGACTCCCTCTGGCACATTTTGGAGGTTGGGAAAGTTGCTAGAGGCTTCAGAACTCC 60
QY 195 AGCCTAATGGATCCCAAACCTCGGGAGAAATGGCTGCGTCCCTGCTGGCTGCTGCTG 254
DB 61 AGCCTAATGGATCCCAAACCTCGGGAGAAATGGCTGCGTCCCTGCTGGCTGCTGCTG 120
QY 255 CTGCTGGAGCGCGGCATGTTCTCCTCACCCCTCCCCCGCCCCCGGCTGTAGAGAAAGTC 314
DB 121 CTGCTGGAGCGCGGCATGTTCTCCTCACCCCTCCCCCGCCCCCGGCTGTAGAGAAAGTC 180
QY 315 TTCCAGTACATTGACCTCCATCAGGATGAATTGTGCAGACGCTGAAGAGTGGGTGGCC 374
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QY 375 ATCGAGAGCGACTCTGTCCAGCCTGTGCTCGCTTCAGACAAAGAGCTCTTCAGAATGATG 434
DB 241 ATCGAGAGCGACTCTGTCCAGCCTGT----- 266
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DB 267 -----GCCTCGGTGGACATGGGT 284
QY 495 CCTCAGCAGCTGCCGATGGTTCAGAGTCTTCCAATACCTCCCGTCATCCTGGCCGAACCTG 554
DB 285 CCTCAGCAGCTGCCGATGGTTCAGAGTCTTCCAATACCTCCCGTCATCCTGGCCGAACCTG 344
QY 555 GGGAGCGATCCCAAGAAAGGACCGGTGTGCTTCTACGGCCACTTGGACGCTGCAGCCTGCT 614
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QY 615 GACCGGGCGATGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACGGAAACTT 674
DB 405 GACCGGGCGATGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACGGAAACTT 464
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QY 1095 GTGGTTCCTTACAGAGAGGAAATAAATACATACAAAGCCATCCATCTAGACCTAGAA 1154
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DB 1185 TCCAAAAGAAATAGTTCCCAACAAGATGGTTGTTTCCATGACTCTAGACTACACCCGTGG 1244
QY 1455 ATTGCAATATTTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGCATCAGAACAGTGTTT 1514
DB 1245 ATTGCAATATTTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGCATCAGAACAGTGTTT 1304
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DB 1305 GGAACAGAACCCAGATATGATCCGGATGGATCCACCATTCCAATTCGCAAAATGTTCCAG 1364
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DB 1365 GAGATCGTCCAAGAGCGGTGCTGAATTCGCTGGAGCTGTGATGATGGAGAACAT 1424
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Db	1545		
Qy	1815	TTTGGGCTAGTATAGTACATTTTCCCTTCCATTTTAAATGTCTTGGGATATCTGGATCA	1874
Db	1605		
Qy	1875	GTAATAAAATATTTCAAAGGCACAGATGTTGGAATGTTTAAAGTCCCCCACTGCACAC	1934
Db	1665		
Qy	1935	CTTCCTCAAGTCATAGCTGCTTGACAGCAACTTGATTTCCCCAAGTCCTGTGCAATAGCCC	1994
Db	1725		
Qy	1995	CAGGATTGGATTCCTTCCAACCTTTTAGCATATCTCCAACCTTGCAATTTGATTGGCATA	2054
Db	1785		
Qy	2055	ATCACTCCGGTTGCTTTCTAGGTCCTCAAGTCTCGTGACACATAATCATTCATCCAA	2114
Db	1845		
Qy	2115	TGATCGCCTTGTCTTACCACCTCTTTCCCTTTATCTTATTAATAAAAAATGTTGGTCTCCA	2174
Db	1905		
Qy	2175	CCACTG 2180	
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RESULT 6			
HSA417564			
LOCUS			
DEFINITION Homo sapiens mRNA for glutamate carboxypeptidase-like protein 2			
(CPGL2 gene).			
ACCESSION AJ417564			
VERSION AJ417564.1 GI:16555791			
KEYWORDS CPGL2 gene; glutamate carboxypeptidase-like protein 2.			
SOURCE Homo sapiens (human)			
ORGANISM Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE 1			
AUTHORS Chen, J.M. and Barrett, A.J.			
TITLE Cloning and sequencing of a second human homologue of glutamate carboxypeptidase in peptidase family M20			
JOURNAL Unpublished			
AUTHORS Chen, J.M.			
TITLE Direct Submission			
JOURNAL Submitted (24-OCT-2001) Chen J.M., MRC Molecular Enzymology Laboratory, Babraham Institute, Babraham Hall, Babraham, Cambridgehire CB2 4AT, UNITED KINGDOM			
FEATURES			
Source			
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Best Local Similarity 99.5%; Pred.No. 0;			
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Db	241	CTGTGCCTCGCTTCAGACAAAGAGCTCTTCAGATGATGGCGTGGCTGCGGACACGCTGC	300
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Db	301	AGCGCCTGGGGCCCGCTGCTGGCCTCGGTGGACATGGGTCTCTCAGCAGCTGCCGATGGTC	360
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Qy	577	CCGTGTGCTTCTACGGCCACTTTGGACGTGCAGCCTGCTGACCGGGCGATGGGTGGCTCA	636
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Qy	637	CGGACCCCTATGTGCTGACGGAGGTAGACGGGAAACTTTTATGGACGAGGAGCGACCGACA	696
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Qy	817	TGGAGGAACCTTGTGGAAAAAGAAAGACCGATTCTTCTCTGGTGTGGACTACATTGTAA	876
Db	661	TGGAGGAACCTTGTGGAAAAAGAAAGACCGATTCTTCTCTGGTGTGGACTACATTGTAA	720
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QY 1657 GGTGGAACATACATAGAGGGAACCAAAATTTTGTGCTCTTTTCTTAGAGATGGCCCCAGC 1716

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QY 1777 CATCCCTAGACAGGGATGGA 1796

Db 1621 CATCCCTAGACAGGGATGGA 1640

RESULT 7

AX231101

LOCUS AX231101 1587 bp DNA linear PAT 11-SEP-2001

DEFINITION Sequence 497 from Patent WO0162787.

ACCESSION AX231101

VERSION AX231101.1 GI:15592456

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.

1

REFERENCE

AUTHORS Herath,H.M., Parekh,R.B., Rohlf,C.O., Terrett,J.A. and Tyson,K.L.

TITLE Diagnosis and treatment of bipolar affective disorder

JOURNAL Patent: WO 0162787-A 497 30-AUG-2001;

FEATURES

source Oxford GlycoSciences (UK) Limited (GB)

Location/Qualifiers

1. .1587

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 68.3%; Score 1531.6; DB 6; Length 1587;

Best Local Similarity 99.1%; Pred. No. 0;

Matches 1533; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 225 GCTGCGTCCCTGCTGGCTGTGCTGCTGCTGCTGGAGCGGSCATGTTCTCTCCTCACCC 284

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QY 285 TCCCCGCCCCCGCGCTGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAA 344

Db 101 TCCCCGCCCCCGCGCTGTTAGAGAAAGTCTTCCAGTACATTGACCTNCAATCAGGATGAA 160

QY 345 TTTGTGCAGACGCTGAAGGAGTGGGTGGCATCGAGAGCGACTCTGTCCAGCCTGTGCCT 404

Db 161 TTTGTGCAGACGCTGAAGGAGTGGGTGGCATCGAGAGCGACTCTGTCCAGCCTGTGCCT 220

QY 405 CGCTTCAGACAAGAGCTCTTCAGAAATGATGGCTGCTGCGGACACGCTGCGAGCGCCTG 464

Db 221 CGCTTCAGACAAGAGCTCTTCANAATGATGGCTGGCTGCGGACACGCTGCGAGCGCCTG 280

QY 465 GGGGCCCGTGGCTCGGTGGACATGGGTGCTCAGCAGCTGCCGATGGTGCAGAGTCTT 524

Db 281 GGGGCCCGTGGCTCGGTGGACATGGGTGCTCAGCAGCTGCCGATGGTGCAGAGTCTT 340

QY 525 CCAATACCTCCCGTCATCCTGGCCGAACCTGGGGAGCGATCCCACGAAAGSCACCGTGTGC 584

Db 341 CCAATACCTCCCGTCATCCTGGCCGAACCTGGGGAGCGATCCCACGAAAGSCACCGTGTGC 400

QY 585 TTCTACGGCCACTTGGACGTGCAGCTGCTGACCGGGCGCATGGGTGGCTACGGACCCC 644

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QY 825 CTTGTGGAAGAAAGAAAGGACCGATTCTTCTGCTGGTGGACTACATTGTAATTTTCAGAT 884

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QY 1005 CTTCTATGAACCAATGGCTGATCTGCTGCTGCTTCTCGGTAGCCTGGTAGACTCGTCTGGT 1064

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Db	941		
QY	1185	TTTCTGTTGATACCTAAGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCTTTCT	1244
Db	1001		
QY	1245	ATTATGGGATCGAGGGCGGTTTGATGAGCCTGGAACTTAAACAGTCATACCTGSCCGA	1304
Db	1061		
QY	1305	GTTATAGAAAATTTTCAATCCGTCATGTCCTTCAATGAATGTGTCTGCGGTGGAATA	1364
Db	1121		
QY	1365	CAGGTGACAGACATCTTGAAGATGTGTTTCCAAAAGAAATAGTTCCAAACAAGATGGTT	1424
Db	1181		
QY	1425	GTTTCCATGACTTAGGACTACACCCGTGGATTGCAAAATATGATGACACCCAGTATCTC	1484
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QY	1545	TCCACCATTTCCAAATGCCAAAATGTTCCAGGAGATCGTCCACAGAGCGTGGTCTAAAT	1604
Db	1361		
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QY	1665	TACATAGAGGGAACCAAAATATTTGCTGCCCTTTTCTTAGAGATGSCCCAGCTCCATTAA	1724
Db	1481		
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Db	1541		
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LOCUS	AX231560		linear
DEFINITION	Sequence 458 from Patent WO0163294.		PAT 11-SEP-2001
ACCESSION	AX231560		
VERSION	AX231560.1	GI:15592465	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Herath,H.M., Parekh,R.B. and Rohlf,C.		
TITLE	Diagnosis of bipolar affective disorder (bad) and unipolar depression		
JOURNAL	Patent: WO 0163294-A 458 30-AUG-2001;		
FEATURES	Oxford GlycoSciences (UK) Limited (GB)		
	Location/Qualifiers		
source	1. .1587		
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				Indels	0;
				Gaps	0;
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Db	41				
QY	285	TCCCCGCCCCCGCGCTGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAA	344		
Db	101				
QY	345	TTTGTGCAGACGCTGAAGGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCCT	404		
Db	161				
QY	405	CGCTTCAGACAAAGAGCTCTTCAAGATGATGGCCGTGGCTGCGGACACGCTGCAGCGCCTG	464		
Db	221				
QY	465	GGGGCCCGTGTGGCCTCGGTGGACATGGGTCTCTCAGCAGCTGCCCGATGGTCAGAGTCTT	524		
Db	281				
QY	525	CCAATACCTCCCGTCATCTGGCCGAACTGGGAGCGATCCACGAAAGGACCCGTGTGC	584		
Db	341				
QY	585	TTCTACGGCCACTTGGACGTGCAGCCTGCTGACCCGGGCGATGGTGGTCACGGACCCC	644		
Db	401				
QY	645	TATGTGCTGACGGAGGTAGACGGGAAAACITTTATGGACGAGGAGCGACCGACAAACAAAGGC	704		
Db	461				
QY	705	CCTGTCTTGGCTTGGATCAATGCTGTGAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCCT	764		
Db	521				
QY	765	GTGAATATCAAAATTCATATTGAGGGGATGGAAGAGCTGGCTCTGTTGCCCTGGAGGAA	824		
Db	581				
QY	825	CTTGTGAAAAAGAAAAAGGACCGATTCTTCTCTGGTGTGGACTACATTGTAATTTTCAGAT	884		
Db	641				
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Db	701				
QY	945	TTTCATGGTGGAGGTGAAATGCAGAGACCCAGGATTTTCACTCAGGAACTTTGGTGGCATC	1004		
Db	761				
QY	1005	CTTCATGAACCAATGGCTGATCTGGTTGCTCTTCTCGGTAGCCTGGTAGACTCGTCTGGT	1064		
Db	821				
QY	1065	CATATCCTGGTCCCTGGAATCTATGATGAAGTGGTTCTCTTACAGAAAGAGGAAATAAAT	1124		
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Db	941				
QY	1185	TTTCTGTTGATACCTAAGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCTTCT	1244		
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AX232218
LOCUS      AX232218          1587 bp      DNA
DEFINITION Sequence 496 from Patent WO0163293.
ACCESSION  AX232218
VERSION     AX232218.1  GI:15592548
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1
REFERENCE
AUTHORS    Herath,M.A., Parekh,R.B. and Rohlf,C.O.
TITLE       Diagnosis and treatment of schizophrenia
JOURNAL     Patent: WO 0163293-A 496 30-AUG-2001;
            Oxford Glycosciences (UK) Limited (GB)
FEATURES
            Location/Qualifiers
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	Best Local Similarity	99.1%;	Pred. No. 0;		
	Matches 1533; Conservative	0;	Mismatches 14;	Indels 0;	Gaps 0;
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Dd	41	CGGTCCTTGCTGGCTGTGCTGCTGCTGCTGCTGAGCGCGGCATGTTCTCCTCACCC	100		
Qy	285	TCCCCGCCCGCGCGCTGTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAA	344		
Dd	101	TCCCCGCCCGCGCGCTGTAGAGAAAGTCTTCCAGTACATTGACCTNCATCAGGATGAA	160		
Qy	345	TTTGTGCAGACGCTGAAGGAGTGGGTGGCCCATCGAGAGCGACTCTGTCCAGCCTGTGCCT	404		


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QY 1665 TACATAGAGGGAACCAAAATATTGCTGCCTTTTCTTAGAGATGGCCAGCTCCATTAA 1724
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RESULT 10
AX233356 1587 bp DNA linear PAT 11-SEP-2001
LOCUS AX233356
DEFINITION Sequence 680 from Patent WO0162785.
ACCESSION AX233356
VERSION AX233356.1 GI:15592690
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Herath,H.M., Parekh,R.B., Rohlf,C.C., Terrett,J.A. and Tyson,K.L.
TITLE Protein and gene and their use for diagnosis and treatment of
schizophrenia
JOURNAL Patent: WO 0162785-A 680 30-AUG-2001;
Oxford GlycoSciences (UK) Limited (GB)
FEATURES
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    Query Match 68.3%; Score 1531.6; DB 6; Length 1587;
    Best Local Similarity 99.1%; Pred. No. 0;
    Matches 1533; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 225 GCTGCGTCCCTGCTGGCTGCTGCTGCTGCTGCTGGAGCGCGCATGTTCTCCTCACCC 284
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QY 525 CCAATACCTCCCGTCATCTGGCCGAACTGGGGAGCGATCCCAAGAAAGGACCGTGTGC 584
Db 341 CCAATACCTCCCGTCATCTGGCCGAACTGGGGAGCGATCCCAAGAAAGGACCGTGTGC 400
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RESULT 11
AX319869
LOCUS AX319869 1524 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 33 from Patent WO0183782.
ACCESSION AX319869
VERSION AX319869.1 GI:17901459
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Plowman,G.D., Whyte,D., Sudarsanam,S., Manning,G., Caenepeel,S. and
Payne,V.
TITLE Novel proteases
JOURNAL Patent: WO 0183782-A 33 08-NOV-2001;
Sugen, Inc. (US)
FEATURES
source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1141 ATGAATGTGCTGCGGTGGAAAAACAGGTGACACGACATCTTGAAGATGTGTTCTCCAAA 1200
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RESULT 12
AX527746
LOCUS AX527746 1521 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 3 from Patent WO026948.

ACCESSION	AX527746
VERSION	AX527746.1 GI:25172276
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Kapeller-Libermann,R.
TITLE	55054, a novel human metalloprotease and uses therefor
JOURNAL	Patent: WO 0226948-A 3 04-APR-2002;
FEATURES	Millennium Pharmaceuticals, Inc. (US) Location/Qualifiers 1..1521 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
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	Query Match 67.8%; Score 1521; DB 6; Length 1521; Best Local Similarity 100.0%; Pred. No. 0; Matches 1521; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Dd	
QY	381 AGCGACTCTGTCCAGCCTGTCCTCGCTTCAGACAAGAGCTCTTCAGAATGATGGCCGTG 440
Dd	
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Dd	
QY	361 GATCCCAAGAACCGCTGCTGTCTTACGGCCACTTGGACGTGCAGCCTGCTGACC GG 420
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QY	621 GCCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACGGAAACTTTATGGA 680
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QY	421 GCCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACGGAAACTTTATGGA 480
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QY	741 AGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAATTCATCATTGAGGGGATGGAAGAG 800
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QY	541 AGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAATTCATCATTGAGGGGATGGAAGAG 600
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QY	861 GTGGACTACATTGTAATTTTTCAGATAAAGTGTGGATCAGCCAAAGGAAGCCAGCAATCACT 920
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QY	661 GTGGACTACATTGTAATTTTTCAGATAAAGTGTGGATCAGCCAAAGGAAGCCAGCAATCACT 720
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ORIGIN

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Best Local Similarity		99.7%;	Pred.	No.	0;			
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							Gaps	1;
QY	201	ATGGATCCCAAACTCGGAGAAATGGCTGCTCCCTGCTGGCTG--TGCTGCTGCTG	257					
Db	1	ATGGATCCCAAACTCGGAGAAATGGCTGCGTCCCTGCTGGCTGCTGCTGCTGCTG	60					
QY	258	CTGGAGCGCGCATGTTCTCTCACCTCCCGCCCGCCCGCGCTGTTAGAGAAAGTCTTC	317					
Db	61	CTGGAGCGCGCATGTTCTCTCACCTCCCGCCCGCCCGCGCTGTTAGAGAAAGTCTTC	120					
QY	318	CAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGAGTGGTGGCCATC	377					
Db	121	CAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGAGTGGTGGCCATC	180					
QY	378	GAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTACAGCAAGAGCTCTTCAGAAATGATGCC	437					
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QY	438	GTGGCTGCGGACACGCTGCAGCGCCTGGGGCCCGTGTGGCCTCGTGGACATGGTCCCT	497					
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QY	498	CAGCAGCTGCCGATGGTCAGAGTCTTCCAAATACCTCCCGTCATCCTGGCCGAACCTGGG	557					
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QY	678	GGACGAGGAGCGACCGACAAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGAGCGCC	737					
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Db	721	ACTTATGGAACCCGGGGAAACAGCTACTTTCATGGTGGAGGTGAAATGCAGAGACCAGGAT	780
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QY	1038	CTCGGTAGCCTGGTAGACTCGTCTGGTCAATATCCTGGTCCCTGGAATCTATGATGAAGTG	1097
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QY	1098	GTTCCCTCTTACAGAAAGAGGAAATAAATACATACAAAAAGCCATCCATCTAGACCTAGAAAGAA	1157
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QY	1638	CAGAAATGAGAAAAATCAACAGGTGGAATACATAGAGGGAAACCAAAATTAATTTGCTGCTTT	1697
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QY	1698	TTCTTAGAGATGGCCAGCTCCAT	1721
Db	1501	TTCTTAGAGATGGCCAGCTCCAT	1524
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LOCUS			
DEFINITION			
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VERSION			
KEYWORDS			
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ORGANISM			
REFERENCE			
AUTHORS			
BC081877			
Rattus norvegicus			
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BC081877.1			
GI:51859149			
MGC.			
Rattus norvegicus (Norway rat)			
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
Rattus.			
1 (bases 1 to 2675)			
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,			
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,			
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,			
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,			
linear			
2675 bp			
mRNA			
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IMAGE:7107931,			
complete cds.			

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 2675)

Director MGC Project.

Direct Submission

Submitted (01-SEP-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Howard Jacobs

cDNA Library Preparation: Express Genomics

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 181 Row: i Column: 1

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers

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ORIGIN

Query Match 46.0%; Score 1031.2; DB 10; Length 2675;
Best Local Similarity 79.9%; Pred. No. 1.4e-227;
Matches 1242; Conservative 0; Mismatches 303; Indels 9; Gaps 2;

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QY	426	AGAATGATGGCCGTGCTGCGGACACCGCTGCAGCGCTGGGGCCCCGTGTGSCCTCGGTG	485
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BC043305			
LOCUS			
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ACCESSION	BC043305		
VERSION	BC043305.1	GI:27695038	
KEYWORDS	MGC.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2774)		
	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,B.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickinson,M.C., Rodriguez,A.C., Grinwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 2774)		
AUTHORS	Strausberg,R.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer		

REMARK	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov
	Contact: MGC help desk
	Email: cgapbs-r@mail.nih.gov
	Tissue Procurement: Jeffrey E. Green, M.D.
	cdna Library Preparation: Life Technologies, Inc.
	cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
	info@bcgsc.bc.ca
	Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angélique Schnerch, Ursula Skalska, Duane Smalhus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 15:45:48 ; Search time 9249 Seconds
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Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 6
Total number of hits satisfying chosen parameters: 8998214

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Post-processing: Listing first 1500 summaries

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- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1602	71.5	1970	9	AK098369 Homo sapi
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7	1521	67.8	1521	6	AX527746 Sequence
8	1427	63.6	1524	6	AX139747 Sequence
9	1375	61.3	1587	6	AX231101 Sequence
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11	1375	61.3	1587	6	AX232218 Sequence
12	1375	61.3	1587	6	AX233356 Sequence
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17	423	18.9	164394	9	AC116904 Homo sapi
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132	59	2.6	190	6	AX985981	Sequence	AR425287	205	59	2.6	682	10	BC049545	Mus muscu
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134	59	2.6	196	6	CQ527157	Sequence	BD120840	207	59	2.6	699	10	BC053692	Mus muscu
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146	59	2.6	270	6	CQ517277	Sequence	CQ506050	219	59	2.6	913	3	AF252289	Leishmani
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253	59	2.6	1413	10	BC026675	BC026675 Mus muscu	326	59	2.6	2307	10	BC057127	BC057127 Mus muscu
254	59	2.6	1417	5	BC067701	BC067701 Danio rer	327	59	2.6	2328	9	BC028034	BC028034 Homo sapi
255	59	2.6	1420	10	BC035539	BC035539 Mus muscu	328	59	2.6	2348	9	BC007998	BC007998 Homo sapi
256	59	2.6	1444	9	BC035354	BC035354 Homo sapi	329	59	2.6	2364	9	BC008711	BC008711 Homo sapi
257	59	2.6	1456	5	BC077897	BC077897 Xenopus l	330	59	2.6	2370	10	BC034555	BC034555 Mus muscu
258	59	2.6	1464	9	IR2005397	AL389978 Homo sapi	331	59	2.6	2375	9	BC028239	BC028239 Homo sapi
259	59	2.6	1480	5	BC074071	BC074071 Danio rer	332	59	2.6	2404	9	BC042542	BC042542 Homo sapi
260	59	2.6	1487	8	BT008916	BT008916 Triticum	333	59	2.6	2413	9	BC002342	BC002342 Homo sapi
261	59	2.6	1490	9	BC063409	BC063409 Homo sapi	334	59	2.6	2422	9	BC043488	BC043488 Homo sapi
262	59	2.6	1513	6	AX921981	AX921981 Sequence	335	59	2.6	2426	9	BC004874	BC004874 Homo sapi
263	59	2.6	1534	10	RNC21	X99257 R.norvegicu	336	59	2.6	2430	5	BC056717	BC056717 Danio rer
264	59	2.6	1554	5	AF065135	AF065135 Xenopus l	337	59	2.6	2435	9	BC051753	BC051753 Homo sapi
265	59	2.6	1554	6	BD132843	BD132843 WA545 com	338	59	2.6	2447	5	BC064881	BC064881 Xenopus t
266	59	2.6	1555	5	BC049526	BC049526 Danio rer	339	59	2.6	2460	10	BC036985	BC036985 Mus muscu
267	59	2.6	1573	10	BC057679	BC057679 Mus muscu	340	59	2.6	2474	9	HSM806789	BX640718 Homo sapi
268	59	2.6	1598	10	BC062643	BC062643 Mus muscu	341	59	2.6	2503	8	AF061107	AF061107 Zea mays
269	59	2.6	1599	9	BC010738	BC010738 Homo sapi	342	59	2.6	2504	6	BD139957	BD139957 Secreted
270	59	2.6	1609	8	BT008970	BT008970 Triticum	343	59	2.6	2507	9	BC006411	BC006411 Homo sapi
271	59	2.6	1620	10	BC046622	BC046622 Mus muscu	344	59	2.6	2630	10	BC064659	BC064659 Rattus no
272	59	2.6	1625	9	BC065733	BC065733 Homo sapi	345	59	2.6	2641	9	BC020219	BC020219 Homo sapi
273	59	2.6	1640	5	BC056535	BC056535 Danio rer	346	59	2.6	2647	9	BC043484	BC043484 Homo sapi
274	59	2.6	1640	9	BC035844	BC035844 Homo sapi	347	59	2.6	2649	5	BC046050	BC046050 Danio rer
275	59	2.6	1651	6	AR374741	AR374741 Sequence	348	59	2.6	2660	10	BC046318	BC046318 Mus muscu
276	59	2.6	1651	6	AX146877	AX146877 Sequence	349	59	2.6	2673	9	BC036711	BC036711 Homo sapi
277	59	2.6	1651	9	AF067420	AF067420 Homo sapi	350	59	2.6	2765	9	BC009113	BC009113 Homo sapi
278	59	2.6	1670	9	HSM806969	BX640854 Homo sapi	351	59	2.6	2817	9	BC000556	BC000556 Homo sapi
279	59	2.6	1693	9	BC042110	BC042110 Homo sapi	352	59	2.6	2825	9	BC028203	BC028203 Homo sapi
280	59	2.6	1704	10	BC048726	BC048726 Mus muscu	353	59	2.6	2836	3	AB016609	AB016609 Dictyoste
281	59	2.6	1705	9	BC032249	BC032249 Homo sapi	354	59	2.6	2841	10	BC045601	BC045601 Mus muscu
282	59	2.6	1754	4	AY312278	AY312278 Bos tauru	355	59	2.6	2931	3	PPTUBEA	X14213 Physarum po
283	59	2.6	1755	9	BC036846	BC036846 Homo sapi	356	59	2.6	2988	9	BC073907	BC073907 Homo sapi
284	59	2.6	1759	6	AX358752	AX358752 Sequence	357	59	2.6	2989	6	AR364635	AR364635 Sequence
285	59	2.6	1759	6	AX362245	AX362245 Sequence	358	59	2.6	2998	10	BC051114	BC051114 Mus muscu
286	59	2.6	1759	9	AY358724	AY358724 Homo sapi	359	59	2.6	3004	10	BC031128	BC031128 Mus muscu
287	59	2.6	1800	10	BC042440	BC042440 Mus muscu	360	59	2.6	3076	8	AF205791	AF205791 Botryococ
288	59	2.6	1812	9	BC018774	BC018774 Homo sapi	361	59	2.6	3095	10	BC063752	BC063752 Mus muscu
289	59	2.6	1815	6	AX098200	AX098200 Sequence	362	59	2.6	3105	9	HSM800649	AL080137 Homo sapi
290	59	2.6	1816	3	AK112765	AK112765 Ciona int	363	59	2.6	3115	10	BC058780	BC058780 Mus muscu
291	59	2.6	1820	9	BC035606	BC035606 Homo sapi	364	59	2.6	3132	9	HSM802176	AL137705 Homo sapi
292	59	2.6	1868	6	AX709314	AX709314 Sequence	365	59	2.6	3160	9	BC028067	BC028067 Homo sapi
293	59	2.6	1878	6	AR217827	AR217827 Sequence	366	59	2.6	3217	6	BD015772	BD015772 Antibody
294	59	2.6	1878	6	AX787069	AX787069 Sequence	367	59	2.6	3315	9	AB056768	AB056768 Macaca fa
295	59	2.6	1881	5	BC049494	BC049494 Danio rer	368	59	2.6	3329	9	BC051862	BC051862 Homo sapi
296	59	2.6	1882	9	BC043565	BC043565 Homo sapi	369	59	2.6	3418	9	BC037539	BC037539 Homo sapi
297	59	2.6	1885	6	CQ412300	CQ412300 Sequence	370	59	2.6	3481	9	BC065509	BC065509 Homo sapi
298	59	2.6	1899	9	BC013872	BC013872 Homo sapi	371	59	2.6	3481	10	BC064007	BC064007 Mus muscu
299	59	2.6	1923	9	BC001349	BC001349 Homo sapi	372	59	2.6	3531	10	BC060084	BC060084 Mus muscu
300	59	2.6	1932	9	BC014126	BC014126 Homo sapi	373	59	2.6	3585	10	BC063072	BC063072 Mus muscu
301	59	2.6	1968	9	BC011262	BC011262 Homo sapi	374	59	2.6	3599	9	BC064543	BC064543 Homo sapi
302	59	2.6	1968	10	BC006016	BC006016 Mus muscu	375	59	2.6	3626	9	BC012147	BC012147 Homo sapi
303	59	2.6	1982	3	AK112713	AK112713 Ciona int	376	59	2.6	3645	10	BC062916	BC062916 Mus muscu
304	59	2.6	1993	9	BC013377	BC013377 Homo sapi	377	59	2.6	3715	9	BC054004	BC054004 Homo sapi
305	59	2.6	1995	10	BC050759	BC050759 Mus muscu	378	59	2.6	3724	9	HSM805632	AL834516 Homo sapi
306	59	2.6	2029	10	BC050265	BC050265 Mus muscu	379	59	2.6	3832	9	HSU75370	U75370 Human mitoc
307	59	2.6	2030	10	BC037434	BC037434 Mus muscu	380	59	2.6	4067	5	BC077182	BC077182 Xenopus l
308	59	2.6	2032	10	BC057123	BC057123 Mus muscu	381	59	2.6	4083	9	BC062341	BC062341 Homo sapi
309	59	2.6	2035	9	BC036799	BC036799 Homo sapi	382	59	2.6	4124	9	BC032311	BC032311 Homo sapi
310	59	2.6	2042	9	BC044947	BC044947 Homo sapi	383	59	2.6	4271	10	BC060275	BC060275 Mus muscu
311	59	2.6	2049	9	BC065235	BC065235 Homo sapi	384	59	2.6	4508	10	BC053013	BC053013 Mus muscu

385	59	2.6	4692	3	AV118673	AV118673 Drosophil	458	58	2.6	453	6	CQ517526	CQ517526 Sequence
386	59	2.6	4710	10	BC060613	BC060613 Mus muscu	C 459	58	2.6	461	6	AX284240	AX284240 Sequence
387	59	2.6	4863	9	HSM808808	BX648657 Homo sapi	460	58	2.6	467	3	AF156168	AF156168 Butus ma
388	59	2.6	5000	3	AY392433	AY392433 Dictyoste	C 461	58	2.6	470	6	BD242015	BD242015 Compounds
389	59	2.6	5124	9	HSM805736	BX537434 Homo sapi	C 462	58	2.6	470	6	AR237198	AR237198 Sequence
390	59	2.6	5344	6	AX470393	AX470393 Sequence	C 463	58	2.6	470	6	AR278222	AR278222 Sequence
391	59	2.6	5701	6	AX470390	AX470390 Sequence	C 464	58	2.6	470	6	AR366918	AR366918 Sequence
392	59	2.6	7028	9	HSM803514	AL832207 Homo sapi	C 465	58	2.6	470	6	AR370814	AR370814 Sequence
393	59	2.6	33651	3	AC114261	AC114261 Dictyoste	C 466	58	2.6	470	6	AR392319	AR392319 Sequence
394	59	2.6	49306	3	AC115606	AC115606 Dictyoste	C 467	58	2.6	470	6	AR399954	AR399954 Sequence
C 395	59	2.6	79284	2	BX927314	BX927314 Danio rer	C 468	58	2.6	470	6	AR405221	AR405221 Sequence
C 396	59	2.6	125958	3	AC115592	AC115592 Dictyoste	C 469	58	2.6	470	6	AR439425	AR439425 Sequence
C 397	59	2.6	130701	2	AC009889	AC009889 Homo sapi	C 470	58	2.6	470	6	AR370814	AR370814 Sequence
C 398	59	2.6	141427	2	AL929185	AL929185 Homo sapi	C 471	58	2.6	470	6	AR392319	AR392319 Sequence
C 399	59	2.6	161823	2	AC136947	AC136947 Homo sapi	C 472	58	2.6	470	6	AR399954	AR399954 Sequence
C 400	59	2.6	167780	9	AL844892	AL844892 Human DNA	C 468	58	2.6	470	6	AR405221	AR405221 Sequence
C 401	59	2.6	170655	2	AP001012	AP001012 Homo sapi	C 469	58	2.6	470	6	AR439425	AR439425 Sequence
C 402	59	2.6	172915	2	AC010160	AC010160 Homo sapi	C 470	58	2.6	470	6	AX106321	AX106321 Sequence
C 403	59	2.6	179739	2	CR352310	CR352310 Danio rer	C 471	58	2.6	470	6	AX140612	AX140612 Sequence
404	59	2.6	184182	2	CR352221	CR352221 Danio rer	477	58	2.6	470	6	AX200472	AX200472 Sequence
405	59	2.6	211091	2	AC132973	AC132973 Rattus no	478	58	2.6	470	6	AX267128	AX267128 Sequence
C 406	59	2.6	223920	2	AC141733	AC141733 Apis mell	479	58	2.6	470	6	AX267128	AX267128 Sequence
C 407	59	2.6	229316	2	AC1117604	AC1117604 Mus muscu	480	58	2.6	470	6	AX267128	AX267128 Sequence
C 408	59	2.6	349980	6	AX344563	AX344563 Sequence	481	58	2.6	470	6	AX267128	AX267128 Sequence
409	58	2.6	80	6	A18777	A18777 5' terminus	482	58	2.6	470	6	BD070251	BD070251 Compounds
410	58	2.6	80	6	AR001312	AR001312 Sequence	483	58	2.6	471	6	CQ515907	CQ515907 Sequence
411	58	2.6	80	6	AR130410	AR130410 Sequence	C 484	58	2.6	471	6	CQ515907	CQ515907 Sequence
C 412	58	2.6	101	6	AX494448	AX494448 Sequence	C 485	58	2.6	483	6	CQ517059	CQ517059 Sequence
413	58	2.6	147	6	CQ677570	CQ677570 Sequence	C 486	58	2.6	485	6	AR252545	AR252545 Sequence
C 414	58	2.6	153	6	AX182151	AX182151 Sequence	C 487	58	2.6	485	6	AR252545	AR252545 Sequence
C 415	58	2.6	177	6	CQ473920	CQ473920 Sequence	C 488	58	2.6	485	6	AX092312	AX092312 Sequence
416	58	2.6	201	6	CQ526416	CQ526416 Sequence	C 489	58	2.6	485	6	AX376118	AX376118 Sequence
417	58	2.6	206	6	CQ525565	CQ525565 Sequence	C 490	58	2.6	485	6	AX403358	AX403358 Sequence
418	58	2.6	234	6	CQ525561	CQ525561 Sequence	C 491	58	2.6	485	9	AY358669	AY358669 Homo sapi
419	58	2.6	247	6	CQ524931	CQ524931 Sequence	C 492	58	2.6	485	6	AX403358	AX403358 Sequence
420	58	2.6	253	6	AR421302	AR421302 Sequence	C 493	58	2.6	485	6	AX376118	AX376118 Sequence
421	58	2.6	253	6	AX981996	AX981996 Sequence	C 494	58	2.6	485	6	AX376118	AX376118 Sequence
422	58	2.6	253	6	BD116855	BD116855 EST and e	C 495	58	2.6	485	6	AX376118	AX376118 Sequence
423	58	2.6	254	6	CQ487594	CQ487594 Sequence	C 496	58	2.6	485	6	AX376118	AX376118 Sequence
424	58	2.6	254	6	CQ517598	CQ517598 Sequence	C 497	58	2.6	485	6	AX376118	AX376118 Sequence
425	58	2.6	260	6	CQ704761	CQ704761 Sequence	C 498	58	2.6	485	6	AX376118	AX376118 Sequence
426	58	2.6	263	6	E15582	E15582 cDNA encodi	499	58	2.6	485	6	AX376118	AX376118 Sequence
427	58	2.6	263	6	AR222772	AR222772 Sequence	500	58	2.6	485	6	AX376118	AX376118 Sequence
C 428	58	2.6	278	6	CQ518107	CQ518107 Sequence	501	58	2.6	485	6	AX376118	AX376118 Sequence
429	58	2.6	282	6	CQ427703	CQ427703 Sequence	502	58	2.6	485	6	AX376118	AX376118 Sequence
430	58	2.6	285	6	AX284863	AX284863 Sequence	503	58	2.6	485	6	AX376118	AX376118 Sequence
C 431	58	2.6	294	6	CQ467734	CQ467734 Sequence	504	58	2.6	485	6	AX376118	AX376118 Sequence
432	58	2.6	312	6	CQ699683	CQ699683 Sequence	505	58	2.6	485	6	AX376118	AX376118 Sequence
C 433	58	2.6	321	6	AX361391	AX361391 Sequence	506	58	2.6	485	6	AX376118	AX376118 Sequence
434	58	2.6	325	6	CQ527169	CQ527169 Sequence	507	58	2.6	485	6	AX376118	AX376118 Sequence
435	58	2.6	342	6	AX381435	AX381435 Sequence	508	58	2.6	485	6	AX376118	AX376118 Sequence
C 436	58	2.6	360	6	CQ482995	CQ482995 Sequence	509	58	2.6	485	6	AX376118	AX376118 Sequence
437	58	2.6	367	6	CQ523839	CQ523839 Sequence	510	58	2.6	485	6	AX376118	AX376118 Sequence
438	58	2.6	372	10	BC027531	BC027531 Mus muscu	511	58	2.6	485	6	AX376118	AX376118 Sequence
439	58	2.6	373	6	CQ526228	CQ526228 Sequence	512	58	2.6	485	6	AX376118	AX376118 Sequence
440	58	2.6	377	6	CQ517394	CQ517394 Sequence	513	58	2.6	485	6	AX376118	AX376118 Sequence
441	58	2.6	390	9	BC035731	BC035731 Homo sapi	514	58	2.6	485	6	AX376118	AX376118 Sequence
C 442	58	2.6	392	6	CQ507200	CQ507200 Sequence	515	58	2.6	485	6	AX376118	AX376118 Sequence
443	58	2.6	396	6	CQ525748	CQ525748 Sequence	516	58	2.6	485	6	AX376118	AX376118 Sequence
C 444	58	2.6	400	6	CQ483089	CQ483089 Sequence	C 517	58	2.6	485	6	AX376118	AX376118 Sequence
C 445	58	2.6	404	6	CQ507110	CQ507110 Sequence	518	58	2.6	485	6	AX376118	AX376118 Sequence
446	58	2.6	409	10	BC055712	BC055712 Mus muscu	519	58	2.6	485	6	AX376118	AX376118 Sequence
C 447	58	2.6	413	6	CQ427117	CQ427117 Sequence	520	58	2.6	485	6	AX376118	AX376118 Sequence
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449	58	2.6	423	6	CQ526104	CQ526104 Sequence	522	58	2.6	485	6	AX376118	AX376118 Sequence
C 450	58	2.6	429	6	CQ473793	CQ473793 Sequence	C 523	58	2.6	485	6	AX376118	AX376118 Sequence
451	58	2.6	441	6	AR344256	AR344256 Sequence	C 524	58	2.6	485	6	AX376118	AX376118 Sequence
452	58	2.6	441	6	AX019230	AX019230 Sequence	525	58	2.6	485	6	AX376118	AX376118 Sequence
453	58	2.6	441	6	BD130456	BD130456 Expressio	526	58	2.6	485	6	AX376118	AX376118 Sequence
454	58	2.6	443	5	PBDRSPB	X72387 P.bicolor m	527	58	2.6	485	6	AX376118	AX376118 Sequence
455	58	2.6	443	6	BD268888	BD268888 Transgeni	528	58	2.6	485	6	AX376118	AX376118 Sequence
456	58	2.6	446	6	CQ487730	CQ487730 Sequence	529	58	2.6	485	6	AX376118	AX376118 Sequence
457	58	2.6	451	6	CQ524930	CQ524930 Sequence	530	58	2.6	485	6	AX376118	AX376118 Sequence

531	58	2.6	638	6	BD181688	BD181688 Polypepti	604	58	2.6	942	6	AX709468	AX709468 Sequence
532	58	2.6	638	6	E49221	E49221 Polypeptide	605	58	2.6	942	6	AX709469	AX709469 Sequence
533	58	2.6	638	6	BD142627	BD142627 Use of po	606	58	2.6	943	6	AX098202	AX098202 Sequence
534	58	2.6	650	9	BC034814	BC034814 Homo sapi	607	58	2.6	945	9	BC002688	BC002688 Homo sapi
535	58	2.6	673	9	BC063401	BC063401 Homo sapi	608	58	2.6	949	6	BD223099	BD223099 98 human
536	58	2.6	679	9	BC073915	BC073915 Homo sapi	609	58	2.6	949	6	AR243797	AR243797 Sequence
537	58	2.6	682	10	BC053379	BC053379 Mus muscu	610	58	2.6	951	6	BD021498	BD021498 Novel gen
538	58	2.6	688	6	AR365490	AR365490 Sequence	611	58	2.6	951	6	BD101436	BD101436 Novel gen
539	58	2.6	693	6	AX055710	AX055710 Sequence	612	58	2.6	973	9	BC043578	BC043578 Homo sapi
540	58	2.6	693	6	AX299998	AX299998 Sequence	613	58	2.6	979	9	BC031875	BC031875 Homo sapi
541	58	2.6	693	6	AX358922	AX358922 Sequence	614	58	2.6	981	9	BC000007	BC000007 Homo sapi
542	58	2.6	693	6	AX362415	AX362415 Sequence	615	58	2.6	990	3	AF466601	AF466601 Aedes aeg
543	58	2.6	693	6	AX454614	AX454614 Sequence	616	58	2.6	995	9	BC043534	BC043534 Homo sapi
544	58	2.6	693	6	AX464366	AX464366 Sequence	617	58	2.6	996	6	AX406866	AX406866 Sequence
545	58	2.6	693	6	AX491092	AX491092 Sequence	618	58	2.6	997	5	BC061271	BC061271 Xenopus t
546	58	2.6	693	6	AX697075	AX697075 Sequence	619	58	2.6	1003	5	BC067645	BC067645 Danio rer
547	58	2.6	693	9	AY358935	AY358935 Homo sapi	620	58	2.6	1004	10	BC045153	BC045153 Mus muscu
548	58	2.6	693	10	BC049621	BC049621 Mus muscu	621	58	2.6	1006	9	AF111112	AF111112 Homo sapi
549	58	2.6	700	10	BC035545	BC035545 Mus muscu	622	58	2.6	1008	6	AR404675	AR404675 Sequence
550	58	2.6	705	10	BC059084	BC059084 Mus muscu	623	58	2.6	1011	6	AX709470	AX709470 Sequence
551	58	2.6	708	5	AY190729	AY190729 Pagrus ma	624	58	2.6	1013	4	AF155148	AF155148 Canis fam
552	58	2.6	710	10	BC024378	BC024378 Mus muscu	625	58	2.6	1013	6	BD211499	BD211499 Canine an
553	58	2.6	710	10	BC049608	BC049608 Mus muscu	c 626	58	2.6	1013	6	BD211500	BD211500 Canine an
554	58	2.6	716	9	BC015172	BC015172 Homo sapi	627	58	2.6	1013	6	AR241477	AR241477 Sequence
555	58	2.6	716	9	BC044236	BC044236 Homo sapi	c 628	58	2.6	1013	6	AR241478	AR241478 Sequence
556	58	2.6	730	3	AY113197	AY113197 Drosophil	629	58	2.6	1013	6	AR254433	AR254433 Sequence
557	58	2.6	732	6	CQ487253	CQ487253 Sequence	c 630	58	2.6	1013	6	AR254434	AR254434 Sequence
c 558	58	2.6	735	6	CQ467402	CQ467402 Sequence	631	58	2.6	1016	6	BD135263	BD135263 110 human
559	58	2.6	737	9	BC013410	BC013410 Homo sapi	632	58	2.6	1016	10	BC024487	BC024487 Mus muscu
c 560	58	2.6	740	6	CQ430280	CQ430280 Sequence	633	58	2.6	1020	5	BC066621	BC066621 Danio rer
561	58	2.6	741	6	AR414257	AR414257 Sequence	634	58	2.6	1026	9	BC031650	BC031650 Homo sapi
562	58	2.6	741	6	AX971091	AX971091 Sequence	635	58	2.6	1032	8	LETHM18GE	X98308 L.esculentu
563	58	2.6	741	6	BD109810	BD109810 EST and e	636	58	2.6	1042	9	BC036790	BC036790 Homo sapi
564	58	2.6	749	10	BC049667	BC049667 Mus muscu	637	58	2.6	1046	9	BC032585	BC032585 Homo sapi
565	58	2.6	759	6	AR429329	AR429329 Sequence	638	58	2.6	1056	3	AY069254	AY069254 Drosophil
566	58	2.6	759	8	BT008966	BT008966 Triticum	639	58	2.6	1062	6	AR438054	AR438054 Sequence
567	58	2.6	759	9	BC043514	BC043514 Homo sapi	640	58	2.6	1063	9	BC047332	BC047332 Homo sapi
568	58	2.6	761	9	BC037214	BC037214 Homo sapi	641	58	2.6	1065	8	ZMYPTM2A	X63278 Z.mays yptm
569	58	2.6	762	9	BC070287	BC070287 Homo sapi	642	58	2.6	1065	9	BC073914	BC073914 Homo sapi
570	58	2.6	763	9	BC040916	BC040916 Homo sapi	643	58	2.6	1069	6	BD192979	BD192979 207 human
571	58	2.6	781	9	AK000690	AK000690 Homo sapi	644	58	2.6	1069	6	CQ821975	CQ821975 Sequence
572	58	2.6	781	9	AK074413	AK074413 Homo sapi	645	58	2.6	1074	9	BC052808	BC052808 Homo sapi
573	58	2.6	791	3	AY156926	AY156926 Pinctada	646	58	2.6	1082	9	BC029908	BC029908 Homo sapi
574	58	2.6	791	8	BT009373	BT009373 Triticum	c 647	58	2.6	1083	9	HSM800561	AL080060 Homo sapi
575	58	2.6	794	9	BC058920	BC058920 Homo sapi	648	58	2.6	1088	10	BC014283	BC014283 Mus muscu
576	58	2.6	809	6	BD252094	BD252094 47 secret	649	58	2.6	1092	10	BC005748	BC005748 Mus muscu
577	58	2.6	814	10	BC025933	BC025933 Mus muscu	650	58	2.6	1097	8	BT009078	BT009078 Triticum
578	58	2.6	815	10	AF035161	AF035161 Mus muscu	651	58	2.6	1102	9	HSM805713	BX537414 Homo sapi
579	58	2.6	816	6	CQ486089	CQ486089 Sequence	652	58	2.6	1105	10	BC005696	BC005696 Mus muscu
580	58	2.6	822	6	BD271590	BD271590 49 human	653	58	2.6	1108	9	BC018104	BC018104 Homo sapi
581	58	2.6	851	9	BC016844	BC016844 Homo sapi	654	58	2.6	1112	5	BC060917	BC060917 Danio rer
582	58	2.6	859	9	BC043551	BC043551 Homo sapi	655	58	2.6	1113	10	BC013777	BC013777 Mus muscu
583	58	2.6	866	10	BC026557	BC026557 Mus muscu	656	58	2.6	1119	9	BC071717	BC071717 Homo sapi
584	58	2.6	868	9	BC033502	BC033502 Homo sapi	657	58	2.6	1120	9	BC035904	BC035904 Homo sapi
c 585	58	2.6	870	6	CQ482086	CQ482086 Sequence	658	58	2.6	1126	6	BD275148	BD275148 48 Human
586	58	2.6	870	8	BT009293	BT009293 Triticum	659	58	2.6	1130	10	BC061770	BC061770 Rattus no
587	58	2.6	872	9	BC058073	BC058073 Homo sapi	660	58	2.6	1133	10	BC044743	BC044743 Mus muscu
588	58	2.6	875	9	AF242525	AF242525 Homo sapi	661	58	2.6	1138	4	AF360872	AF360872 Oryctolag
589	58	2.6	878	9	BC009521	BC009521 Homo sapi	662	58	2.6	1148	8	OSY15009	Y15009 Oryza sativ
590	58	2.6	880	9	AF207829	AF207829 Homo sapi	663	58	2.6	1159	9	BC067119	BC067119 Homo sapi
591	58	2.6	880	9	BC018139	BC018139 Homo sapi	664	58	2.6	1164	9	BC006332	BC006332 Homo sapi
592	58	2.6	882	10	BC062186	BC062186 Mus muscu	665	58	2.6	1174	9	AF094850	AF094850 Homo sapi
593	58	2.6	887	3	AY099474	AY099474 Haematobi	666	58	2.6	1178	6	BD275922	BD275922 Uncouplin
594	58	2.6	892	9	BC000077	BC000077 Homo sapi	667	58	2.6	1178	10	BC048734	BC048734 Mus muscu
595	58	2.6	900	10	BC002073	BC002073 Mus muscu	668	58	2.6	1183	10	BC046431	BC046431 Mus muscu
596	58	2.6	907	10	BC058959	BC058959 Mus muscu	669	58	2.6	1195	9	HSM802132	AL137429 Homo sapi
597	58	2.6	910	10	BC049687	BC049687 Mus muscu	670	58	2.6	1197	9	BC031811	BC031811 Homo sapi
598	58	2.6	914	9	BC036297	BC036297 Homo sapi	671	58	2.6	1197	10	BC036984	BC036984 Mus muscu
599	58	2.6	923	10	BC026487	BC026487 Mus muscu	672	58	2.6	1198	9	BC000051	BC000051 Homo sapi
600	58	2.6	931	9	BC064491	BC064491 Homo sapi	673	58	2.6	1198	10	BC033305	BC033305 Mus muscu
601	58	2.6	935	10	BC049693	BC049693 Mus muscu	674	58	2.6	1200	10	BC038126	BC038126 Mus muscu
602	58	2.6	939	5	BC061437	BC061437 Xenopus t	675	58	2.6	1203	8	AF187063	AF187063 Oryza sat
603	58	2.6	940	10	BC060548	BC060548 Rattus no	676	58	2.6	1208	9	BC046635	BC046635 Homo sapi

677	58	2.6	1238	5	BC041264	BC041264 Xenopus l	750
678	58	2.6	1238	9	BC025970	Homo sapi	751
679	58	2.6	1238	9	HSM802295	AL137556 Homo sapi	752
680	58	2.6	1242	9	BC017721	Homo sapi	753
681	58	2.6	1244	10	MMBASIII	Y16258 Mus musculu	754
682	58	2.6	1254	9	BC054506	BC054506 Homo sapi	755
683	58	2.6	1257	8	AY367058	Pisum sat	756
684	58	2.6	1259	5	BC051778	BC051778 Danio rer	757
685	58	2.6	1265	9	BC018847	BC018847 Homo sapi	758
686	58	2.6	1271	9	BC029647	BC029647 Homo sapi	759
687	58	2.6	1276	6	A57389	A57389 Sequence 4	760
688	58	2.6	1290	9	BC062599	BC062599 Homo sapi	761
689	58	2.6	1294	8	AF394890	AF394890 Filobasid	762
690	58	2.6	1298	5	BC053261	BC053261 Danio rer	763
691	58	2.6	1298	10	MMBASII	Y16257 Mus musculu	764
692	58	2.6	1299	6	BD227288	BD227288 Secreted	765
693	58	2.6	1302	6	E02756	E02756 DNA encodin	766
694	58	2.6	1302	6	BD140113	BD140113 Secreted	767
695	58	2.6	1302	10	MMBASI	Y16256 Mus musculu	768
696	58	2.6	1303	9	HSM802259	AL137526 Homo sapi	769
697	58	2.6	1311	3	BT011164	BT011164 Drosophil	770
698	58	2.6	1311	10	BC030932	BC030932 Mus muscu	771
699	58	2.6	1315	5	BC055585	BC055585 Danio rer	772
700	58	2.6	1316	9	BC069049	BC069049 Homo sapi	773
701	58	2.6	1317	10	BC059775	BC059775 Mus muscu	774
702	58	2.6	1319	10	BC057971	BC057971 Mus muscu	775
703	58	2.6	1329	9	BC071737	BC071737 Homo sapi	776
704	58	2.6	1330	10	BC064023	BC064023 Mus muscu	777
705	58	2.6	1339	9	BC016998	BC016998 Homo sapi	778
706	58	2.6	1339	9	BC048255	BC048255 Homo sapi	779
707	58	2.6	1342	6	BD223153	BD223153 98 human	780
708	58	2.6	1342	6	AR243851	AR243851 Sequence	781
709	58	2.6	1343	5	BC057508	BC057508 Danio rer	782
710	58	2.6	1343	9	BC052989	BC052989 Homo sapi	783
711	58	2.6	1344	8	BT009299	BT009299 Triticum	784
712	58	2.6	1348	5	BC057423	BC057423 Danio rer	785
713	58	2.6	1350	10	BC057639	BC057639 Mus muscu	786
714	58	2.6	1362	3	AY070872	AY070872 Drosophil	787
715	58	2.6	1366	9	BC065486	BC065486 Homo sapi	788
716	58	2.6	1368	5	BC064278	BC064278 Xenopus t	789
717	58	2.6	1372	8	ATCOQ3	Y15055 Arabidopsis	790
718	58	2.6	1377	5	BC063336	BC063336 Xenopus t	791
719	58	2.6	1388	3	AF182511	AF182511 Drosophil	792
720	58	2.6	1389	5	XLNLPNO38	X56039 X.laavis mR	793
721	58	2.6	1391	5	BC074604	BC074604 Xenopus t	794
722	58	2.6	1402	9	BC040630	BC040630 Homo sapi	795
723	58	2.6	1405	6	AR337570	AR337570 Sequence	796
724	58	2.6	1405	6	BD130049	BD130049 Human ser	797
725	58	2.6	1412	6	AR452913	AR452913 Sequence	798
726	58	2.6	1414	10	BC049767	BC049767 Mus muscu	799
727	58	2.6	1416	8	AY443040	AY443040 Arabidops	800
728	58	2.6	1416	9	BC004950	BC004950 Homo sapi	801
729	58	2.6	1418	9	BC075806	BC075806 Homo sapi	802
730	58	2.6	1423	6	I09360	I09360 Sequence 1	803
731	58	2.6	1424	5	BC063367	BC063367 Xenopus t	804
732	58	2.6	1441	9	BC050568	BC050568 Homo sapi	805
733	58	2.6	1444	9	BC064535	BC064535 Homo sapi	806
734	58	2.6	1444	9	HSM801370	AL133093 Homo sapi	807
735	58	2.6	1452	10	BC030672	BC030672 Mus muscu	808
736	58	2.6	1455	5	BC053247	BC053247 Danio rer	809
737	58	2.6	1456	9	BC025257	BC025257 Homo sapi	810
738	58	2.6	1460	5	BC065641	BC065641 Danio rer	811
739	58	2.6	1469	5	XLB50GAP4	X87582 X.laavis B-	812
740	58	2.6	1469	10	BC055305	BC055305 Mus muscu	813
741	58	2.6	1475	6	BD249092	BD249092 49 human	814
742	58	2.6	1479	9	BC018977	BC018977 Homo sapi	815
743	58	2.6	1480	10	BC062376	BC062376 Mus muscu	816
744	58	2.6	1481	6	BD275459	BD275459 47 Human	817
745	58	2.6	1486	6	BD223469	BD223469 94 human	818
746	58	2.6	1486	6	AR243103	AR243103 Sequence	819
747	58	2.6	1486	6	AR404284	AR404284 Sequence	820
748	58	2.6	1493	6	E05822	E05822 DNA encodin	821
749	58	2.6	1493	6	I19901	I19901 Sequence 24	822

58	2.6	1493	6	I40996	I40996 Sequence 24	750
58	2.6	1500	5	BC065586	BC065586 Danio rer	751
58	2.6	1500	10	BC049755	BC049755 Mus muscu	752
58	2.6	1500	10	BC065307	BC065307 Rattus no	753
58	2.6	1507	9	BC002839	BC002839 Homo sapi	754
58	2.6	1509	10	BC071190	BC071190 Mus muscu	755
58	2.6	1510	5	BC074510	BC074510 Xenopus t	756
58	2.6	1511	10	BC061104	BC061104 Mus muscu	757
58	2.6	1516	8	OSABTUB1	X78142 O.sativa (A	758
58	2.6	1519	6	AX546769	AX546769 Sequence	759
58	2.6	1520	9	AK026597	AK026597 Homo sapi	760
58	2.6	1523	10	BC027081	BC027081 Mus muscu	761
58	2.6	1525	6	AR142178	AR142178 Sequence	762
58	2.6	1525	6	AR144464	AR144464 Sequence	763
58	2.6	1525	6	BD224149	BD224149 REC2 kina	764
58	2.6	1525	6	AR214787	AR214787 Sequence	765
58	2.6	1525	6	BD003352	BD003352 Mammalian	766
58	2.6	1525	10	MMU92068	U92068 Mus musculu	767
58	2.6	1531	9	BC042073	BC042073 Homo sapi	768
58	2.6	1535	9	BC025659	BC025659 Homo sapi	769
58	2.6	1537	8	CAR400861	AJ400861 Cicer ari	770
58	2.6	1540	9	BC053865	BC053865 Homo sapi	771
58	2.6	1547	5	BC076743	BC076743 Xenopus l	772
58	2.6	1547	6	BD275163	BD275163 48 Human	773
58	2.6	1551	9	BC017072	BC017072 Homo sapi	774
58	2.6	1559	9	BC009822	BC009822 Homo sapi	775
58	2.6	1570	6	AX376268	AX376268 Sequence	776
58	2.6	1570	6	AX697223	AX697223 Sequence	777
58	2.6	1570	9	AY358532	AY358532 Homo sapi	778
58	2.6	1577	9	BC025726	BC025726 Homo sapi	779
58	2.6	1580	6	BD231696	BD231696 31 human	780
58	2.6	1580	9	BC037569	BC037569 Homo sapi	781
58	2.6	1584	5	BC042270	BC042270 Xenopus l	782
58	2.6	1588	5	BC049408	BC049408 Danio rer	783
58	2.6	1588	9	BC032381	BC032381 Homo sapi	784
58	2.6	1591	9	HSM807298	BX647154 Homo sapi	785
58	2.6	1591	10	AB041801	AB041801 Mus muscl	786
58	2.6	1598	9	AK000432	AK000432 Homo sapi	787
58	2.6	1601	9	BC010419	BC010419 Homo sapi	788
58	2.6	1609	9	BC040703	BC040703 Homo sapi	789
58	2.6	1624	6	AX464048	AX464048 Sequence	790
58	2.6	1624	9	AY359115	AY359115 Homo sapi	791
58	2.6	1636	8	ATASKDZET	X94938 A.thaliana	792
58	2.6	1637	6	BD193083	BD193083 207 human	793
58	2.6	1637	6	CQ822079	CQ822079 Sequence	794
58	2.6	1641	9	BC010739	BC010739 Homo sapi	795
58	2.6	1642	9	HSM805977	BX537512 Homo sapi	796
58	2.6	1646	8	AF058708	AF058708 Zea mays	797
58	2.6	1646	9	BC051812	BC051812 Homo sapi	798
58	2.6	1652	8	BT009431	BT009431 Triticum	799
58	2.6	1654	9	AB055370	AB055370 Macaca fa	800
58	2.6	1660	3	AY069770	AY069770 Drosophil	801
58	2.6	1660	9	BC032309	BC032309 Homo sapi	802
58	2.6	1660	10	BC062018	BC062018 Rattus no	803
58	2.6	1662	8	AY243851	AY243851 Galdieria	804
58	2.6	1664	9	BC048288	BC048288 Homo sapi	805
58	2.6	1674	3	AY070845	AY070845 Drosophil	806
58	2.6	1674	6	AR252574	AR252574 Sequence	807
58	2.6	1674	6	AX403413	AX403413 Sequence	808
58	2.6	1674	6	AX454576	AX454576 Sequence	809
58	2.6	1674	6	AX464320	AX464320 Sequence	810
58	2.6	1674	6	AX491054	AX491054 Sequence	811
58	2.6	1674	9	AY358950	AY358950 Homo sapi	812
58	2.6	1676	3	DDRAX	Z11804 D.discoideu	813
58	2.6	1677	5	BC074594	BC074594 Xenopus t	814
58	2.6	1685	5	BC048049	BC048049 Danio rer	815
58	2.6	1685	9	BC009889	BC009889 Homo sapi	816
58	2.6	1685	9	BC018841	BC018841 Homo sapi	817
58	2.6	1691	3	AF044679	AF044679 Leishmani	818
58	2.6	1691	9	AK025549	AK025549 Homo sapi	819
58	2.6	1691	10	BC019184	BC019184 Mus muscu	820
58	2.6	1692	6	AR360374	AR360374 Sequence	821
58	2.6	1692	9	AF132676	AF132676 Homo sapi	822

I40996	Sequence 24
BC065586	Danio rer
BC049755	Mus muscu
BC065307	Rattus no
BC002839	Homo sapi
BC071190	Mus muscu
BC074510	Xenopus t
BC061104	Mus muscu
X78142	O.sativa (A
AX546769	Sequence
AK026597	Homo sapi
BC027081	Mus muscu
AR142178	Sequence
AR144464	Sequence
BD224149	REC2 kina
AR214787	Sequence
BD003352	Mammalian
U92068	Mus musculu
BC042073	Homo sapi
BC025659	Homo sapi
AJ400861	Cicer ari
BC053865	Homo sapi
BC076743	Xenopus l
BD275163	48 Human
BC017072	Homo sapi
BC009822	Homo sapi
AX376268	Sequence
AX697223	Sequence
AY358532	Homo sapi
BC025726	Homo sapi
BD231696	31 human
BC037569	Homo sapi
BC042270	Xenopus l
BC049408	Danio rer
BC032381	Homo sapi
BX647154	Homo sapi
AB041801	Mus muscl
AK000432	Homo sapi
BC010419	Homo sapi
BC040703	Homo sapi
AX464048	Sequence
AY359115	Homo sapi
X94938	A.thaliana
BD193083	207 human
CQ822079	Sequence
BC010739	Homo sapi
BX537512	Homo sapi
AF058708	Zea mays
BC051812	Homo sapi
BT009431	Triticum
AB055370	Macaca fa
AY069770	Drosophil
BC032309	Homo sapi
BC062018	Rattus no
AY243851	Galdieria
BC048288	Homo sapi
AY070845	Drosophil
AR252574	Sequence
AX403413	Sequence
AX454576	Sequence
AX464320	Sequence
AX491054	Sequence
AY358950	Homo sapi
Z11804	D.discoideu
BC074594	Xenopus t
BC048049	Danio rer
BC009889	Homo sapi
BC018841	Homo sapi
AF044679	Leishmani
AK025549	Homo sapi
BC019184	Mus muscu
AR360374	Sequence
AF132676	Homo sapi

823	58	2.6	1697	10	AF166267	AF166267 Rattus no	896	58	2.6	1960	9	BC007355	BC007355 Homo sapi
824	58	2.6	1702	9	BC006832	BC006832 Homo sapi	897	58	2.6	1962	9	BC009848	BC009848 Homo sapi
825	58	2.6	1710	9	AB047897	AB047897 Macaca fa	898	58	2.6	1966	10	BC024430	BC024430 Mus muscu
826	58	2.6	1717	5	BC056693	BC056693 Danio rer	899	58	2.6	1975	9	BC017376	BC017376 Homo sapi
827	58	2.6	1725	6	AR451632	AR451632 Sequence	900	58	2.6	1981	3	AFACHA	X64584 A.fulica Fe
828	58	2.6	1733	10	BC017530	BC017530 Mus muscu	901	58	2.6	1984	9	AB071103	AB071103 Macaca fa
829	58	2.6	1738	9	HSM801162	AL117626 Homo sapi	902	58	2.6	1985	6	BD175393	BD175393 Secretary
830	58	2.6	1744	8	BT009253	BT009253 Triticum	903	58	2.6	1985	6	AR410771	AR410771 Sequence
831	58	2.6	1761	9	BC054519	BC054519 Homo sapi	904	58	2.6	1985	6	AR439135	AR439135 Sequence
832	58	2.6	1762	10	BC022118	BC022118 Mus muscu	905	58	2.6	1985	6	AR473155	AR473155 Sequence
833	58	2.6	1768	8	SCSACPD	X78935 S.commerson	906	58	2.6	1985	6	AX375960	AX375960 Sequence
834	58	2.6	1769	9	BC025749	BC025749 Homo sapi	907	58	2.6	1985	6	AX697621	AX697621 Sequence
835	58	2.6	1780	10	BC062053	BC062053 Rattus no	908	58	2.6	1985	6	BD075542	BD075542 Secretary
836	58	2.6	1788	9	BC044944	BC044944 Homo sapi	909	58	2.6	1985	6	BD172402	BD172402 Secreted
837	58	2.6	1788	9	HSM801263	AL122106 Homo sapi	910	58	2.6	1985	6	BD172721	BD172721 Secreted
838	58	2.6	1790	10	BC024638	BC024638 Mus muscu	911	58	2.6	1985	6	BD173040	BD173040 Secreted
839	58	2.6	1791	9	BC015779	BC015779 Homo sapi	912	58	2.6	1985	6	BD173359	BD173359 Secreted
840	58	2.6	1797	9	AK027161	AK027161 Homo sapi	913	58	2.6	1985	6	AY358500	AY358500 Homo sapi
841	58	2.6	1798	9	BC042845	BC042845 Homo sapi	914	58	2.6	1987	9	BX957216	BX957216 Homo sapi
842	58	2.6	1805	6	CQ413955	BC066434 Danio rer	915	58	2.6	1993	9	AK026793	AK026793 Homo sapi
843	58	2.6	1805	8	AY036609	CQ413955 Sequence	916	58	2.6	1996	9	BC062574	BC062574 Homo sapi
844	58	2.6	1808	9	AK000636	AY036609 Triticum	917	58	2.6	2005	9	BC040276	BC040276 Homo sapi
845	58	2.6	1811	6	CQ414890	AK000636 Homo sapi	918	58	2.6	2005	9	HSM803426	AL832119 Homo sapi
846	58	2.6	1817	9	BC020499	BC020499 Homo sapi	919	58	2.6	2009	9	BC050391	BC050391 Homo sapi
847	58	2.6	1819	9	BC009930	BC009930 Homo sapi	920	58	2.6	2009	10	BC031165	BC031165 Mus muscu
848	58	2.6	1820	5	BC066434	BC066434 Danio rer	921	58	2.6	2016	8	AF428076	AF428076 Paracocci
849	58	2.6	1820	9	BC064387	BC064387 Homo sapi	922	58	2.6	2018	5	BC066638	BC066638 Danio rer
850	58	2.6	1822	9	AF061836	AF061836 Homo sapi	923	58	2.6	2021	5	BC044045	BC044045 Xenopus l
851	58	2.6	1822	10	BC058602	BC058602 Mus muscu	924	58	2.6	2027	10	BC052191	BC052191 Mus muscu
852	58	2.6	1823	9	BC008904	BC008904 Homo sapi	925	58	2.6	2030	9	BC041637	BC041637 Homo sapi
853	58	2.6	1824	9	BC028094	BC028094 Homo sapi	926	58	2.6	2030	10	BC058229	BC058229 Mus muscu
854	58	2.6	1825	9	BC063388	BC063388 Homo sapi	927	58	2.6	2033	10	BC021915	BC021915 Mus muscu
855	58	2.6	1831	10	BC028896	BC028896 Mus muscu	928	58	2.6	2034	5	BC067669	BC067669 Danio rer
856	58	2.6	1833	9	HSM802685	AL359583 Homo sapi	929	58	2.6	2045	6	AR229196	AR229196 Sequence
857	58	2.6	1838	5	BC053151	BC053151 Danio rer	930	58	2.6	2045	6	AX810698	AX810698 Sequence
858	58	2.6	1839	10	BC053440	BC053440 Mus muscu	931	58	2.6	2045	6	BD084173	BD084173 28 human
859	58	2.6	1842	10	BC055473	BC055473 Mus muscu	932	58	2.6	2047	10	BC053455	BC053455 Mus muscu
860	58	2.6	1846	9	BC008280	BC008280 Homo sapi	933	58	2.6	2048	9	BC044243	BC044243 Homo sapi
861	58	2.6	1847	3	AY069729	AY069729 Drosophil	934	58	2.6	2050	5	BC066614	BC066614 Danio rer
862	58	2.6	1849	5	BC061396	BC061396 Xenopus t	935	58	2.6	2060	10	BC049179	BC049179 Mus muscu
863	58	2.6	1851	10	BC017684	BC017684 Mus muscu	936	58	2.6	2063	10	BC003900	BC003900 Mus muscu
864	58	2.6	1856	3	BT003792	BT003792 Drosophil	937	58	2.6	2064	8	BT009245	BT009245 Triticum
865	58	2.6	1860	9	BC058897	BC058897 Homo sapi	938	58	2.6	2065	9	BC024260	BC024260 Homo sapi
866	58	2.6	1864	14	SMVAJ6202	AJ006202 Sugarcane	939	58	2.6	2069	9	BC007641	BC007641 Homo sapi
867	58	2.6	1872	6	AR208578	AR208578 Sequence	940	58	2.6	2070	10	BC046278	BC046278 Mus muscu
868	58	2.6	1872	8	BT009301	BT009301 Triticum	941	58	2.6	2072	9	BC044245	BC044245 Homo sapi
869	58	2.6	1872	10	BC023437	BC023437 Mus muscu	942	58	2.6	2073	10	BC060677	BC060677 Mus muscu
870	58	2.6	1879	10	BC060146	BC060146 Mus muscu	943	58	2.6	2074	9	BC035912	BC035912 Homo sapi
871	58	2.6	1880	6	CQ769491	CQ769491 Sequence	944	58	2.6	2076	10	BC010309	BC010309 Mus muscu
872	58	2.6	1884	9	AF086921	AF086921 Homo sapi	945	58	2.6	2079	10	BC029014	BC029014 Mus muscu
873	58	2.6	1885	10	BC051143	BC051143 Mus muscu	946	58	2.6	2081	5	BC064187	BC064187 Xenopus t
874	58	2.6	1888	5	BC068332	BC068332 Danio rer	947	58	2.6	2082	9	HSM802275	AL137538 Homo sapi
875	58	2.6	1889	5	AB025103	AB025103 Gallus ga	948	58	2.6	2090	9	BC071171	BC071171 Homo sapi
876	58	2.6	1889	9	AB066553	AB066553 Macaca fa	949	58	2.6	2090	10	BC038500	BC038500 Mus muscu
877	58	2.6	1890	9	AK025208	AK025208 Homo sapi	950	58	2.6	2094	10	BC033384	BC033384 Mus muscu
878	58	2.6	1892	9	BC065843	BC065843 Homo sapi	951	58	2.6	2095	9	BC006472	BC006472 Homo sapi
879	58	2.6	1894	9	BC011889	BC011889 Homo sapi	952	58	2.6	2096	3	AY061097	AY061097 Drosophil
880	58	2.6	1894	9	HSM803495	AL832188 Homo sapi	953	58	2.6	2103	10	BC022603	BC022603 Mus muscu
881	58	2.6	1900	9	BC025963	BC025963 Homo sapi	954	58	2.6	2104	10	BC023321	BC023321 Mus muscu
882	58	2.6	1900	9	BC063603	BC063603 Homo sapi	955	58	2.6	2106	9	BC027948	BC027948 Homo sapi
883	58	2.6	1903	10	BC023012	BC023012 Mus muscu	956	58	2.6	2115	5	BC051611	BC051611 Danio rer
884	58	2.6	1908	9	AK025209	AK025209 Homo sapi	957	58	2.6	2116	10	BC030862	BC030862 Mus muscu
885	58	2.6	1915	10	BC046597	BC046597 Mus muscu	958	58	2.6	2119	8	BT009049	BT009049 Triticum
886	58	2.6	1920	10	BC059229	BC059229 Mus muscu	959	58	2.6	2122	9	BC037277	BC037277 Homo sapi
887	58	2.6	1928	9	BC039741	BC039741 Homo sapi	960	58	2.6	2134	5	XLCTG	X84990 X.laavis Cc
888	58	2.6	1929	10	BC058811	BC058811 Mus muscu	961	58	2.6	2138	9	BC067301	BC067301 Homo sapi
889	58	2.6	1932	9	AK026947	AK026947 Homo sapi	962	58	2.6	2140	9	BC062566	BC062566 Homo sapi
890	58	2.6	1934	9	AK025407	AK025407 Homo sapi	963	58	2.6	2145	9	BC037968	BC037968 Homo sapi
891	58	2.6	1936	9	BC042416	BC042416 Homo sapi	964	58	2.6	2149	9	BC072428	BC072428 Homo sapi
892	58	2.6	1945	9	BC072393	BC072393 Homo sapi	965	58	2.6	2151	9	BC032474	BC032474 Homo sapi
893	58	2.6	1953	9	BC029049	BC029049 Homo sapi	966	58	2.6	2153	10	RNP4502C	X55446 Rat mRNA fo
894	58	2.6	1956	9	BC052580	BC052580 Homo sapi	967	58	2.6	2159	3	AY119209	AY119209 Drosophil
895	58	2.6	1958	5	BC064256	BC064256 Xenopus t	968	58	2.6	2164	9	BC028132	BC028132 Homo sapi

969 58 2.6 2207 9 BC058880 BC058880 Homo sapi
970 58 2.6 2217 9 BC073932 BC073932 Homo sapi
971 58 2.6 2220 9 BC007556 BC007556 Homo sapi
972 58 2.6 2237 9 BC069230 BC069230 Homo sapi
973 58 2.6 2238 10 AF356506 AF356506 Mus muscu
974 58 2.6 2246 6 AR212256 AR212256 Sequence
975 58 2.6 2246 6 AR265251 AR265251 Sequence
976 58 2.6 2246 10 AF017152 AF017152 Mus muscu
977 58 2.6 2247 5 BC058510 BC058510 Danio rer
978 58 2.6 2257 6 AX048774 AX048774 Sequence
979 58 2.6 2266 9 BC041164 BC041164 Homo sapi
980 58 2.6 2275 9 AF218023 AF218023 Homo sapi
981 58 2.6 2287 9 BC044220 BC044220 Homo sapi
982 58 2.6 2291 9 AK000753 AK000753 Homo sapi
983 58 2.6 2298 5 BC074532 BC074532 Xenopus t
984 58 2.6 2298 9 BC029162 BC029162 Homo sapi
985 58 2.6 2313 10 BC029670 BC029670 Mus muscu
986 58 2.6 2322 9 BC017240 BC017240 Homo sapi
987 58 2.6 2324 5 BC062381 BC062381 Danio rer
988 58 2.6 2327 10 MMU96683 U96683 Mus musculus
989 58 2.6 2330 9 BC006555 BC006555 Homo sapi
990 58 2.6 2366 9 BC017481 BC017481 Homo sapi
991 58 2.6 2368 9 HSM802593 AL162062 Homo sapi
992 58 2.6 2369 9 AK074384 AK074384 Homo sapi
993 58 2.6 2371 9 HSM805927 BX537833 Homo sapi
994 58 2.6 2374 3 AY119126 AY119126 Drosophil
995 58 2.6 2379 9 BC025698 BC025698 Homo sapi
996 58 2.6 2388 10 BC030895 BC030895 Mus muscu
997 58 2.6 2397 9 BC052990 BC052990 Homo sapi
998 58 2.6 2400 9 BC053347 BC053347 Homo sapi
999 58 2.6 2403 9 HSM808752 BX648601 Homo sapi
1000 58 2.6 2415 9 BC028002 BC028002 Homo sapi
1001 58 2.6 2415 9 BC032459 BC032459 Homo sapi
1002 58 2.6 2432 10 BC003959 BC003959 Mus muscu
1003 58 2.6 2438 6 AR310306 AR310306 Sequence
1004 58 2.6 2438 6 AX097774 AX097774 Sequence
1005 58 2.6 2443 9 BC063448 BC063448 Homo sapi
1006 58 2.6 2445 9 BC038798 BC038798 Homo sapi
1007 58 2.6 2453 9 HSM807676 BX647530 Homo sapi
1008 58 2.6 2454 10 BC031113 BC031113 Mus muscu
1009 58 2.6 2465 5 BC070798 BC070798 Xenopus l
1010 58 2.6 2466 9 HSM802197 AL137712 Homo sapi
1011 58 2.6 2468 8 AF503585 AF503585 Oryza sat
1012 58 2.6 2474 3 AY220909 AY220909 Helicover
1013 58 2.6 2490 9 BC073845 BC073845 Homo sapi
1014 58 2.6 2496 5 BC079755 BC079755 Xenopus l
1015 58 2.6 2500 9 BC035690 BC035690 Homo sapi
1016 58 2.6 2533 5 BC064702 BC064702 Danio rer
1017 58 2.6 2533 9 HSM803787 AL832479 Homo sapi
1018 58 2.6 2533 10 BC006690 BC006690 Mus muscu
1019 58 2.6 2539 10 BC006050 BC006050 Mus muscu
1020 58 2.6 2542 10 BC060983 BC060983 Mus muscu
1021 58 2.6 2553 10 BC061558 BC061558 Rattus no
1022 58 2.6 2562 6 AX477654 AX477654 Sequence
1023 58 2.6 2562 9 AK025708 AK025708 Homo sapi
1024 58 2.6 2564 9 BC017181 BC017181 Homo sapi
1025 58 2.6 2565 9 BC007198 BC007198 Homo sapi
1026 58 2.6 2565 9 BC017438 BC017438 Homo sapi
1027 58 2.6 2565 9 BC030233 BC030233 Homo sapi
1028 58 2.6 2578 9 BC064805 BC064805 Homo sapi
1029 58 2.6 2586 9 BC006207 BC006207 Homo sapi
1030 58 2.6 2594 6 A45787 A45787 Sequence 25
1031 58 2.6 2594 8 CMACON X82840 C.melo mRNA
1032 58 2.6 2600 9 BC035596 BC035596 Homo sapi
1033 58 2.6 2601 5 BC072034 BC072034 Xenopus l
1034 58 2.6 2626 10 BC013637 BC013637 Mus muscu
1035 58 2.6 2628 5 BC053210 BC053210 Danio rer
1036 58 2.6 2628 6 I66342 I66342 Sequence 1
1037 58 2.6 2630 9 BC033813 BC033813 Homo sapi
1038 58 2.6 2634 6 AR241385 AR241385 Sequence
1039 58 2.6 2634 6 AX006092 AX006092 Sequence
1040 58 2.6 2634 6 BD080224 BD080224 Starch de
1041 58 2.6 2634 8 AY132998 AY132998 Solanum t

1042 58 2.6 2667 5 BC064852 BC064852
1043 58 2.6 2690 10 BC058562 BC058562
1044 58 2.6 2699 9 BC013364 BC013364 Homo sapi
1045 58 2.6 2702 9 BC017163 BC017163 Homo sapi
1046 58 2.6 2710 3 DMORDPROT X92840 D.melanogas
1047 58 2.6 2736 9 HSM801348 AL133077 Homo sapi
1048 58 2.6 2754 10 BC066817 BC066817 Mus muscu
1049 58 2.6 2762 10 BC006698 BC006698 Mus muscu
1050 58 2.6 2771 10 BC027055 BC027055 Mus muscu
1051 58 2.6 2773 10 BC064468 BC064468 Mus muscu
1052 58 2.6 2789 10 BC026672 BC026672 Mus muscu
1053 58 2.6 2789 10 BC046625 BC046625 Mus muscu
1054 58 2.6 2800 9 BC014632 BC014632 Homo sapi
1055 58 2.6 2800 9 BC053596 BC053596 Homo sapi
1056 58 2.6 2809 10 BC053333 BC053333 Mus muscu
1057 58 2.6 2811 10 BC051178 BC051178 Mus muscu
1058 58 2.6 2813 9 AF217991 AF217991 Homo sapi
1059 58 2.6 2816 9 BC013975 BC013975 Homo sapi
1060 58 2.6 2827 9 HSM807053 BX649191 Homo sapi
1061 58 2.6 2855 6 AX574572 AX574572 Sequence
1062 58 2.6 2855 9 AY358127 AY358127 Homo sapi
1063 58 2.6 2873 9 BC042488 BC042488 Homo sapi
1064 58 2.6 2873 10 BC046232 BC046232 Mus muscu
1065 58 2.6 2874 6 AX815603 AX815603 Sequence
1066 58 2.6 2875 9 HSM808745 BX648594 Homo sapi
1067 58 2.6 2881 9 IR2004669 AL389951 Homo sapi
1068 58 2.6 2886 10 BC025599 BC025599 Mus muscu
1069 58 2.6 2890 10 BC036168 BC036168 Mus muscu
1070 58 2.6 2907 9 BC042125 BC042125 Homo sapi
1071 58 2.6 2908 10 BC043702 BC043702 Mus muscu
1072 58 2.6 2909 10 BC053050 BC053050 Mus muscu
1073 58 2.6 2924 6 AX683129 AX683129 Sequence
1074 58 2.6 2924 9 BC063554 BC063554 Homo sapi
1075 58 2.6 2924 10 S68736 S68736 Rattus sp.
1076 58 2.6 2940 9 BC037172 BC037172 Homo sapi
1077 58 2.6 2943 9 HSM803526 AL832219 Homo sapi
1078 58 2.6 2968 9 BC041697 BC041697 Homo sapi
1079 58 2.6 2975 9 BC012172 BC012172 Homo sapi
1080 58 2.6 2980 6 BD270060 BD270060 Secreted
1081 58 2.6 2993 10 BC052189 BC052189 Mus muscu
1082 58 2.6 3002 6 AX354181 AX354181 Sequence
1083 58 2.6 3002 9 HSM808510 BX648362 Homo sapi
1084 58 2.6 3039 3 AY280848 AY280848 Apis mell
1085 58 2.6 3046 9 AY129024 AY129024 Homo sapi
1086 58 2.6 3048 10 BC054124 BC054124 Mus muscu
1087 58 2.6 3055 6 AX430977 AX430977 Sequence
1088 58 2.6 3057 9 BC019256 BC019256 Homo sapi
1089 58 2.6 3061 10 AF180525 AF180525 Rattus no
1090 58 2.6 3096 9 BC035284 BC035284 Homo sapi
1091 58 2.6 3120 9 BC038443 BC038443 Homo sapi
1092 58 2.6 3124 6 AR235862 AR235862 Sequence
1093 58 2.6 3124 6 AR432042 AR432042 Sequence
1094 58 2.6 3124 6 AX350342 AX350342 Sequence
1095 58 2.6 3141 10 BC017634 BC017634 Mus muscu
1096 58 2.6 3143 3 BT011466 BT011466 Drosophil
1097 58 2.6 3151 9 BC029653 BC029653 Homo sapi
1098 58 2.6 3154 10 BC027028 BC027028 Mus muscu
1099 58 2.6 3154 10 BC065074 BC065074 Mus muscu
1100 58 2.6 3164 9 BC041161 BC041161 Homo sapi
1101 58 2.6 3166 10 BC053054 BC053054 Mus muscu
1102 58 2.6 3211 10 BC060096 BC060096 Mus muscu
1103 58 2.6 3224 6 AX754970 AX754970 Sequence
1104 58 2.6 3224 9 BC032429 BC032429 Homo sapi
1105 58 2.6 3250 5 BC068779 BC068779 Xenopus l
1106 58 2.6 3254 10 AF522186 AF522186 Rattus no
1107 58 2.6 3275 9 BC030523 BC030523 Homo sapi
1108 58 2.6 3282 10 AF030513 AF030513 Mus muscu
1109 58 2.6 3287 10 BC028272 BC028272 Mus muscu
1110 58 2.6 3305 10 BC040407 BC040407 Mus muscu
1111 58 2.6 3325 9 BC035372 BC035372 Homo sapi
1112 58 2.6 3327 9 HSM802260 BC035372 Homo sapi
1113 58 2.6 3329 10 BC054371 BC054371 Mus muscu
1114 58 2.6 3330 9 BC037992 BC037992 Homo sapi

BC064852 Xenopus t
BC058562 Mus muscu
BC013364 Homo sapi
BC017163 Homo sapi
X92840 D.melanogas
AL133077 Homo sapi
BC066817 Mus muscu
BC006698 Mus muscu
BC027055 Mus muscu
BC064468 Mus muscu
BC026672 Mus muscu
BC046625 Mus muscu
BC014632 Homo sapi
BC053596 Homo sapi
BC053333 Mus muscu
BC051178 Mus muscu
AF217991 Homo sapi
BC013975 Homo sapi
BX649191 Homo sapi
AX574572 Sequence
AY358127 Homo sapi
BC042488 Homo sapi
BC046232 Mus muscu
AX815603 Sequence
BX648594 Homo sapi
AL389951 Homo sapi
BC025599 Mus muscu
BC036168 Mus muscu
BC042125 Homo sapi
BC043702 Mus muscu
BC053050 Mus muscu
AX683129 Sequence
BC063554 Homo sapi
S68736 Rattus sp.
BC037172 Homo sapi
AL832219 Homo sapi
BC041697 Homo sapi
BC012172 Homo sapi
BD270060 Secreted
BC052189 Mus muscu
AX354181 Sequence
BX648362 Homo sapi
AY280848 Apis mell
AY129024 Homo sapi
BC054124 Mus muscu
AX430977 Sequence
AX430977 Sequence
BC019256 Homo sapi
AF180525 Rattus no
BC035284 Homo sapi
BC038443 Homo sapi
AR235862 Sequence
AR432042 Sequence
AX350342 Sequence
BC017634 Mus muscu
BT011466 Drosophil
BC029653 Homo sapi
BC027028 Mus muscu
BC065074 Mus muscu
BC041161 Homo sapi
BC053054 Mus muscu
BC060096 Mus muscu
AX754970 Sequence
BC032429 Homo sapi
BC068779 Xenopus l
AF522186 Rattus no
BC030523 Homo sapi
AF030513 Mus muscu
BC028272 Mus muscu
BC040407 Mus muscu
BC035372 Homo sapi
AL137527 Homo sapi
BC054371 Mus muscu
BC037992 Homo sapi

1115	58	2.6	3350	6	AR068182	AR068182 Sequence	1188	58	2.6	4856	10	BC052326	BC052326 Mus muscu
1116	58	2.6	3350	6	AR076934	AR076934 Sequence	1189	58	2.6	4857	10	BC030187	BC030187 Mus muscu
1117	58	2.6	3350	6	AR078767	AR078767 Sequence	1190	58	2.6	5223	5	BC044985	BC044985 Xenopus l
1118	58	2.6	3392	3	AF300334	AF300334 Dictyoste	1191	58	2.6	5280	10	BC052198	BC052198 Mus muscu
1119	58	2.6	3395	9	HSM801962	AL137294 Homo sapi	1192	58	2.6	5344	9	HSM807425	BX647281 Homo sapi
1120	58	2.6	3399	5	BC077830	BC077830 Xenopus l	c1193	58	2.6	5418	6	AX346356	AX346356 Sequence
1121	58	2.6	3401	9	BC041867	BC041867 Homo sapi	1194	58	2.6	5559	9	HSM803673	AL832365 Homo sapi
1122	58	2.6	3402	3	BT003641	BT003641 Drosophil	1195	58	2.6	5644	9	HSM808247	BX648100 Homo sapi
1123	58	2.6	3410	10	BC037109	BC037109 Mus muscu	1196	58	2.6	5735	10	BC063260	BC063260 Mus muscu
1124	58	2.6	3412	10	BC006648	BC006648 Mus muscu	1197	58	2.6	5775	5	AB034701	AB034701 Xenopus l
1125	58	2.6	3415	10	BC023677	BC023677 Mus muscu	1198	58	2.6	6163	10	BC052150	BC052150 Mus muscu
1126	58	2.6	3418	9	HSM804646	AL833333 Homo sapi	1199	58	2.6	6200	9	AF324064	AF324064 Homo sapi
1127	58	2.6	3430	3	BT003625	BT003625 Drosophil	1200	58	2.6	6239	9	HSM803498	AL832191 Homo sapi
1128	58	2.6	3447	9	BC052983	BC052983 Homo sapi	1201	58	2.6	6430	6	CQ491854	CQ491854 Sequence
1129	58	2.6	3447	9	HSM801484	AL133619 Homo sapi	1202	58	2.6	6430	6	CQ497756	CQ497756 Sequence
1130	58	2.6	3459	9	BC052964	BC052964 Homo sapi	1203	58	2.6	6559	5	BC063724	BC063724 Xenopus l
1131	58	2.6	3469	9	HSM800438	AL050138 Homo sapi	1204	58	2.6	7165	9	HSM803503	AL832196 Homo sapi
1132	58	2.6	3505	9	HSM806327	BX537608 Homo sapi	1205	58	2.6	7240	9	HSM808174	BX648028 Homo sapi
1133	58	2.6	3505	10	BC068304	BC068304 Mus muscu	1206	58	2.6	8000	6	BD138791	BD138791 Alphaviru
1134	58	2.6	3506	9	BC062616	BC062616 Homo sapi	1207	58	2.6	8100	6	BD226819	BD226819 Alphaviru
1135	58	2.6	3520	9	HSM804704	AL833391 Homo sapi	1208	58	2.6	8100	6	AR243302	AR243302 Sequence
1136	58	2.6	3544	10	BC042521	BC042521 Mus muscu	1209	58	2.6	8694	9	HSM808392	BX648244 Homo sapi
1137	58	2.6	3582	10	BC053927	BC053927 Mus muscu	c1210	58	2.6	10467	6	AX323839	AX323839 Sequence
1138	58	2.6	3620	9	HSM804516	AL833205 Homo sapi	1211	58	2.6	11000	6	BD138792	BD138792 Alphaviru
1139	58	2.6	3621	5	BC068908	BC068908 Xenopus l	1212	58	2.6	11517	6	A18788	A18788 complete nu
1140	58	2.6	3657	10	BC050054	BC050054 Mus muscu	1213	58	2.6	11517	6	AR001293	AR001293 Sequence
1141	58	2.6	3694	10	AF085809	AF085809 Mus muscu	1214	58	2.6	11517	6	AR130391	AR130391 Sequence
1142	58	2.6	3697	9	AB048948	AB048948 Homo sapi	1215	58	2.6	12295	6	BD138799	BD138799 Alphaviru
1143	58	2.6	3713	9	HSM807381	BX647237 Homo sapi	1216	58	2.6	12464	6	BD263357	BD263357 Compositi
1144	58	2.6	3724	5	BC068927	BC068927 Xenopus l	1217	58	2.6	12972	3	AF088979	AF088979 Dictyoste
1145	58	2.6	3747	9	HSM805597	AL834489 Homo sapi	1218	58	2.6	15418	6	BD226816	BD226816 Alphaviru
1146	58	2.6	3768	9	BC051845	BC051845 Homo sapi	1219	58	2.6	15528	6	A93016	A93016 Sequence 4
1147	58	2.6	3782	9	HSM804515	AL833204 Homo sapi	1220	58	2.6	15528	12	PEAVGEN	Y07862 Cloning vec
1148	58	2.6	3836	9	BC063854	BC063854 Homo sapi	1221	58	2.6	15538	6	AR243299	AR243299 Sequence
1149	58	2.6	3857	10	BC040362	BC040362 Mus muscu	c1222	58	2.6	39984	3	AC114258	AC114258 Dictyoste
1150	58	2.6	3864	3	AY122110	AY122110 Drosophil	1223	58	2.6	64814	8	NCB21J21	AL355929 Neurospor
1151	58	2.6	3870	9	HSM806049	BX537527 Homo sapi	1224	58	2.6	79554	8	NCB11B23	AL669991 Neurospor
1152	58	2.6	3911	10	BC031166	BC031166 Mus muscu	1225	58	2.6	80272	5	AL591180	AL591180 Zebrafish
1153	58	2.6	3916	10	BC018439	BC018439 Mus muscu	1226	58	2.6	83340	3	AC004438	AC004438 Drosophil
1154	58	2.6	3919	10	BC067070	BC067070 Mus muscu	1227	58	2.6	89232	5	AL591175	AL591175 Zebrafish
1155	58	2.6	3960	9	BC038239	BC038239 Homo sapi	c1228	58	2.6	94153	2	AC139443	AC139443 Rattus no
1156	58	2.6	4008	10	BC025619	BC025619 Mus muscu	1229	58	2.6	110000	2	AC131059_2	Continuation (3 of
1157	58	2.6	4050	9	BC047244	BC047244 Homo sapi	c1230	58	2.6	111158	9	AC004987	AC004987 Homo sapi
1158	58	2.6	4121	6	AR344255	AR344255 Sequence	c1231	58	2.6	126590	2	AP001112	AP001112 Homo sapi
1159	58	2.6	4121	6	AX019229	AX019229 Sequence	1232	58	2.6	126611	10	AL928592	AL928592 Mouse DNA
1160	58	2.6	4121	6	BD130455	BD130455 Expressio	c1233	58	2.6	133949	10	AC146471	AC146471 Mus muscu
1161	58	2.6	4143	5	GSDYNACT	X62773 Gallus gall	c1234	58	2.6	136240	3	AC117070	AC117070 Dictyoste
1162	58	2.6	4168	6	AX393305	AX393305 Sequence	c1235	58	2.6	137436	9	AF348209	AF348209 Homo sapi
1163	58	2.6	4169	10	BC053919	BC053919 Mus muscu	c1236	58	2.6	138376	9	AF069333	AF069333 Homo sapi
1164	58	2.6	4184	10	BC058993	BC058993 Mus muscu	c1237	58	2.6	138426	10	AC142451	AC142451 Mus muscu
1165	58	2.6	4204	10	BC052212	BC052212 Mus muscu	c1238	58	2.6	139936	2	AC139411	AC139411 Rattus no
1166	58	2.6	4236	5	BC071048	BC071048 Xenopus l	c1239	58	2.6	139947	9	AY293855	AY293855 Homo sapi
1167	58	2.6	4250	9	HSM803434	AL832127 Homo sapi	1240	58	2.6	142951	2	CR391966	CR391966 Danio rer
1168	58	2.6	4274	6	AX402021	AX402021 Sequence	1241	58	2.6	146846	2	AC150264	AC150264 Aedes aeg
1169	58	2.6	4274	10	AF192401	AF192401 Rattus no	1242	58	2.6	147889	2	AC018534	AC018534 Homo sapi
1170	58	2.6	4295	10	BC057367	BC057367 Mus muscu	c1243	58	2.6	148250	9	AL353625	AL353625 Human DNA
1171	58	2.6	4318	9	BC016029	BC016029 Homo sapi	c1244	58	2.6	149152	10	AC124388	AC124388 Mus muscu
1172	58	2.6	4362	10	BC052329	BC052329 Mus muscu	1245	58	2.6	157847	10	AC122511	AC122511 Mus muscu
1173	58	2.6	4380	9	AF000145	AF000145 Homo sapi	c1246	58	2.6	157998	10	AC140354	AC140354 Mus muscu
1174	58	2.6	4432	3	AY095206	AY095206 Drosophil	1247	58	2.6	162972	10	AC144579	AC144579 Mus muscu
1175	58	2.6	4486	10	BC054123	BC054123 Mus muscu	c1248	58	2.6	163121	2	AC122406	AC122406 Mus muscu
1176	58	2.6	4487	10	BC023962	BC023962 Mus muscu	1249	58	2.6	165978	2	AC087132	AC087132 Mus muscu
1177	58	2.6	4493	9	BC064843	BC064843 Homo sapi	c1250	58	2.6	172830	10	AC131329	AC131329 Mus muscu
1178	58	2.6	4499	9	HSM803130	AL831817 Homo sapi	1251	58	2.6	175611	2	AC020621	AC020621 Homo sapi
1179	58	2.6	4508	10	AF192402	AF192402 Rattus no	1252	58	2.6	176306	3	AC007186	AC007186 Drosophil
1180	58	2.6	4519	10	BC058994	BC058994 Mus muscu	c1253	58	2.6	176329	2	AC117968	AC117968 Rattus no
1181	58	2.6	4538	5	AF182215	AF182215 Tilapia m	1254	58	2.6	179439	2	AC018874	AC018874 Homo sapi
1182	58	2.6	4543	10	BC049133	BC049133 Mus muscu	c1255	58	2.6	179676	2	AC012221	AC012221 Homo sapi
1183	58	2.6	4598	9	BC032463	BC032463 Homo sapi	c1256	58	2.6	186950	10	BX855608	BX855608 Mouse DNA
1184	58	2.6	4659	9	HSM806121	BX537988 Homo sapi	c1257	58	2.6	190516	10	AC110376	AC110376 Mus muscu
1185	58	2.6	4723	5	BC063192	BC063192 Xenopus t	1258	58	2.6	190792	10	AC129019	AC129019 Mus muscu
1186	58	2.6	4841	9	BC052565	BC052565 Homo sapi	1259	58	2.6	192874	10	AL672019	AL672019 Mouse DNA
1187	58	2.6	4845	9	HSM808798	BX648647 Homo sapi	1260	58	2.6	197571	10	BX890555	BX890555 Mouse DNA

1261	58	2.6	199372	2	AC135219	AC135219 Sus scrofa	1334	57	2.5	165	6	AX977324	AX977324 Sequence
1262	58	2.6	203225	5	BX255942	BX255942 Zebrafish	1335	57	2.5	165	6	BD112183	BD112183 EST and e
c1263	58	2.6	204021	2	AC139352	AC139352 Rattus no	1336	57	2.5	169	6	CQ663079	CQ663079 Sequence
1264	58	2.6	204394	10	AC079644	AC079644 Mus muscu	1337	57	2.5	169	6	AR419752	AR419752 Sequence
c1265	58	2.6	204591	2	AC136341	AC136341 Mus muscu	1338	57	2.5	169	6	AX980446	AX980446 Sequence
c1266	58	2.6	205515	2	AC118905	AC118905 Rattus no	1339	57	2.5	169	6	BD115305	BD115305 EST and e
c1267	58	2.6	210688	2	AC139257	AC139257 Homo sapi	1340	57	2.5	173	6	AX284784	AX284784 Sequence
1268	58	2.6	213167	9	AC008588	AC008588 Homo sapi	1341	57	2.5	175	6	CQ769330	CQ769330 Sequence
1269	58	2.6	213565	2	CR354428	CR354428 Danilo rer	1342	57	2.5	176	6	CQ677241	CQ677241 Sequence
1270	58	2.6	217279	2	AC117787	AC117787 Mus muscu	1343	57	2.5	176	6	AR422406	AR422406 Sequence
c1271	58	2.6	217327	2	AC111930	AC111930 Rattus no	1344	57	2.5	176	6	AX983100	AX983100 Sequence
1272	58	2.6	219673	2	AC139263	AC139263 Homo sapi	1345	57	2.5	176	6	BD117959	BD117959 EST and e
c1273	58	2.6	219941	2	AC099717	AC099717 Mus muscu	1346	57	2.5	177	6	AR413410	AR413410 Sequence
1274	58	2.6	227074	2	AC060772	AC060772 Mus muscu	1347	57	2.5	177	6	AX970244	AX970244 Sequence
1275	58	2.6	228428	2	AC099217	AC099217 Rattus no	1348	57	2.5	177	6	BD108963	BD108963 EST and e
c1276	58	2.6	228878	2	AC112329	AC112329 Rattus no	1349	57	2.5	178	6	CQ486695	CQ486695 Sequence
c1277	58	2.6	230886	10	AL935264	AL935264 Mouse DNA	1350	57	2.5	179	6	AR418078	AR418078 Sequence
1278	58	2.6	236489	2	AC110553	AC110553 Mus muscu	1351	57	2.5	179	6	AX978772	AX978772 Sequence
c1279	58	2.6	237913	2	AC104208	AC104208 Mus muscu	1352	57	2.5	179	6	BD113631	BD113631 EST and e
c1280	58	2.6	244105	2	AC098897	AC098897 Rattus no	1353	57	2.5	185	6	CQ524628	CQ524628 Sequence
1281	58	2.6	249995	2	AC121434	AC121434 Rattus no	1354	57	2.5	187	6	CQ701146	CQ701146 Sequence
1282	58	2.6	253149	2	AC107527	AC107527 Rattus no	1355	57	2.5	188	6	CQ527214	CQ527214 Sequence
1283	58	2.6	253313	2	AC102731	AC102731 Mus muscu	1356	57	2.5	189	6	AX284585	AX284585 Sequence
1284	58	2.6	254733	3	AC117075	AC117075 Dictyoste	1357	57	2.5	194	6	AR413164	AR413164 Sequence
1285	58	2.6	256673	2	AC087146	AC087146 Mus muscu	1358	57	2.5	194	6	AX969998	AX969998 Sequence
c1286	58	2.6	263283	2	AC109389	AC109389 Rattus no	1359	57	2.5	194	6	BD108717	BD108717 EST and e
1287	58	2.6	263319	2	AC125258	AC125258 Mus muscu	1360	57	2.5	195	6	AX361368	AX361368 Sequence
c1288	58	2.6	272652	2	AC109709	AC109709 Rattus no	1361	57	2.5	196	6	CQ525476	CQ525476 Sequence
c1289	58	2.6	274909	2	AC131169	AC131169 Rattus no	1362	57	2.5	198	6	CQ487384	CQ487384 Sequence
1290	58	2.6	289460	3	AE003630	AE003630 Drosophil	1363	57	2.5	198	6	CQ820245	CQ820245 Sequence
1291	58	2.6	302156	3	AC116977	AC116977 Dictyoste	1364	57	2.5	198	6	CQ820246	CQ820246 Sequence
c1292	58	2.6	308479	2	AC094671	AC094671 Rattus no	1365	57	2.5	199	6	CQ523406	CQ523406 Sequence
1293	58	2.6	318145	2	AC122576	AC122576 Rattus no	1366	57	2.5	201	11	BV199973	BV199973 sqnm20284
c1294	58	2.6	349980	6	AX344553	AX344553 Sequence	1367	57	2.5	201	11	BV200358	BV200358 sqnm20393
c1295	58	2.6	349980	6	AX344558	AX344558 Sequence	1368	57	2.5	201	11	BV200361	BV200361 sqnm20395
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1297	57	2.5	92	6	AX982817	AX982817 Sequence	1370	57	2.5	201	11	BV200379	BV200379 sqnm20400
1298	57	2.5	92	6	BD117676	BD117676 EST and e	c1371	57	2.5	201	11	BV200460	BV200460 sqnm20420
1299	57	2.5	97	6	AR417589	AR417589 Sequence	c1372	57	2.5	201	11	BV201749	BV201749 sqnm20728
1300	57	2.5	97	6	AX978283	AX978283 Sequence	1373	57	2.5	201	11	BV202083	BV202083 sqnm20814
1301	57	2.5	97	6	BD113142	BD113142 EST and e	1374	57	2.5	201	11	BV202595	BV202595 sqnm20945
1302	57	2.5	106	6	BD021994	BD021994 Secreted	1375	57	2.5	201	11	BV204012	BV204012 sqnm21375
c1303	57	2.5	107	9	S77771S1	S77771 aspartyglu	1376	57	2.5	201	11	BV204551	BV204551 sqnm21558
1304	57	2.5	109	6	AR423095	AR423095 Sequence	1377	57	2.5	201	11	BV207013	BV207013 sqnm22249
1305	57	2.5	109	6	AX983789	AX983789 Sequence	1378	57	2.5	201	11	BV208193	BV208193 sqnm22575
1306	57	2.5	109	6	BD118648	BD118648 EST and e	1379	57	2.5	202	11	BV088301	BV088301 RPAMMSEQ0
1307	57	2.5	127	6	AR422436	AR422436 Sequence	1380	57	2.5	202	11	BV097344	BV097344 RPAMMSEQ0
1308	57	2.5	127	6	AX983130	AX983130 Sequence	1381	57	2.5	205	6	CQ525020	CQ525020 Sequence
1309	57	2.5	127	6	BD117989	BD117989 EST and e	1382	57	2.5	209	10	BC036353	BC036353 Mus muscu
1310	57	2.5	134	6	AR426936	AR426936 Sequence	1383	57	2.5	210	6	CQ525883	CQ525883 Sequence
1311	57	2.5	134	6	AX987630	AX987630 Sequence	1384	57	2.5	214	6	CQ487824	CQ487824 Sequence
1312	57	2.5	134	6	BD122489	BD122489 EST and e	1385	57	2.5	215	6	CQ526670	CQ526670 Sequence
1313	57	2.5	137	6	AR426937	AR426937 Sequence	1386	57	2.5	216	6	CQ525470	CQ525470 Sequence
1314	57	2.5	137	6	AX987631	AX987631 Sequence	1387	57	2.5	218	6	CQ517186	CQ517186 Sequence
1315	57	2.5	137	6	BD122490	BD122490 EST and e	1388	57	2.5	218	9	BC055094	BC055094 Homo sapi
1316	57	2.5	142	6	AR419304	AR419304 Sequence	1389	57	2.5	221	6	CQ563915	CQ563915 Sequence
1317	57	2.5	142	6	AX979998	AX979998 Sequence	1390	57	2.5	224	6	CQ525227	CQ525227 Sequence
1318	57	2.5	142	6	BD114857	BD114857 EST and e	1391	57	2.5	235	6	CQ677257	CQ677257 Sequence
1319	57	2.5	147	6	AR418757	AR418757 Sequence	1392	57	2.5	236	6	CQ664217	CQ664217 Sequence
1320	57	2.5	147	6	AX979451	AX979451 Sequence	1393	57	2.5	241	6	CQ487383	CQ487383 Sequence
1321	57	2.5	147	6	BD114310	BD114310 EST and e	1394	57	2.5	241	6	CQ526281	CQ526281 Sequence
1322	57	2.5	150	6	AR417159	AR417159 Sequence	1395	57	2.5	244	6	AX408053	AX408053 Sequence
1323	57	2.5	150	6	AX977853	AX977853 Sequence	1396	57	2.5	247	6	CQ524135	CQ524135 Sequence
1324	57	2.5	150	6	BD112712	BD112712 EST and e	1397	57	2.5	249	6	AR427647	AR427647 Sequence
1325	57	2.5	153	6	CQ700107	CQ700107 Sequence	1398	57	2.5	249	6	AX988341	AX988341 Sequence
1326	57	2.5	160	6	AR418838	AR418838 Sequence	1399	57	2.5	249	6	BD123200	BD123200 EST and e
1327	57	2.5	160	6	AX979532	AX979532 Sequence	1400	57	2.5	250	6	CQ526214	CQ526214 Sequence
1328	57	2.5	160	6	BD114391	BD114391 EST and e	1401	57	2.5	253	6	BD219575	BD219575 Human gen
c1329	57	2.5	161	6	AX381305	AX381305 Sequence	1402	57	2.5	255	6	CQ484634	CQ484634 Sequence
1330	57	2.5	163	6	AR418111	AR418111 Sequence	1403	57	2.5	255	6	CQ521197	CQ521197 Sequence
1331	57	2.5	163	6	AX978805	AX978805 Sequence	1404	57	2.5	256	6	CQ525624	CQ525624 Sequence
1332	57	2.5	163	6	BD113664	BD113664 EST and e	1405	57	2.5	258	10	BC014856	BC014856 Mus muscu
1333	57	2.5	165	6	AR416630	AR416630 Sequence	1406	57	2.5	260	6	CQ525782	CQ525782 Sequence

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PDQSLPIPPVILAEIGSDPTKGTVCFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYG									
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ORIGIN									
Query Match		100.0%;	Score 2242;	DB 9;	Length 2242;				
Best Local Similarity		100.0%;	Pred. No. 0;						
Matches 2242;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
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QY	61	TCGTCTTCCTCCGGGGGACAAACGTGGGTCAGGGCACAGAGAGATATTTAATGTCAACCT	120						
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QY	121	CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTTTGGAGGTTGGGAAAGTTGCTAGA	180						
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QY	181	GGCTTCAGAACTCCAGCCTAATGGATCCCAAACTCGGGAGAAATGGCTGCGTCCCTGCTGG	240						
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QY	241	CTGTGCTGCTGCTGCTGGAGCGCGGCATGTTCTCCTCACCTCCCGGCCCGCGCGC	300						
Db	241	CTGTGCTGCTGCTGCTGGAGCGCGGCATGTTCTCCTCACCTCCCGGCCCGCGCGC	300						
QY	301	TGTTAGAGAAAGTCTTCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA	360						
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QY	361	AGGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAAGAGC	420						
Db	361	AGGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAAGAGC	420						
QY	421	TCTTCAGAAATGATGGCCGTGGCTGCGGACACGCTGCAGCGCTTGGGGGCCCTGTGGCCT	480						
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QY	481	CGGTGGACATGGGTCTCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCA	540						
Db	481	CGGTGGACATGGGTCTCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCA	540						
QY	541	TCCTTGGCCGAACTGGGGAGCGGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGG	600						
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QY	601	ACGTGCAGCCTGCTGACCCGGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGG	660						
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QY	661	TAGACGGGAAACTTTATGGACGAGGACGACCGACAACAAAGGCCCTGTCTTGGCTTGA	720						
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QY	721	TCAATGCTGTGAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCCTGTGAATATCAAATTCA	780						
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QY	781	TCATTGAGGGGATGGAAGAGGCTGGCTCTGTGTGCCCTGGAGGAACCTGTGGAAAAAGAAA	840						
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QY	841	AGGACCGATTCTTCTCTGGTGTGGACTACATTGTAATTTTCAGATAAACCTGTGGATCAGCC	900						
Db	841	AGGACCGATTCTTCTCTGGTGTGGACTACATTGTAATTTTCAGATAAACCTGTGGATCAGCC	900						

QY	901	AAAGGAAGCCAGCAATCACCTTATGGAACCCGGGGAAACAGCTACTTCATGGTGGAGGTGA	960
Db	901	AAAGGAAGCCAGCAATCACCTTATGGAACCCGGGGAAACAGCTACTTCATGGTGGAGGTGA	960
QY	961	AATGCAGAGACCAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGG	1020
Db	961	AATGCAGAGACCAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGG	1020
QY	1021	CTGATCTGGTTCCTTCTCGGTAGCCTCGGTAGACTCGTCTGGTCATATCCTGGTCCCTG	1080
Db	1021	CTGATCTGGTTCCTTCTCGGTAGCCTCGGTAGACTCGTCTGGTCATATCCTGGTCCCTG	1080
QY	1081	GAATCTATGATGAAGTGGTTCCTCTTACAGAAGAGGAAATAAAATACATACAAAGCCATCC	1140
Db	1081	GAATCTATGATGAAGTGGTTCCTCTTACAGAAGAGGAAATAAAATACATACAAAGCCATCC	1140
QY	1141	ATCTAGACCTAGAAATACCGGAATAGCAGCCGGGTTGAGAAAATTTCTGTTTCGATACTA	1200
Db	1141	ATCTAGACCTAGAAATACCGGAATAGCAGCCGGGTTGAGAAAATTTCTGTTTCGATACTA	1200
QY	1201	AGGAGGAGATCTTAATGCACCTCTGGAGGTACCCATCTCTTTCTATTCATGGGATCGAGG	1260
Db	1201	AGGAGGAGATCTTAATGCACCTCTGGAGGTACCCATCTCTTTCTATTCATGGGATCGAGG	1260
QY	1261	CGCGGTTTGTATGAGCCTGGAACCTAAACAGTACATACCTGGCCGAGTTATAGGAAAATTTT	1320
Db	1261	CGCGGTTTGTATGAGCCTGGAACCTAAACAGTACATACCTGGCCGAGTTATAGGAAAATTTT	1320
QY	1321	CAATCCGCTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAACAGGTGACACGACATC	1380
Db	1321	CAATCCGCTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAACAGGTGACACGACATC	1380
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QY	1501	TCAGAACAGTGTTTGGAACAGAACCCAGATATGATCCGGGATGGATCCACCAATTCOAATTG	1560
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QY	1561	CCAAAATGTTCCAGGAGATCGTCCACAAGACGCGTGGTGTAAATTCGCTGGGAGCTGTTG	1620
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QY 2221 AAAAAAAAAAAAAAAAAAAAAA 2242
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RESULT 2
AX527744
LOCUS AX527744 2784 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 1 from Patent WO0226948.
ACCESSION AX527744
VERSION AX527744.1 GI:25172275
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kapeller-Libermann,R.
TITLE 55054, a novel human metalloprotease and uses therefor
JOURNAL Patent: WO 0226948-A 1 04-APR-2002;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source 1.
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ORIGIN

Query Match 97.2%; Score 2180; DB 6; Length 2784;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 TCGTCTTCTTCCGGGGACAACGTGGGTCAGGGCACAGAGAGATATTTAATGTCACCCCT 120
Db |||||||
462 TCGTCTTCTTCCGGGGACAACGTGGGTCAGGGCACAGAGAGATATTTAATGTCACCCCT 521
QY 121 CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTGTGGAGGTTGGGAAAGTTGCTAGA 180
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522 CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTGTGGAGGTTGGGAAAGTTGCTAGA 581
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QY 241 CTGTGCTGCTGCTGTGGAGCGCGGCATGTTCTCTCACCCTCCCGCCCCCGGCGC 300
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RESULT 3

BD205653

LOCUS

DEFINITION 97 human secreted proteins.

ACCESSION BD205653

VERSION BD205653.1 GI:33015423

KEYWORDS JP 2002533058-A/30.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2152)

AUTHORS Ruben,S.M., Florence,K., Ni,J., Rosen,C.A., Carter,K.C., Moore,P.A., Olsen,H.S., Shi,Y., Young,P.E., Wei,F.F., Brewer,L.A., Soppet,D.R., Lafleur,D.W., Endress,G.A. and Ebner,R.

97 human secreted proteins

PATENT: JP 2002533058-A 30 08-OCT-2002;

HUMAN GENOME SCIENCES INC

OS Homo sapiens (human)

PN JP 2002533058-A/30

PD 08-OCT-2002

PF 06-MAY-1999 JP 2000548451

PR 12-MAY-1998 US 60/085093,12-MAY-1998 US 60/085094 PR

12-MAY-1998 US 60/085105,12-MAY-1998 US 60/085180 PR

18-MAY-1998 US 60/085927,18-MAY-1998 US 60/085906 PR

18-MAY-1998 US 60/085924,18-MAY-1998 US 60/085922 PR

18-MAY-1998 US 60/085923,18-MAY-1998 US 60/085921 PR

18-MAY-1998 US 60/085925,18-MAY-1998 US 60/085928 PR

18-MAY-1998 US 60/085920

PI STEVEN M RUBEN,KIMBERLY FLORENCE,JIAN NI,CRAIG A ROSEN,KENNETH

PI C CARTER,

PI PAUL A MOORE,HENRIK S OLSEN,YANGGU SHI,PAUL E YOUNG,FING FEI

PI WEI,

PI LAURIE A BREWER,DANIEL R SOPPET,DAVID W LAFLEUR,GREGORY A PI

ENDRESS,

PI REINHARD EBNER

PC C12N15/09,C07K14/00,C07K14/435,C07K16/18,C12N1/15,C12N1/19, PC

C12N1/21,

PC C12N5/10,C12P21/02,C12N15/00,C12N5/00

CC 97 human secreted proteins.

PH Key Location/Qualifiers

FT source 1..2152

FT /organism='Homo sapiens (human)'.

FEATURES

source

1..2152

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Query Match 84.3%; Score 1891; DB 6; Length 2152;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 TGCTGCTGCTGCTGGAGCGCGCATGTTCTCCTCACCCCTCCCGCCCCGCGCTGT 303

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QY 1924 CCACTGCACACCTTCCTCAAGTCATAGTCTGTTGACAGCAACTTGATTTCCCCCAAGTCTCTG 1983

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Db |||||||
2089 ATTCCATCCAATGATCGCCTTTTGCTTTTACCA 2119

RESULT 4
AX059560
LOCUS AX059560 2235 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 8 from Patent WO0075298.
ACCESSION AX059560
VERSION AX059560.1 GI:12311667
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Hodgson,D.M., Lincoln,S.E., Russo,F.D., Spiro,P.A., Banville,S.C.,
Bratcher,S.R., Dufour,G.E., Cohen,H.J., Rosen,B.H., Chalup,M.S.,
Hillman,J.L., Jones,A.L., Yu,J.Y., Greenawalt,L.B., Panzer,S.R.,
Roseberry,A.M., Wright,R.J. and Daniels,S.E.
TITLE Molecules for disease detection and treatment
JOURNAL Patent: WO 0075298-A 8 14-DEC-2000;
Incyte Genomics, Inc. (US)
FEATURES
source Location/Qualifiers
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VERSION
KEYWORDS
SOURCE
ORGANISM

SOURCE ORGANISM

ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

REFERENCES AND AUTHORS

Tanigami, A., Fujiwara, T., Shibahara, T., Goto, Y., Hirao, M.,
 Shimizu, F., Wakebe, H., Ono, T., Hishigaki, H., Watanabe, T., Ozaki, K.,
 Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M.,
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 Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and
 Sugano, S.

TITLE NEDO human cDNA sequencing project

IIIE
JOURNAL
Unpublished
NEDO Haman

BOOKS
REFERENCE
2 (bases 1 to 1970)

REFERENCE
AUTHORS
Sugano, S. and Suzuki, Y.
2 (Pages 1 to 157)

AUTHORS	SUGANO, S: ana suz
TITLE	Direct Submission

ILLI
 JOURNAL
 Direct submission
 Submitted (08-JUL-2002) Sumio Sugano, Institute of Medical Science,
 University of Tokyo, Laboratory of Genome Structure, Human Genome
 Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
 (E-mail: fllcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
 Fax:81-3-5449-5416)

COMMENT

COMMENT

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.

REPLY

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VERSION AX139747.1 GI:14275329
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REFERENCE 1
AUTHORS Saudek,V., Smirnova-Robert,T. and Teufel,M.
TITLE Human carnosinase, its isolation and uses
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AX231560

LOCUS AX231560 1587 bp DNA linear PAT 11-SEP-2001

DEFINITION Sequence 458 from Patent WO0163294.

ACCESSION AX231560

VERSION AX231560.1 GI:15592465

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Herath,H.M., Parekh,R.B. and Rohlff,C.

TITLE Diagnosis of bipolar affective disorder (bad) and unipolar depression

JOURNAL Patent: WO 0163294-A 458 30-AUG-2001; Oxford Glycosciences (UK) Limited (GB)

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Location/Qualifiers

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Best Local Similarity 99.8%; Pred. No. 0;

Matches 1525; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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LOCUS AX232218 1587 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 496 from Patent WO0163293.
ACCESSION AX232218
VERSION AX232218.1 GI:15592548
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Herath,M.A., Parekh,R.B. and Rohlff,C.O.
TITLE Diagnosis and treatment of schizophrenia
JOURNAL Patent: WO 0163293-A 496 30-AUG-2001;
Oxford GlycoSciences (UK) Limited (GB)
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DEFINITION Sequence 680 from Patent WO0162785.
ACCESSION  AX2333356
VERSION    AX2333356.1  GI:15592690
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Herath,H.M., Parekh,R.B., Rohlf,C.C., Terrett,J.A. and Tyson,K.L.
TITLE      Protein and gene and their use for diagnosis and treatment of
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JOURNAL    Patent: WO 0162785-A 680 30-AUG-2001;
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Best Local Similarity 99.8%; Pred. No. 0;
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Db 1560 TGATCTGATCCACTGACAGATTTCACCTC 1587

RESULT 13

HSA417564

LOCUS HSA417564 1640 bp mRNA linear PRI 30-OCT-2001

DEFINITION Homo sapiens mRNA for glutamate carboxypeptidase-like protein 2 (CPGL2 gene).

ACCESSION AJ417564

VERSION AJ417564.1 GI:16555791

KEYWORDS CPGL2 gene; glutamate carboxypeptidase-like protein 2.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Chen,J.M. and Barrett,A.J.

TITLE Cloning and sequencing of a second human homologue of glutamate carboxypeptidase in peptidase family M20

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1640)

AUTHORS Chen,J.M.

TITLE Direct Submission

JOURNAL Submitted (24-OCT-2001) Chen J.M., MRC Molecular Enzymology Laboratory, Babraham Institute, Babraham Hall, Babraham, Cambridgeshire CB2 4AT, UNITED KINGDOM

FEATURES

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QY	1084	TCTATGATGAAGTGGTCTCTTTACAGAAGAGGAATAAATACATACAAAGCCATCCATC	1143
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Db	1468	ATGGAGAACATTCGAGAAATGAGAAATCAACAGGTGGAACCTACATAGAGGGAACCAAT	1527
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QY	1744	TGATCTGATCCACTGACAGATTACCTCCCCACATCCCTTAGACAGGGATGGA	1796
Db	1588	TGATCTGATCCACTGACAGATTACCTCCCCACATCCCTTAGACAGGGATGGA	1640

RESULT 14
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LOCUS
DEFINITION Homo sapiens chromosome 18 clone RP13-482C18 map 18, WORKING DRAFT
SEQUENCE, 3 unordered pieces.
AC127485
VERSION AC127485.2 GI:22267793
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 175905)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 18, clone RP13-482C18
JOURNAL Unpublished

REFERENCE
AUTHORS

2 (bases 1 to 175905)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schubback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesyfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (17-JUL-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 175905)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
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Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schubback,R., Seaman,S., Severy,P.,
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Tesyfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (16-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Aug 16, 2002 this sequence version replaced gi:21886892.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L27777

Center clone name: 482_C_18

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 174971 bases at least Q40

Consensus quality: 175423 bases at least Q30

Consensus quality: 175606 bases at least Q20

Insert size: 175000; agarose-fp

Insert size: 175705; sum-of-contigs

Quality coverage: 15.3 in Q20 bases; agarose-fp

Quality coverage: 15.3 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 47188: contig of 47188 bp in length
* 47189 47288: gap of 100 bp
* 47289 55377: contig of 8089 bp in length
* 55378 55477: gap of 100 bp
* 55478 175905: contig of 120428 bp in length.

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/note="assembly_fragment"

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55478..175905
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clone_end:T7
vector_side:right"

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QY 1776 ACATCCCTAGACAGGGATGGAATGTAATATCCAGAGAAATTTGGTCTAGTATAGTACAT 1835
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Db 174578 ACATCCCTAGACAGGGATGGAATGTAATATCCAGAGAAATTTGGTCTAGTATAGTACAT 174637

QY 1836 TTTCCTTCCATTAAATGTCTTGGGATATCTGGATCAGTAAATAAAATATTTCAAAGGC 1895
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Db 174638 TTTCCTTCCATTAAATGTCTTGGGATATCTGGATCAGTAAATAAAATATTTCAAAGGC 174697

QY 1896 ACAGATGTTGGAAATGGTTTAAGGTCCTTCAAGTCCCTCAAGTCATAGCTGCT 1955
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Db 174698 ACAGATGTTGGAAATGGTTTAAGGTCCTTCAAGTCCCTCAAGTCATAGCTGCT 174757

QY 1956 TGCAGCAACTTGATTTCCCAAGTCCTGTGCAATAGCCCCAGGATTGGATTCCCTTCCAAC 2015
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Db 174758 TGCAGCAACTTGATTTCCCAAGTCCTGTGCAATAGCCCCAGGATTGGATTCCCTTCCAAC 174817

QY 2016 CTTTGTAGCATATCTCCAACCTTGCAATTGGATGGCATAATCACTCCGGTTTGCTTTCTA 2075
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LOCUS CQ845803 3755 bp DNA linear PAT 02-AUG-2004

DEFINITION Sequence 4450 from Patent EP1440981.
ACCESSION CQ845803
VERSION CQ845803.1 GI:50895402
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J., Isono,Y., Nagai,K. and Irie,R.
TITLE Full-length human cdna
JOURNAL Patent: EP 1440981-A 4450 28-JUL-2004;
Research Association for Biotechnology (JP)
FEATURES
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ORIGIN

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Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1836 TTTCCTTCCATTAAATGTCTTGGGATATCTGGATCAGTAAATAAAATATTTCAAAGGC 1895
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Db 3478 ACAGATGTTGGAAATGGTTTAAGGTCCTTCAAGTCCCTCAAGTCATAGCTGCT 3537

QY 1956 TGCAGCAACTTGATTTCCCAAGTCCTGTGCAATAGCCCCAGGATTGGATTCCCTTCCAAC 2015
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Db 3538 TGCAGCAACTTGATTTCCCAAGTCCTGTGCAATAGCCCCAGGATTGGATTCCCTTCCAAC 3597

QY 2016 CTTTGTAGCATATCTCCAACCTTGCAATTGGATGGCATAATCACTCCGGTTTGCTTTCTA 2075
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Db 3598 CTTTGTAGCATATCTCCAACCTTGCAATTGGATGGCATAATCACTCCGGTTTGCTTTCTA 3657

QY 2076 GGTCCTCAAGTGCTCGTGACACATAATCAATCCCAATGATCGCCTTTGCTTTACCAC 2135
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Db 3658 GGTCCTCAAGTGCTCGTGACACATAATCAATCCCAATGATCGCCTTTGCTTTACCAC 3717

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Perfect score: 2242
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Total number of hits satisfying chosen parameters: 8142013
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 1						
ID	AAA96348	standard; cDNA; 2242 BP.				
DE	CDNA encoding a novel polypeptide designated PRO4380.					
PN	WQ200056889-A2.					
PD	28-SEP-2000.					
PA	(GETH) GENENTECH INC.					
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ID	ACD28837	standard; cDNA; 2242 BP.				
DE	Human secreted / transmembrane polypeptide PRO4380 cDNA.					
PN	US2003027249-A1.					
PD	06-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 2242;	DB 8;	Length 2242;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 3						
ID	ACA06111	standard; cDNA; 2242 BP.				
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PN	US2003008348-A1.					
PD	09-JAN-2003.					
PA	(GETH) GENENTECH INC.					
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PN	US2002192751-A1.					
PD	19-DEC-2002.					
PA	(GETH) GENENTECH INC.					
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Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 5						
ID	ADA76581	standard; cDNA; 2242 BP.				
DE	Novel human secreted and transmembrane protein PRO4380 cDNA.					
PN	US2003036114-A1.					
PD	20-FEB-2003.					
PA	(GETH) GENENTECH INC.					
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Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 6						
ID	ACD42296	standard; cDNA; 2242 BP.				

DE Human cDNA encoding secreted/transmembrane protein PRO4380.
PN US2003044842-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2242; DB 9; Length 2242;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 7

ID AAD59362 standard; cDNA; 2242 BP.
DE Human PRO4380 cDNA.
PN US2003049733-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
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RESULT 8

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DE Human PRO4380 cDNA.
PN US2003049734-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2242; DB 10; Length 2242;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 9

ID ADC29812 standard; cDNA; 2242 BP.
DE Novel human secreted and transmembrane protein PRO4380 cDNA.
PN US2003092063-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2242; DB 10; Length 2242;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 10

ID ACA06168 standard; cDNA; 2242 BP.
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PN US2003032061-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;

RESULT 11

ID ADF09255 standard; cDNA; 2242 BP.
DE Human secreted and transmembrane protein PRO4380 cDNA.
PN US2003134327-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;

RESULT 12

ID ABL58476 standard; cDNA; 2784 BP.
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PN WO200226948-A2.
PD 04-APR-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 97.2%; Score 2180; DB 6; Length 2784;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 13

ID ADF90847 standard; DNA; 2851 BP.
DE Human hepatic-fibrosis disease marker SEQ ID 309.
PN JP2003259877-A.
PD 16-SEP-2003.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 97.2%; Score 2180; DB 10; Length 2851;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 14

ID AAZ65270 standard; DNA; 2152 BP.
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PN WO9958660-A1.
PD 18-NOV-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
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RESULT 15

ID ACC50470 standard; cDNA; 2152 BP.
DE Human secreted protein coding sequence, SEQ ID 137.

PN WO200295010-A2.
PD 28-NOV-2002.
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 16
ID ABZ71261 standard; cDNA; 2152 BP.
DE Human secreted protein-encoding gene 72 cDNA clone HHPEN62, SEQ ID NO:82.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 84.3%; Score 1891; DB 8; Length 2152;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 17
ID ADE91167 standard; cDNA; 2152 BP.
DE Human secreted protein cDNA #SEQ ID 113.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 84.3%; Score 1891; DB 9; Length 2152;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 18
ID ADC73537 standard; DNA; 2152 BP.
DE Human secreted protein-related DNA - SEQ ID 170.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 19
ID ADE11660 standard; cDNA; 2152 BP.
DE Human secreted polypeptide cDNA #22.
PN US2003100051-A1.
PD 29-MAY-2003.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (CART/) CARTER K C.
PA (MOOR/) MOORE P A.
PA (OLSE/) OLSEN H S.
PA (SHIY/) SHI Y.
PA (YOUN/) YOUNG P E.
PA (WEIY/) WEI Y.
PA (BREW/) BREWER L A.
PA (SOPP/) SOPPET D R.
PA (LAFL/) LAFLEUR D W.
PA (ENDR/) ENDRESS G A.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 84.3%; Score 1891; DB 10; Length 2152;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 20
ID AAH64725 standard; cDNA; 2201 BP.
DE Human secreted protein cDNA, SEQ ID NO: 1.
PN WO200142451-A2.
PD 14-JUN-2001.
PA (GEST) GENSET.
Query Match 84.1%; Score 1886; DB 5; Length 2201;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 21
ID AAC84452 standard; cDNA; 2235 BP.
DE Nucleotide sequence of mddt cDNA clone ID No: 436857.2.
PN WO200075298-A2.
PD 14-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 83.2%; Score 1865; DB 4; Length 2235;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 22
ID AAS97191 standard; cDNA; 1524 BP.
DE Human metalloprotease partial DNA sequence #20.
PN WO200183782-A2.
PD 08-NOV-2001.

PA (SUGE-) SUGEN INC.
Query Match 68.0%; Score 1524; DB 6; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 23
ID ABL58477 standard; cDNA; 1521 BP.
DE Human metalloprotease, 55054 coding sequence.
PN WO200226948-A2.
PD 04-APR-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 67.8%; Score 1521; DB 6; Length 1521;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 24
ID AAH27154 standard; cDNA; 1524 BP.
DE Human carnosinase cDNA.
PN EP1097997-A1.
PD 09-MAY-2001.
PA (SNFI) SANOFI-SYNTHELABO.
Query Match 63.6%; Score 1427; DB 4; Length 1524;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 25
ID AAS12574 standard; DNA; 1587 BP.
DE DNA encoding DPI-45 and DPI-213.
PN WO200162787-A1.
PD 30-AUG-2001.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Query Match 61.3%; Score 1375; DB 4; Length 1587;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 26
ID AAS42478 standard; DNA; 1587 BP.
DE Human Schizophrenia-Associated Protein Isoform (SPI) 238/240 DNA.
PN WO200162785-A2.
PD 30-AUG-2001.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Query Match 61.3%; Score 1375; DB 4; Length 1587;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 27
ID AAS43075 standard; DNA; 1587 BP.
DE EST AAS26679/AI589129 complete sequence.
PN WO200163294-A2.
PD 30-AUG-2001.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Query Match 61.3%; Score 1375; DB 4; Length 1587;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 28
ID AAS23811 standard; DNA; 1587 BP.
DE DNA encoding schizophrenia-associated isoform SPI-238/240.
PN WO200163293-A2.
PD 30-AUG-2001.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Query Match 61.3%; Score 1375; DB 5; Length 1587;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 29
ID ADO79057 standard; DNA; 1587 BP.
DE Schizophrenia-Associated Protein Isoform SPI-238/SPI-240 cDNA.
PN US2004110938-A1.
PD 10-JUN-2004.
PA (PARE/) PAREKH R B.
PA (HERA/) CHANDRASIRI HERATH H M A.
PA (ROHL/) ROHLFF C.
PA (TERR/) TERRETT J A.
PA (TYSO/) TYSON K L.
Query Match 61.3%; Score 1375; DB 12; Length 1587;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 30
ID ADC77690 standard; cDNA; 1640 BP.
DE Human 55054 protein encoding cDNA SEQ ID NO:53.
PN WO2003073983-A2.
PD 12-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 57.9%; Score 1298; DB 10; Length 1640;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 31
ID AAI59305 standard; cDNA; 1343 BP.

DE Human polynucleotide SEQ ID NO 1508.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 52.8%; Score 1184; DB 4; Length 1343;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 32
ID AAI61091 standard; cDNA; 1569 BP.
DE Human polynucleotide SEQ ID NO 5080.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 45.5%; Score 1021; DB 4; Length 1569;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 33
ID ABL90090 standard; cDNA; 2039 BP.
DE Human polynucleotide SEQ ID NO 652.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 42.1%; Score 945; DB 6; Length 2039;
Best Local Similarity 99.5%; Pred. No. 1.1e-311;
RESULT 34
ID ADF90810 standard; DNA; 742 BP.
DE Human hepatic-fibrosis disease marker SEQ ID 272.
PN JP2003259877-A.
PD 16-SEP-2003.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 25.7%; Score 576; DB 10; Length 742;
Best Local Similarity 100.0%; Pred. No. 3e-186;
RESULT 35
ID AAH98942 standard; cDNA; 639 BP.
DE Human EST-derived coding sequence SEQ ID NO: 799.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.8%; Score 332; DB 4; Length 639;
Best Local Similarity 100.0%; Pred. No. 2.4e-103;
RESULT 36
ID AAH99853 standard; cDNA; 639 BP.
DE Human protein encoding cDNA sequence SEQ ID NO:688.
PN WO200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.8%; Score 332; DB 4; Length 639;
Best Local Similarity 100.0%; Pred. No. 2.4e-103;
RESULT 37
ID ACH13751 standard; cDNA; 456 BP.
DE Human adult brain cDNA #963.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 14.0%; Score 313; DB 9; Length 456;
Best Local Similarity 100.0%; Pred. No. 7.3e-97;
RESULT 38
ID AAC09875 standard; cDNA; 300 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 13950.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 8.0%; Score 180; DB 3; Length 300;
Best Local Similarity 99.6%; Pred. No. 1.2e-51;
RESULT 39
ID ACH74305 standard; DNA; 582 BP.
DE Human genome derived single exon probe #7500.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.
Query Match 6.8%; Score 152; DB 12; Length 582;
Best Local Similarity 100.0%; Pred. No. 3.4e-42;
RESULT 40
ID ACH88005 standard; DNA; 156 BP.
DE Human genome derived single exon probe #21200.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 6.7%; Score 150; DB 12; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.2e-41;
RESULT 41
ID AAS65841 standard; cDNA; 643 BP.
DE DNA encoding novel human diagnostic protein #1645.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 144; DB 5; Length 643;
Best Local Similarity 99.5%; Pred. No. 1.7e-39;
RESULT 42
ID AAS65840 standard; cDNA; 497 BP.
DE DNA encoding novel human diagnostic protein #1644.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 132; DB 5; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.2e-35;
RESULT 43
ID AAX10638 standard; DNA; 127 BP.
DE Human biallelic polymorphic DNA fragment WI-15225.
PN WO9820165-A2.
PD 14-MAY-1998.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 3.6%; Score 80; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.4e-17;
RESULT 44
ID AAI84805 standard; cDNA; 402 BP.
DE Human polynucleotide SEQ ID NO 4865.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.7%; Score 61; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 3e-11;
RESULT 45
ID ABA77130 standard; DNA; 433 BP.
DE Proliferative glomerular nephritis-associated gene sequence SEQ ID:137.
PN WO200173022-A1.
PD 04-OCT-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 2.7%; Score 61; DB 4; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
RESULT 46
ID ABN96930 standard; DNA; 770 BP.
DE Gene #3428 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 61; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
RESULT 47
ID ADQ22074 standard; DNA; 980 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4894.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 61; DB 12; Length 980;
Best Local Similarity 100.0%; Pred. No. 2.4e-11;
RESULT 48
ID ADQ23279 standard; DNA; 1225 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6099.
PN WO2004048938-A2.

PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 61; DB 12; Length 1225;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
RESULT 49
ID AAD16506 standard; DNA; 1367 BP.
DE Human ABC transporter-encoding gene 3 cDNA clone HJMBP48, SEQ ID NO:21.
PN WO200155208-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 4; Length 1367;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
RESULT 50
ID AAS29733 standard; cDNA; 1367 BP.
DE Human endocrine polypeptide encoding cDNA SEQ ID No 233.
PN WO200155364-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 5; Length 1367;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
RESULT 51
ID ADA27261 standard; cDNA; 1367 BP.
DE cDNA encoding human ABC transport receptor #11.
PN US2003049652-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 9; Length 1367;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
RESULT 52
ID ADA12864 standard; cDNA; 1367 BP.
DE Human ABC transporter-related cDNA HJMBP48 #2.
PN US2002161208-A1.
PD 31-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 61; DB 10; Length 1367;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
RESULT 53
ID ACC72015 standard; DNA; 1422 BP.
DE BCU0021 gene #SEQ ID 7.
PN WO2003029421-A2.
PD 10-APR-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 2.7%; Score 61; DB 8; Length 1422;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
RESULT 54
ID AAS27477 standard; cDNA; 1661 BP.
DE cDNA encoding novel signal transduction pathway protein, Seq ID 512.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 4; Length 1661;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
RESULT 55
ID AAL02553 standard; cDNA; 1661 BP.
DE Human reproductive system related antigen cDNA SEQ ID NO: 2554.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 4; Length 1661;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
RESULT 56
ID ABA07672 standard; cDNA; 1661 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 229.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 4; Length 1661;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
RESULT 57
ID ABK43975 standard; cDNA; 1661 BP.
DE DNA encoding novel central nervous system protein #555.

PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 4; Length 1661;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
RESULT 58
ID ADB93655 standard; cDNA; 1661 BP.
DE Human cDNA encoding a novel protein #502.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 61; DB 10; Length 1661;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
RESULT 59
ID ADI54362 standard; cDNA; 1661 BP.
DE cDNA encoding novel human protein seq id 565.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 61; DB 12; Length 1661;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
RESULT 60
ID ABQ54695 standard; cDNA; 1663 BP.
DE Human ovarian antigen HCOMM05 cDNA, SEQ ID NO:575.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 6; Length 1663;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
RESULT 61
ID AAV81394 standard; DNA; 1733 BP.
DE Human tumour antigen zsig15 coding sequence.
PN WO9850552-A1.
PD 12-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 2.7%; Score 61; DB 2; Length 1733;
Best Local Similarity 100.0%; Pred. No. 2.1e-11;
RESULT 62
ID ADN04967 standard; cDNA; 2161 BP.
DE Antipsoriatic cDNA sequence #698.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 61; DB 12; Length 2161;
Best Local Similarity 100.0%; Pred. No. 2e-11;
RESULT 63
ID ABK69135 standard; cDNA; 3714 BP.
DE DNA encoding human secreted protein, SEQ ID No 59.
PN WO200224721-A1.
PD 28-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 6; Length 3714;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
RESULT 64
ID ABQ54814 standard; cDNA; 3714 BP.
DE Human ovarian antigen HSPSI42 cDNA, SEQ ID NO:694.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 6; Length 3714;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
RESULT 65
ID ABV07975 standard; cDNA; 309 BP.
DE Human prostate expression marker cDNA 7966.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 60; DB 5; Length 309;
Best Local Similarity 100.0%; Pred. No. 7e-11;

RESULT 66
ID ADL37681 standard; DNA; 309 BP.
DE Human ovarian cancer DNA marker #11571.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 60; DB 5; Length 309;
Best Local Similarity 100.0%; Pred. No. 7e-11;
RESULT 67
ID ADI72542 standard; DNA; 309 BP.
DE Human ovarian cancer DNA marker #5284.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 60; DB 5; Length 309;
Best Local Similarity 100.0%; Pred. No. 7e-11;
RESULT 68
ID ABX41000 standard; cDNA; 321 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6165.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.7%; Score 60; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 6.9e-11;
RESULT 69
ID AAC78443 standard; cDNA; 386 BP.
DE Human cancer associated gene sequence SEQ ID NO:837.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 60; DB 3; Length 386;
Best Local Similarity 100.0%; Pred. No. 6.6e-11;
RESULT 70
ID AAI92146 standard; cDNA; 386 BP.
DE Human polynucleotide SEQ ID NO 12206.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.7%; Score 60; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 6.6e-11;
RESULT 71
ID ADK61475 standard; DNA; 438 BP.
DE Ovarian cancer-related DNA #630 with altered ovarian cancer expression.
PN WO2003068054-A2.
PD 21-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 2.7%; Score 60; DB 10; Length 438;
Best Local Similarity 100.0%; Pred. No. 6.4e-11;
RESULT 72
ID AAS60503 standard; cDNA; 509 BP.
DE Human cancer agent-sensitive marker #234.
PN WO200179556-A2.
PD 25-OCT-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 60; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 6.2e-11;
RESULT 73
ID AAF81806 standard; cDNA; 712 BP.
DE Human secreted protein gene 20 SEQ ID NO:30.
PN WO200112775-A2.
PD 22-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 60; DB 4; Length 712;
Best Local Similarity 100.0%; Pred. No. 5.7e-11;
RESULT 74
ID AAL23455 standard; cDNA; 752 BP.
DE Human breast cancer expressed polynucleotide 15912.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 60; DB 4; Length 752;
Best Local Similarity 100.0%; Pred. No. 5.7e-11;
RESULT 75
ID ADI15961 standard; cDNA; 759 BP.
DE Human PP 83 cDNA.
PN WO2003008450-A1.
PD 30-JAN-2003.
PA (ITOH/) ITOH K.
Query Match 2.7%; Score 60; DB 10; Length 759;
Best Local Similarity 100.0%; Pred. No. 5.7e-11;
RESULT 76
ID ADE58855 standard; DNA; 774 BP.
DE Human gene AK026608, SEQ ID NO 4743.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 2.7%; Score 60; DB 10; Length 774;
Best Local Similarity 100.0%; Pred. No. 5.6e-11;
RESULT 77
ID ADE58852 standard; DNA; 774 BP.
DE Human gene AK026608, SEQ ID NO 4740.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 2.7%; Score 60; DB 10; Length 774;
Best Local Similarity 100.0%; Pred. No. 5.6e-11;
RESULT 78
ID AAL24400 standard; cDNA; 781 BP.
DE Human breast cancer expressed polynucleotide 16857.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 60; DB 4; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.6e-11;
RESULT 79
ID AAD64841 standard; cDNA; 1249 BP.
DE M. charantia FUSCA homologue transcription factor EST cDNA #2.
PN US2003119165-A1.
PD 26-JUN-2003.
PA (CAHO/) CAHOON R E.
PA (LUGG/) LU G.
PA (WILL/) WILLIAMS M E.
Query Match 2.7%; Score 60; DB 10; Length 1249;
Best Local Similarity 100.0%; Pred. No. 5e-11;
RESULT 80
ID ADI42365 standard; DNA; 1262 BP.
DE Plant transcription factor polynucleotide #503.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 2.7%; Score 60; DB 12; Length 1262;
Best Local Similarity 100.0%; Pred. No. 5e-11;
RESULT 81
ID ADO02769 standard; cDNA; 1262 BP.
DE Soybean orthologue of Thalecress transcription factor, cDNA #103.
PN US2004045049-A1.

PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 2.7%; Score 60; DB 12; Length 1262;
Best Local Similarity 100.0%; Pred. No. 5e-11;
RESULT 82
ID AAA99029 standard; cDNA; 1360 BP.
DE Human TGC839 nucleotide sequence.
PN WO200055197-A1.
PD 21-SEP-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 2.7%; Score 60; DB 3; Length 1360;
Best Local Similarity 100.0%; Pred. No. 4.9e-11;
RESULT 83
ID ADM47789 standard; DNA; 1455 BP.
DE Polynucleotide sequence #207 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 2.7%; Score 60; DB 12; Length 1455;
Best Local Similarity 100.0%; Pred. No. 4.9e-11;
RESULT 84
ID ADQ24546 standard; DNA; 1478 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7366.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 60; DB 12; Length 1478;
Best Local Similarity 100.0%; Pred. No. 4.8e-11;
RESULT 85
ID AAD07771 standard; cDNA; 1480 BP.
DE Human secreted protein-encoding gene 2 cDNA clone HCGBE81, SEQ ID NO:12.
PN WO200132687-A1.
PD 10-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 60; DB 4; Length 1480;
Best Local Similarity 100.0%; Pred. No. 4.8e-11;
RESULT 86
ID ABQ54640 standard; cDNA; 1583 BP.
DE Human ovarian antigen HMWU46 cDNA, SEQ ID NO:520.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 60; DB 6; Length 1583;
Best Local Similarity 100.0%; Pred. No. 4.8e-11;
RESULT 87
ID AAC68122 standard; cDNA; 1751 BP.
DE Human secreted protein cDNA sequence #42.
PN WO200058335-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 2.7%; Score 60; DB 3; Length 1751;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
RESULT 88

ID AAH33173 standard; cDNA; 1751 BP.
DE Human colon Cancer antigen encoding cDNA SEQ ID NO:229.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 60; DB 4; Length 1751;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
RESULT 89
ID AAS21293 standard; cDNA; 1904 BP.
DE Human cDNA sequence encoding for PRO4403 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 4; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 90
ID ACA03652 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 8; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 91
ID ABX89190 standard; cDNA; 1904 BP.
DE DNA encoding novel secreted and transmembrane protein PRO4403.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 8; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 92
ID ACD41844 standard; cDNA; 1904 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #50.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 8; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 93
ID ACA04073 standard; cDNA; 1904 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 99.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 8; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 94
ID ADA45618 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 95
ID ADA76049 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 96
ID ADA18699 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 97
ID ADA61322 standard; cDNA; 1904 BP.

DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 98
ID ADB19107 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 99
ID ADB27648 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 100
ID ADA86127 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 101
ID ADB15691 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 102
ID ADA47477 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 103
ID ADA67272 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 104
ID ADB30279 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 105
ID ADA85575 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 106
ID ADA96787 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.

PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 107
ID ADA79091 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 108
ID ADA87230 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 109
ID ADB16432 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 110
ID ADA91524 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 111
ID ADB14587 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 112
ID ADB18548 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 113
ID ADA93763 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 114
ID ADB19659 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 115
ID ADB12971 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082710-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 116
ID ACD98473 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 117
ID ADA74225 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 118
ID ADB24458 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide SEQ ID NO 99.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 119
ID ADA81982 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 120
ID ADA74945 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 121
ID ADA85023 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 122
ID ADA84471 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 123
ID ADB29727 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 124
ID ADA80255 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082761-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 125
ID ADA75497 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 126
ID ADA46722 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 127
ID ADB25018 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide SEQ ID NO 99.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 128
ID ADA93194 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 129
ID ADB26544 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 130
ID ADB30831 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 131
ID ADA60759 standard; cDNA; 1904 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 132
ID ADB23906 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide SEQ ID NO 99.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 133
ID ADA96235 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 134
ID ADA80807 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 135
ID ADA95683 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 136
ID ADB25992 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 137
ID ADB21477 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 138
ID ADA77256 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 139
ID ADB17996 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 140
ID ADA86679 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 141
ID ADA87782 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 142
ID ADA46170 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;

Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 143
ID ADB28200 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 144
ID ADB28752 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 145
ID ADA76704 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 146
ID ADA8334 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 147
ID ADA97339 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 148
ID ADB27096 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 149
ID ADB22029 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 150
ID ADA66720 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 151
ID ADB22581 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 152
ID ADB23354 standard; cDNA; 1904 BP.

DE Human PRO polynucleotide SEQ ID NO 99.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 153
ID ADA92076 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 154
ID ADB15139 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 155
ID ADB38391 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 156
ID ADB37839 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 157
ID ADB66311 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 158
ID ADB89391 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 159
ID ADB90123 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 160
ID ADB39224 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 161
ID ADB46847 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.

PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 162
ID ADB86454 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 163
ID ADB77059 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 164
ID ADB34216 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide SEQ ID NO 99.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 165
ID ADB35320 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide SEQ ID NO 99.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 166
ID ADB33664 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide SEQ ID NO 99.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 167
ID ADB34768 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide SEQ ID NO 99.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 168
ID ADB35872 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide SEQ ID NO 99.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 169
ID ADB46267 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 170
ID ADC50140 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003092106-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 171
ID ADC71687 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 172
ID ADC59666 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 173
ID ADC52673 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID99.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 174
ID ADC57027 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID99.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 175
ID ADC60218 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 176
ID ADC50693 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 177
ID ADC65220 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 178
ID ADC54318 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID99.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 179
ID ADC53279 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID99.
PN US2003087364-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 180
ID ADC58802 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID99.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 181
ID ADC55680 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID99.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 182
ID ADC58250 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID99.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 183
ID ADD02924 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 184
ID ADC89916 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 185
ID ADC69335 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 186
ID ADC48224 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 187
ID ADD09753 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 188
ID ADD04328 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 189
ID ADC80284 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 190
ID ADD10791 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 191
ID ADC47672 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 192
ID ADC79732 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 193
ID ADD09201 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 194
ID ADD40914 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 195
ID ADD52053 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 196
ID ADD52793 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 197
ID ADD53345 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;

Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 198
ID ADD51501 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 199
ID ADD02300 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 200
ID ADD01734 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 201
ID ADD53916 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 202
ID ADD92233 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 203
ID ADD91129 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 204
ID ADE03743 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 205
ID ADE32040 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 206
ID ADE21972 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;

RESULT 207
ID ADD79196 standard; cDNA; 1904 BP.
DE CDNA encoding human PRO polypeptide #50.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 208
ID ADE41732 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 209
ID ADE17549 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 210
ID ADD91681 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 211
ID ADE33144 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 212
ID ADE33696 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 213
ID ADD79748 standard; cDNA; 1904 BP.
DE CDNA encoding human PRO polypeptide #50.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 214
ID ADD92785 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 215
ID ADE19205 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 216
ID ADE40612 standard; cDNA; 1904 BP.

ID ADE18653 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 217
ID ADE42849 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 218
ID ADD95638 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 219
ID ADE22524 standard; cDNA; 1904 BP.
DE CDNA encoding human PRO polypeptide #50.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 220
ID ADD78642 standard; cDNA; 1904 BP.
DE CDNA encoding human PRO polypeptide #50.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 221
ID ADE32592 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 222
ID ADE42284 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 223
ID ADD80300 standard; cDNA; 1904 BP.
DE CDNA encoding human PRO polypeptide #50.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 224
ID ADD89328 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 225
ID ADE40612 standard; cDNA; 1904 BP.

DE Human PRO polynucleotide #50.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 226
ID ADE04411 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 227
ID ADE92540 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 228
ID ADG21249 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 229
ID ADG22890 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 230
ID ADF97225 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 231
ID ADG80289 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 232
ID ADG79737 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 233
ID ADH55029 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 234
ID ADH55581 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.

PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 235
ID ADI63800 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 236
ID ADI64749 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 237
ID ADI63248 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 238
ID ADH81662 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 239
ID ADH81110 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 240
ID ACD23902 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 241
ID ACA67043 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 242
ID ADM82279 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 11; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 243
ID ADN15678 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087353-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 11; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 244
ID ADN16307 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 11; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 245
ID ADN15126 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 11; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 246
ID ADN14574 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 11; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 247
ID ADC80836 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 248
ID ADD76284 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 249
ID ADD87648 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 250
ID ADD86052 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 251
ID ADE75500 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 252
ID ADE23076 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003092108-A1.
PD 15-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 253
ID ADE23628 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 254
ID ADE24271 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 255
ID ADD87096 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 256
ID ADE88962 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 257
ID ADE18101 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 258
ID ADE88410 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 259
ID ADE94430 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 260
ID ADE90841 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 261
ID ADE94982 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 262
ID ADE93092 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 263
ID ADF34673 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 264
ID ADE91988 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 265
ID ADE90289 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 266
ID ADE91436 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 267
ID ADG02015 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 268
ID ADG21801 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 269
ID ADG19871 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 270
ID ADF97777 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;

Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 271
ID ADG23994 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 272
ID ADF98348 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 273
ID ADG03179 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 274
ID ADF98900 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 275
ID ADG16485 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 276
ID ADG04944 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 277
ID ADG19211 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 278
ID ADG13048 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 279
ID ADG08105 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;

RESULT 280
ID ADG15275 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 281
ID ADF96673 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 282
ID ADG05858 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 283
ID ADG23442 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 284
ID ADG03731 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 285
ID ADG24632 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 286
ID ADG06929 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 287
ID ADG07481 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 288
ID ADG54976 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 289

ID ADG60640 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 290
ID ADG61744 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 291
ID ADG81945 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 292
ID ADG57184 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 293
ID ADG56632 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 294
ID ADG55528 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 295
ID ADG58288 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 296
ID ADG70654 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 297
ID ADG57736 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 298
ID ADG53320 standard; cDNA; 1904 BP.

DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 299
ID ADG71206 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 300
ID ADG81393 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 301
ID ADH30355 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 302
ID ADH11722 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 303
ID ADG52144 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 304
ID ADG53872 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 305
ID ADG80841 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 306
ID ADG56080 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 307
ID ADH12346 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207378-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 308
ID ADG61192 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 309
ID ADH28279 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 310
ID ADG54424 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 311
ID ADG59464 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 312
ID ADI80888 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 313
ID ADG09631 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 314
ID ADI15102 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 315
ID ADG08979 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 316
ID ADI14434 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 317
ID ADI18029 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 318
ID ADJ63310 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 319
ID ADJ77205 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 320
ID ADJ65327 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 321
ID ADM27463 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 322
ID ADM42187 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 323
ID ADM28049 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 324
ID ABL39593 standard; cDNA; 1964 BP.
DE Human cancer suppressing gene PP928 encoding cDNA SEQ ID NO:30.
PN CN1313318-A.
PD 19-SEP-2001.
PA (SHAN-) SHANGHAI INST ONCOLOGY.
Query Match 2.7%; Score 60; DB 6; Length 1964;
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
RESULT 325
ID ADQ21276 standard; DNA; 2072 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4096.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match 2.7%; Score 60; DB 12; Length 2072;
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
RESULT 326
ID ADI57346 standard; cDNA; 2169 BP.
DE Human pyruvate kinase, liver cDNA SEQ ID NO:30.
PN WO2003066086-A2.
PD 14-AUG-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 2.7%; Score 60; DB 10; Length 2169;
Best Local Similarity 100.0%; Pred. No. 4.4e-11;
RESULT 327
ID AAD07661 standard; cDNA; 2329 BP.
DE Human secreted protein-encoding gene 7 cDNA clone HNTDL21, SEQ ID NO:17.
PN WO200134644-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 60; DB 5; Length 2329;
Best Local Similarity 100.0%; Pred. No. 4.4e-11;
RESULT 328
ID ADQ24017 standard; DNA; 3554 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6837.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 60; DB 12; Length 3554;
Best Local Similarity 100.0%; Pred. No. 4e-11;
RESULT 329
ID AAA16677 standard; cDNA; 4086 BP.
DE Human secreted protein clone kv10_8 nucleotide sequence SEQ ID NO:119.
PN WO200009552-A1.
PD 24-FEB-2000.
PA (GEMY) GENETICS INST INC.
Query Match 2.7%; Score 60; DB 3; Length 4086;
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
RESULT 330
ID ABK39753 standard; cDNA; 4086 BP.
DE cDNA encoding clone #50560 (L987P) of lung tumour protein.
PN WO200204514-A2.
PD 17-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 2.7%; Score 60; DB 6; Length 4086;
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
RESULT 331
ID ACA12082 standard; cDNA; 4086 BP.
DE Human lung cancer-associated cDNA L987P extended sequence.
PN US2002197669-A1.
PD 26-DEC-2002.
PA (BANG/) BANGUR C S.
PA (FANG/) FANGER G R.
PA (WANG/) WANG A.
PA (WANG/) WANG T.
PA (SWIT/) SWITZER A P.
PA (MCNE/) MCNEILL P D.
PA (CLAP/) CLAPPER J D.
Query Match 2.7%; Score 60; DB 8; Length 4086;
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
RESULT 332
ID ACA03268 standard; cDNA; 4086 BP.
DE Lung cancer therapyand diagnosis associated cDNA #1755.
PN US2002172952-A1.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 2.7%; Score 60; DB 8; Length 4086;
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
RESULT 333
ID ADH47320 standard; cDNA; 4086 BP.
DE Human lung tumour cDNA clone, SEQ ID NO 1801.
PN WO2003037267-A2.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 2.7%; Score 60; DB 10; Length 4086;
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
RESULT 334

ID ABV30288 standard; cDNA; 4397 BP.
DE Human prostate expression marker cDNA 30279.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 60; DB 5; Length 4397;
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
RESULT 335
ID ADQ22371 standard; DNA; 4824 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5191.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 60; DB 12; Length 4824;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
RESULT 336
ID ACC00398 standard; cDNA; 10569 BP.
DE Human cell adhesion and extracellular matrix protein, CADECM-7, DNA.
PN WO2003027230-A2.
PD 03-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.7%; Score 60; DB 8; Length 10569;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
RESULT 337
ID ABK55279 standard; cDNA; 81 BP.
DE Human colon cancer-associated cDNA, SEQ ID No 749.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 59; DB 6; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
RESULT 338
ID ABK54687 standard; cDNA; 90 BP.
DE Human colon cancer-associated cDNA, SEQ ID No 157.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 59; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 2e-10;
RESULT 339
ID AAV00430 standard; cDNA; 106 BP.
DE 3' fragment of clone H298_23.
PN WO9740069-A2.
PD 30-OCT-1997.
PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 59; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2e-10;
RESULT 340
ID ADD33553 standard; DNA; 111 BP.
DE Mouse mitochondrial DNA sequence SEQ ID NO:1326.
PN WO2003020220-A2.
PD 13-MAR-2003.
PA (UYEM-) UNIV EMORY.
Query Match 2.6%; Score 59; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
RESULT 341
ID ABX61397 standard; DNA; 115 BP.
DE Arabidopsis thaliana polynucleotide #743.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANYI/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUYI/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match 2.6%; Score 59; DB 5; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
RESULT 342
ID AAD56370 standard; DNA; 169 BP.
DE Human secreted protein-encoding gene 8 cDNA clone HDMSA74, SEQ ID NO:30.
PN WO2003038038-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 9; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
RESULT 343
ID ABT23025 standard; DNA; 178 BP.
DE Breast cancer marker gene SEQ ID No 1398.
PN WO200285298-A2.
PD 31-OCT-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.6%; Score 59; DB 10; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
RESULT 344
ID ABV59005 standard; cDNA; 196 BP.
DE Human prostate expression marker cDNA 58996.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
RESULT 345
ID ABV19718 standard; cDNA; 198 BP.
DE Human prostate expression marker cDNA 19709.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
RESULT 346
ID ADP10592 standard; DNA; 200 BP.
DE Reference mRNA sequences for marker probe #269.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 2.6%; Score 59; DB 12; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
RESULT 347
ID ABV19351 standard; cDNA; 211 BP.
DE Human prostate expression marker cDNA 19342.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
RESULT 348
ID AAL08212 standard; cDNA; 220 BP.
DE Human breast cancer expressed polynucleotide 669.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
RESULT 349
ID ABV61062 standard; cDNA; 228 BP.
DE Human prostate expression marker cDNA 61053.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
RESULT 350
ID AAH42844 standard; DNA; 244 BP.
DE Nucleotide sequence of a human ribosomal protein L18a.
PN WO200153524-A2.
PD 26-JUL-2001.
PA (UYNO-) UNIV NOTTINGHAM TRENT.
Query Match 2.6%; Score 59; DB 5; Length 244;

Best Local Similarity 100.0%; Pred. No. 1.6e-10;
RESULT 351
ID ADI72681 standard; DNA; 246 BP.
DE Human ovarian cancer DNA marker #5423.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
RESULT 352
ID ADL37820 standard; DNA; 246 BP.
DE Human ovarian cancer DNA marker #11710.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
RESULT 353
ID ABV83658 standard; cDNA; 254 BP.
DE Human breast specific gene SEQ ID NO 101.
PN WO200266605-A2.
PD 29-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 2.6%; Score 59; DB 6; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
RESULT 354
ID ABV37898 standard; cDNA; 257 BP.
DE Human prostate expression marker cDNA 37889.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
RESULT 355
ID ABV49125 standard; cDNA; 270 BP.
DE Human prostate expression marker cDNA 49116.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 270;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
RESULT 356
ID ABV61841 standard; cDNA; 281 BP.
DE Human prostate expression marker cDNA 61832.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
RESULT 357
ID ABZ08427 standard; cDNA; 290 BP.
DE Human leukocyte derived cDNA SEQ ID NO 8418.
PN WO200257414-A2.
PD 25-JUL-2002.
PA (BIOC-) BIOCARDIA INC.
Query Match 2.6%; Score 59; DB 6; Length 290;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 358
ID ABV61015 standard; cDNA; 294 BP.
DE Human prostate expression marker cDNA 61006.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 359
ID ABX48782 standard; cDNA; 299 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #13947.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.

PA (WARR/) WARREN W C.
Query Match 2.6%; Score 59; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 360
ID ABV19334 standard; cDNA; 305 BP.
DE Human prostate expression marker cDNA 19325.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 361
ID ABV49426 standard; cDNA; 308 BP.
DE Human prostate expression marker cDNA 49417.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 362
ID ADK60878 standard; DNA; 308 BP.
DE Ovarian cancer-related DNA #33 with altered ovarian cancer expression.
PN WO2003068054-A2.
PD 21-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 2.6%; Score 59; DB 10; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 363
ID AAH70139 standard; cDNA; 309 BP.
DE Human cervical cancer marker nucleic acid 1413.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 364
ID AAL25957 standard; cDNA; 313 BP.
DE Human breast cancer expressed polynucleotide 18414.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 365
ID ADL43989 standard; DNA; 324 BP.
DE Human ovarian cancer DNA marker #17879.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 324;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 366
ID ABV19659 standard; cDNA; 333 BP.
DE Human prostate expression marker cDNA 19650.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 367
ID AAI83209 standard; cDNA; 356 BP.
DE Human polynucleotide SEQ ID NO 3269.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 356;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 368
ID ABL87200 standard; cDNA; 359 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:10178.
PN WO200192581-A2.
PD 06-DEC-2001.

PA (CORI-).CORIXA CORP. 2.6%; Score 59; DB 6; Length 359;
Query Match 100.0%; Pred. No. 1.5e-10;
Best Local Similarity
RESULT 369
ID ABV60981 standard; cDNA; 360 BP.
DE Human prostate expression marker cDNA 60972.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 370
ID ADK61648 standard; DNA; 360 BP.
DE Ovarian cancer-related DNA #803 with altered ovarian cancer expression.
PN WO2003068054-A2.
PD 21-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 2.6%; Score 59; DB 10; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 371
ID AAI83219 standard; cDNA; 362 BP.
DE Human polynucleotide SEQ ID NO 3279.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 372
ID ABX42829 standard; cDNA; 373 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #7994.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 59; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 373
ID ABV14963 standard; cDNA; 374 BP.
DE Human prostate expression marker cDNA 14954.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 374
ID AAI88772 standard; cDNA; 375 BP.
DE Human polynucleotide SEQ ID NO 8832.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 375
ID ABV05794 standard; cDNA; 375 BP.
DE Human prostate expression marker cDNA 5785.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 376
ID ABV57992 standard; cDNA; 376 BP.
DE Human prostate expression marker cDNA 57983.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 377
ID ABV56400 standard; cDNA; 376 BP.

DE Human prostate expression marker cDNA 56391.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 378
ID ABT22632 standard; DNA; 378 BP.
DE Breast cancer marker gene SEQ ID NO 1005.
PN WO200285298-A2.
PD 31-OCT-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.6%; Score 59; DB 10; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 379
ID ABZ08196 standard; cDNA; 384 BP.
DE Human leukocyte derived cDNA SEQ ID NO 8187.
PN WO200257414-A2.
PD 25-JUL-2002.
PA (BIOC-) BIOCARDIA INC.
Query Match 2.6%; Score 59; DB 6; Length 384;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 380
ID AAI90569 standard; cDNA; 393 BP.
DE Human polynucleotide SEQ ID NO 10629.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 381
ID ADL44065 standard; DNA; 394 BP.
DE Human ovarian cancer DNA marker #17955.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 382
ID AAI83099 standard; cDNA; 395 BP.
DE Human polynucleotide SEQ ID NO 3159.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 383
ID AAI88643 standard; cDNA; 396 BP.
DE Human polynucleotide SEQ ID NO 8703.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 384
ID ABV13524 standard; cDNA; 396 BP.
DE Human prostate expression marker cDNA 13515.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 385
ID AAI87808 standard; cDNA; 399 BP.
DE Human polynucleotide SEQ ID NO 7868.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 386
ID ABX47608 standard; cDNA; 399 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12773.

PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match 2.6%; Score 59; DB 8; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 387
ID AAS44813 standard; DNA; 400 BP.
DE Mouse contig polynucleotide sequence #66.
PN WO200164834-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 388
ID ABV14838 standard; cDNA; 400 BP.
DE Human prostate expression marker cDNA 14829.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 389
ID ADL44204 standard; DNA; 402 BP.
DE Human ovarian cancer DNA marker #18094.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 390
ID AAI87975 standard; cDNA; 403 BP.
DE Human polynucleotide SEQ ID NO 8035.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 391
ID AAI83327 standard; cDNA; 405 BP.
DE Human polynucleotide SEQ ID NO 3387.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 392
ID AAI93716 standard; cDNA; 411 BP.
DE Human polynucleotide SEQ ID NO 13776.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 393
ID AAI88867 standard; cDNA; 416 BP.
DE Human polynucleotide SEQ ID NO 8927.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 394
ID AAL25912 standard; cDNA; 417 BP.
DE Human breast cancer expressed polynucleotide 18369.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 395

ID AAI85189 standard; cDNA; 417 BP.
DE Human polynucleotide SEQ ID NO 5249.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 396
ID AAI90979 standard; cDNA; 417 BP.
DE Human polynucleotide SEQ ID NO 11039.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 397
ID AAI82925 standard; cDNA; 417 BP.
DE Human polynucleotide SEQ ID NO 2985.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 398
ID AAI80556 standard; cDNA; 420 BP.
DE Human polynucleotide SEQ ID NO 616.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 399
ID ABV56528 standard; cDNA; 421 BP.
DE Human prostate expression marker cDNA 56519.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 421;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 400
ID AAI82066 standard; cDNA; 422 BP.
DE Human polynucleotide SEQ ID NO 2126.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 401
ID ADL41653 standard; DNA; 425 BP.
DE Human ovarian cancer DNA marker #15543.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 402
ID ABV60871 standard; cDNA; 426 BP.
DE Human prostate expression marker cDNA 60862.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 403
ID ABV44832 standard; cDNA; 433 BP.
DE Human prostate expression marker cDNA 44823.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 404
ID ABX45215 standard; cDNA; 435 BP.

DE Bovine EST associated with lactation/muscle/fat deposition #10380.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 59; DB 8; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 405
ID ABV39046 standard; cDNA; 436 BP.
DE Human prostate expression marker cDNA 39037.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 436;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 406
ID ABV38926 standard; cDNA; 436 BP.
DE Human prostate expression marker cDNA 38917.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 436;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 407
ID ABV44714 standard; cDNA; 436 BP.
DE Human prostate expression marker cDNA 44705.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 436;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 408
ID ABV34639 standard; cDNA; 442 BP.
DE Human prostate expression marker cDNA 34630.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 442;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 409
ID ABV43495 standard; cDNA; 442 BP.
DE Human prostate expression marker cDNA 43486.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 442;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 410
ID AAI83052 standard; cDNA; 452 BP.
DE Human polynucleotide SEQ ID NO 3112.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 411
ID ABX35770 standard; cDNA; 452 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #935.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 59; DB 8; Length 452;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 412
ID AAS60714 standard; cDNA; 456 BP.
DE Human cancer agent-resistance marker #469.
PN WO200179556-A2.
PD 25-OCT-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 413
ID ABV36028 standard; cDNA; 459 BP.
DE Human prostate expression marker cDNA 36019.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 459;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 414
ID ABV37900 standard; cDNA; 459 BP.
DE Human prostate expression marker cDNA 37891.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 459;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 415
ID AAH64924 standard; cDNA; 462 BP.
DE Human secreted protein cDNA, SEQ ID NO: 200.
PN WO200142451-A2.
PD 14-JUN-2001.
PA (GEST) GENSET.
Query Match 2.6%; Score 59; DB 5; Length 462;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 416
ID AAL19122 standard; cDNA; 472 BP.
DE Human breast cancer expressed polynucleotide 11579.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 4; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 417
ID ADL43530 standard; DNA; 476 BP.
DE Human ovarian cancer DNA marker #17420.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 418
ID ABV61013 standard; cDNA; 478 BP.
DE Human prostate expression marker cDNA 61004.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 419
ID AAL19077 standard; cDNA; 486 BP.
DE Human breast cancer expressed polynucleotide 11534.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 4; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 420
ID ADL44998 standard; DNA; 501 BP.
DE Human ovarian cancer DNA marker #18888.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 421
ID ABV57765 standard; cDNA; 502 BP.
DE Human prostate expression marker cDNA 57756.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 2.6%; Score 59; DB 5; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 422
ID ABV35805 standard; cDNA; 503 BP.
DE Human prostate expression marker cDNA 35796.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 423
ID ABV44605 standard; cDNA; 503 BP.
DE Human prostate expression marker cDNA 44596.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 424
ID ABV56784 standard; cDNA; 505 BP.
DE Human prostate expression marker cDNA 56775.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 505;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 425
ID ACH23748 standard; cDNA; 506 BP.
DE Human adult ovary cDNA #2128.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.6%; Score 59; DB 9; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 426
ID ABL87166 standard; cDNA; 508 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:10144.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 59; DB 6; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 427
ID ABV49485 standard; cDNA; 516 BP.
DE Human prostate expression marker cDNA 49476.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 516;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 428
ID ADL43674 standard; DNA; 526 BP.
DE Human ovarian cancer DNA marker #17564.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 429
ID AAS60111 standard; cDNA; 530 BP.
DE Human cancer agent-sensitive marker #112.
PN WO200179556-A2.
PD 25-OCT-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 4; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 430
ID ABV56384 standard; cDNA; 535 BP.
DE Human prostate expression marker cDNA 56375.

PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 535;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 431
ID AAH34620 standard; cDNA; 545 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1702.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 545;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 432
ID ABV56662 standard; cDNA; 549 BP.
DE Human prostate expression marker cDNA 56653.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 433
ID ABV56468 standard; cDNA; 549 BP.
DE Human prostate expression marker cDNA 56459.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 434
ID ABV14728 standard; cDNA; 555 BP.
DE Human prostate expression marker cDNA 14719.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 435
ID AAS29149 standard; cDNA; 565 BP.
DE cDNA encoding for human DNA-binding protein #120.
PN WO200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 5; Length 565;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 436
ID ABS68289 standard; cDNA; 565 BP.
DE cDNA encoding human DNA-binding protein #120.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.6%; Score 59; DB 6; Length 565;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 437
ID ADC25283 standard; cDNA; 565 BP.
DE Human cDNA from extracellular matrix gene 120.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 10; Length 565;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 438
ID ADL43620 standard; DNA; 566 BP.
DE Human ovarian cancer DNA marker #17510.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 566;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 439
ID ABL87230 standard; cDNA; 585 BP.

DE Human ovarian cancer related cDNA clone SEQ ID NO:10208.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP. 2.6%; Score 59; DB 6; Length 585;
Query Match 100.0%; Pred. No. 1.3e-10;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 440
ID ADL37504 standard; DNA; 610 BP.
DE Human ovarian cancer DNA marker #11394.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 441
ID ADI72360 standard; DNA; 610 BP.
DE Human ovarian cancer DNA marker #5102.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 442
ID AAH71564 standard; cDNA; 611 BP.
DE Human cervical cancer marker nucleic acid 2838.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 4; Length 611;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 443
ID ABT22374 standard; DNA; 620 BP.
DE Breast cancer marker gene SEQ ID No 747.
PN WO200285298-A2.
PD 31-OCT-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.6%; Score 59; DB 10; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 444
ID ADK61473 standard; DNA; 631 BP.
DE Ovarian cancer-related DNA #628 with altered ovarian cancer expression.
PN WO2003068054-A2.
PD 21-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 2.6%; Score 59; DB 10; Length 631;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 445
ID AAZ98055 standard; cDNA; 639 BP.
DE Human secreted protein encoding nucleotide sequence SEQ ID NO:49.
PN WO200004140-A1.
PD 27-JAN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 3; Length 639;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 446
ID AAD11668 standard; cDNA; 639 BP.
DE Human secreted protein-encoding gene 39 cDNA clone HE2DY70, SEQ ID NO:49.
PN WO200151504-A1.
PD 19-JUL-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 639;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 447
ID ABK69764 standard; cDNA; 639 BP.
DE Human secreted protein gene 39.
PN WO200226931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 6; Length 639;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 448
ID ADA39770 standard; cDNA; 639 BP.

DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 8; Length 639;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 449
ID ADA55961 standard; DNA; 639 BP.
DE Gene encoding human secreted protein #140.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 10; Length 639;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 450
ID ADI71997 standard; DNA; 664 BP.
DE Human ovarian cancer DNA marker #4739.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 664;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 451
ID ADL37146 standard; DNA; 664 BP.
DE Human ovarian cancer DNA marker #11036.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 664;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 452
ID AAS62239 standard; cDNA; 681 BP.
DE cDNA sequence #26 encoding novel human secreted protein.
PN WO200177291-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 59; DB 6; Length 681;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 453
ID ABA06495 standard; cDNA; 758 BP.
DE Human cDNA SEQ ID NO: 161.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 758;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 454
ID ABV83832 standard; cDNA; 758 BP.
DE Human polynucleotide SEQ ID NO 161.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH, S C.
Query Match 2.6%; Score 59; DB 6; Length 758;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 455
ID AA195164 standard; cDNA; 771 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 1239.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 2.6%; Score 59; DB 4; Length 771;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 456
ID ADL38237 standard; DNA; 810 BP.
DE Human ovarian cancer DNA marker #12127.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 810;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;

RESULT 457
ID ADI73104 standard; DNA; 810 BP.
DE Human ovarian cancer DNA marker #5846.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 810;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 458
ID ABK34898 standard; cDNA; 811 BP.
DE Human cDNA encoding secreted protein #36.
PN WO200177288-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 59; DB 6; Length 811;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 459
ID AAC78094 standard; cDNA; 827 BP.
DE Human cancer associated gene sequence SEQ ID NO:488.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 3; Length 827;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 460
ID AAX89609 standard; cDNA; 831 BP.
DE Human secreted protein clone bg570_1 encoding cDNA.
PN WO9935253-A1.
PD 15-JUL-1999.
PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 59; DB 2; Length 831;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 461
ID AAS59240 standard; cDNA; 831 BP.
DE Human cDNA encoding a secreted protein bg570_1.
PN WO200175068-A2.
PD 11-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 59; DB 4; Length 831;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 462
ID ABA90909 standard; cDNA; 831 BP.
DE Human polynucleotide SEQ ID NO 67.
PN US200103935-A1.
PD 08-NOV-2001.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LAVA/) LAVALLIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (AGOS/) AGOSTINO M J.
PA (STEI/) STEININGER R J.
PA (SPAU/) SPAULDING V.
PA (WONG/) WONG G G.
PA (CLAR/) CLARK H.
PA (FECH/) FECHTEL K.
Query Match 2.6%; Score 59; DB 6; Length 831;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 463
ID ADC78824 standard; DNA; 835 BP.
DE Human PRO protein coding sequence #27.
PN WO2003034984-A2.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 835;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 464
ID AAS25860 standard; cDNA; 836 BP.
DE Human cDNA encoding a novel secreted protein, Seq ID 39.
PN WO200155322-A2.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 836;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 465
ID ABX73201 standard; DNA; 836 BP.
DE Human novel polynucleotide #29.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.6%; Score 59; DB 8; Length 836;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 466
ID ABZ78019 standard; cDNA; 841 BP.
DE Human breast specific nucleic acid #33.
PN WO200268645-A2.
PD 06-SEP-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 2.6%; Score 59; DB 6; Length 841;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 467
ID ADK67944 standard; cDNA; 860 BP.
DE Mouse cDNA clone F38, related to serine/threonine kinase.
PN WO2004013289-A2.
PD 12-FEB-2004.
PA (UYOH-) UNIV OHIO.
Query Match 2.6%; Score 59; DB 12; Length 860;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 468
ID ABA06476 standard; cDNA; 912 BP.
DE Human cDNA SEQ ID NO: 142.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 912;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 469
ID ABV83813 standard; cDNA; 912 BP.
DE Human polynucleotide SEQ ID NO 142.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.6%; Score 59; DB 6; Length 912;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 470
ID AAS40889 standard; cDNA; 913 BP.
DE cDNA encoding novel human enzyme polypeptide #105.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 913;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 471
ID ABA06682 standard; cDNA; 913 BP.
DE Human cDNA SEQ ID NO: 348.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 913;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 472
ID AAS29696 standard; cDNA; 913 BP.
DE Human endocrine polypeptide encoding cDNA SEQ ID No 196.
PN WO200155364-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 5; Length 913;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 473
ID ABV84019 standard; cDNA; 913 BP.

DE Human polynucleotide SEQ ID NO 348.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.6%; Score 59; DB 6; Length 913;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 474
ID ABQ80003 standard; cDNA; 925 BP.
DE Secreted human protein cDNA.
PN WO2003002138-A1.
PD 09-JAN-2003.
PA (PEKE) PE CORP NY.
Query Match 2.6%; Score 59; DB 8; Length 925;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 475
ID AAA78431 standard; cDNA; 952 BP.
DE Human secreted protein gene 46 SEQ ID NO:61.
PN WO200035937-A1.
PD 22-JUN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 3; Length 952;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 476
ID AAC69107 standard; DNA; 995 BP.
DE Human secreted protein gene 24 clone HAMFL84.
PN WO200055371-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 3; Length 995;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 477
ID ABK35340 standard; cDNA; 995 BP.
DE Human cDNA encoding secreted protein #478.
PN WO200177288-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 59; DB 6; Length 995;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 478
ID AAX20414 standard; DNA; 1071 BP.
DE Human secreted protein gene 3.
PN WO9906423-A1.
PD 11-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 2; Length 1071;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 479
ID ADD90198 standard; cDNA; 1071 BP.
DE Novel human secreted protein cDNA seq id 13.
PN US2003199683-A1.
PD 23-OCT-2003.
PA (RUBE/) RUBEN S M.
PA (FENG/) FENG P.
PA (LAF/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (CART/) CARTER K C.
PA (ENDR/) ENDRESS G A.
PA (WEIY/) WEI Y.
PA (FANP/) FAN P.
PA (ROSE/) ROSEN C A.
Query Match 2.6%; Score 59; DB 10; Length 1071;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 480
ID ADG90017 standard; cDNA; 1071 BP.
DE Human cDNA from secreted protein gene 3.
PN US2003166541-A1.
PD 04-SEP-2003.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 10; Length 1071;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 481
ID ADO62876 standard; DNA; 1091 BP.
DE Transcription factor G3055 orthologous sequence, SEQ ID 1343.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 2.6%; Score 59; DB 12; Length 1091;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 482
ID AAA29167 standard; cDNA; 1106 BP.
DE Rice 4-hydroxyphenylpyruvate dioxygenase partial cDNA.
PN WO200032757-A2.
PD 08-JUN-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 2.6%; Score 59; DB 3; Length 1106;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 483
ID ABT02999 standard; DNA; 1107 BP.
DE Human breast specific coding sequence SEQ ID NO: 4.
PN WO200240672-A2.
PD 23-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 2.6%; Score 59; DB 6; Length 1107;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 484
ID AAS28831 standard; cDNA; 1125 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 77.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 1125;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 485
ID ADB31556 standard; cDNA; 1125 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 77.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 10; Length 1125;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 486
ID AAV84347 standard; cDNA; 1180 BP.
DE Human Apo-2DCR cDNA clone DNA33085.
PN WO9858062-A1.
PD 23-DEC-1998.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 2; Length 1180;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 487
ID ABS53571 standard; cDNA; 1180 BP.
DE cDNA encoding native human Apo-2DCR #2.
PN US2002102706-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 6; Length 1180;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 488
ID ABS53570 standard; cDNA; 1180 BP.
DE cDNA encoding native human Apo-2DCR #1.
PN US2002102706-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 6; Length 1180;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 489
ID AAD64037 standard; cDNA; 1180 BP.
DE Human Apo-2DCR cDNA #1.
PN US2003138915-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.

Query Match 2.6%; Score 59; DB 10; Length 1180;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 490
ID AAD64038 standard; cDNA; 1180 BP.
DE Human Apo-2DcR cDNA #2.
PN US2003138915-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1180;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 491
ID ACC00704 standard; cDNA; 1249 BP.
DE Zea mays oil trait related cDNA sequence SEQ ID NO:157.
PN WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 2.6%; Score 59; DB 8; Length 1249;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 492
ID AAA93129 standard; cDNA; 1293 BP.
DE Human secreted protein coding sequence SEQ ID NO: 57.
PN WO200049134-A1.
PD 24-AUG-2000.
PA (ALPH-) ALPHAGEN INC.
Query Match 2.6%; Score 59; DB 3; Length 1293;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 493
ID ACC00651 standard; cDNA; 1307 BP.
DE Zea mays oil trait related cDNA sequence SEQ ID NO:51.
PN WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 2.6%; Score 59; DB 8; Length 1307;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 494
ID ADC23530 standard; cDNA; 1307 BP.
DE cDNA encodes protein involved in altering plant oil phenotype (SeqID 35).
PN WO2003001902-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 2.6%; Score 59; DB 10; Length 1307;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 495
ID ADQ23192 standard; DNA; 1383 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6012.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.6%; Score 59; DB 12; Length 1383;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 496
ID ADQ24215 standard; DNA; 1469 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7035.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.6%; Score 59; DB 12; Length 1469;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 497
ID ADI16785 standard; cDNA; 1513 BP.
DE Human NOVX cDNA to treat human pathological conditions SeqID321.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 2.6%; Score 59; DB 6; Length 1513;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 498
ID ADN42439 standard; cDNA; 1513 BP.
DE Human cDNA encoding NOV 99.
PN US2004033493-A1.

PD 19-FEB-2004.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (GANG/) GANGOLLI E A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELLI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENNA C E A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEFLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
Query Match 2.6%; Score 59; DB 12; Length 1513;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 499
ID AAX16675 standard; DNA; 1554 BP.
DE Xenopus WA545 protein encoding DNA.
PN WO9902678-A1.
PD 21-JAN-1999.
PA (GEMY) GENETICS INST INC.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 2.6%; Score 59; DB 2; Length 1554;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 500
ID ABK35953 standard; cDNA; 1554 BP.
DE cDNA sequence #344 encoding novel human secreted protein.
PN WO200177289-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 59; DB 6; Length 1554;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 501
ID AAF21791 standard; DNA; 1614 BP.
DE Human breast and ovarian cancer associated antigen gene SEQ ID 178.
PN WO200055173-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 3; Length 1614;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 502
ID AAA15694 standard; cDNA; 1651 BP.
DE Cancer suppressor gene down-regulated in large intestine cancer.
PN WO200018911-A1.
PD 06-APR-2000.
PA (ZHEN/) ZHENG S.
Query Match 2.6%; Score 59; DB 3; Length 1651;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 503
ID AAF97914 standard; cDNA; 1651 BP.
DE Human secreted protein cDNA, SEQ ID NO: 41.
PN WO200121658-A1.
PD 29-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 1651;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 504
ID AAD07360 standard; DNA; 1651 BP.
DE Human DNA encoding SNC73 protein (marker 11).
PN WO200136674-A2.
PD 25-MAY-2001.
PA (ASTR) ASTRAZENECA AB.

PA (ASTR) ASTRAZENECA UK LTD.
Query Match 2.6%; Score 59; DB 4; Length 1651;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 505
ID ADI82272 standard; DNA; 1683 BP.
DE Human DNA differentially expressed in embryonic stem cells #2.
PN US2003224411-A1.
PD 04-DEC-2003.
PA (STAN/) STANTON L W.
PA (BRAN/) BRANDENBERGER R.
PA (GOLD/) GOLD J D.
PA (IRVI/) IRVING J M.
PA (MAND/) MANDALAM R.
PA (MOKM/) MOK M.
PA (SHEL/) SHELTON D.
Query Match 2.6%; Score 59; DB 12; Length 1683;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 506
ID ADP10415 standard; DNA; 1705 BP.
DE Reference mRNA sequences for marker probe #92.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 2.6%; Score 59; DB 12; Length 1705;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 507
ID ABK99825 standard; cDNA; 1724 BP.
DE Babesia cDNA sequence for clone 60s.2.
PN WO200253016-A2.
PD 11-JUL-2002.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 59; DB 6; Length 1724;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 508
ID ABK33538 standard; cDNA; 1759 BP.
DE cDNA encoding human PRO protein, Seq ID No 5.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 6; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 509
ID ACA68499 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 8; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 510
ID ABT44228 standard; cDNA; 1759 BP.
DE Human PRO7174 cDNA.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 9; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 511
ID ABT44511 standard; cDNA; 1759 BP.
DE Human PRO7174 cDNA.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 9; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 512
ID ACD82178 standard; cDNA; 1759 BP.
DE Human secreted/transmembrane polypeptide PRO 7174 cDNA.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 9; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;

RESULT 513
ID ABT43884 standard; cDNA; 1759 BP.
DE Human membrane bound receptor/protein PRO7174 cDNA sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 9; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 514
ID ADB83495 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 9; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 515
ID ADB80601 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 9; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 516
ID ADB73142 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 9; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 517
ID ADB78224 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 9; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 518
ID ADB84872 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 519
ID ADB77978 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 520
ID ADB87044 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 521
ID ADB84626 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 522
ID ADB84626 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;

ID ADB83741 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 523
ID ADB72896 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 524
ID ADC36734 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 525
ID ADC21724 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 526
ID ADC49755 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 527
ID ADC48954 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 528
ID ADC49471 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 529
ID ADC47332 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 530
ID ADC47077 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 531
ID ADC77952 standard; cDNA; 1759 BP.

DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 532
ID ADD06187 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 533
ID ADC77706 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 534
ID ADD50669 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 535
ID ADD50915 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 536
ID ADD50396 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 537
ID ADD50150 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 538
ID ADD51161 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 539
ID ACA66843 standard; cDNA; 1759 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 540
ID ACD68595 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.

PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 541
ID ADC48708 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 542
ID ADE20879 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 543
ID ADE05723 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 544
ID ADD74952 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 545
ID ADD75698 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 546
ID ADD84930 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 547
ID ADD86756 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 548
ID ADE20633 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 549
ID ADE38930 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096362-A1.

PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 550
ID ADE05477 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 551
ID ADD73462 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 552
ID ADD78302 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 553
ID ADE21125 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 554
ID ADD77240 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 555
ID ADE20387 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 556
ID ADD75452 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 557
ID ADD73968 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 558
ID ADD74214 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100709-A1.
PD 29-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 559
ID ADD75944 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 560
ID ADD85436 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 561
ID ADE04985 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 562
ID ADD75198 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 563
ID ADD76742 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 564
ID ADD86510 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 565
ID ADD77978 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 566
ID ADD77486 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 567
ID ADD77732 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 568
ID ADD85190 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 569
ID ADD73722 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 570
ID ADD74460 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 571
ID ADD76988 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 572
ID ADD85682 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 573
ID ADE05231 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 574
ID ADD74706 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 575
ID ADG05518 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 576
ID ADG27072 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 577
ID ADD77732 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 577
ID ADG11135 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 578
ID ADG11914 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 579
ID ADF94471 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 580
ID ADG06567 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 581
ID ADH38911 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 582
ID ADG34001 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 583
ID ADI33471 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 584
ID ADH69565 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 585
ID ADI29726 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;

RESULT 586
ID ADM27123 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 587
ID ADK66481 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 588
ID ADC77664 standard; cDNA; 1764 BP.
DE Human 27410 protein encoding cDNA SEQ ID NO:27.
PN WO2003073983-A2.
PD 12-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.6%; Score 59; DB 10; Length 1764;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 589
ID ABK99853 standard; cDNA; 1769 BP.
DE Babesia cDNA sequence for clone 60s.55.
PN WO200253016-A2.
PD 11-JUL-2002.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 59; DB 6; Length 1769;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 590
ID ADI42816 standard; DNA; 1803 BP.
DE Plant transcription factor polynucleotide #820.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 2.6%; Score 59; DB 12; Length 1803;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 591
ID ADO03025 standard; cDNA; 1803 BP.
DE Corn orthologue of Thalecress transcription factor, cDNA #126.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.

PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 2.6%; Score 59; DB 12; Length 1803;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 592
ID AAF98705 standard; DNA; 1815 BP.
DE Human ovarian cancer cell expressed sequence 10805.
PN WO200118542-A2.
PD 15-MAR-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 1815;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 593
ID AAD33245 standard; cDNA; 1817 BP.
DE Human secreted protein-encoding gene 9 cDNA clone HDABU01, SEQ ID NO:19.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 6; Length 1817;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 594
ID AAS41019 standard; cDNA; 1854 BP.
DE cDNA encoding novel human enzyme polypeptide #235.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 1854;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 595
ID ABK87609 standard; cDNA; 1868 BP.
DE cDNA encoding novel extracellular signal-regulated kinase.
PN US2001053844-A1.
PD 20-DEC-2001.
PA (YANC/) YAN C.
PA (ABUT/) ABU-THREIDEH J.
PA (SHAO/) SHAO W.
PA (MERK/) MERKULOV G V.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 2.6%; Score 59; DB 6; Length 1868;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 596
ID ADH00897 standard; cDNA; 1868 BP.
DE Human kinase cDNA.
PN US2003166219-A1.
PD 04-SEP-2003.
PA (PEKE) PE CORP NY.
Query Match 2.6%; Score 59; DB 10; Length 1868;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 597
ID AAK98915 standard; cDNA; 1878 BP.
DE cDNA of a human MAP/extracellular signal-regulated kinase subfamily.
PN US2001051360-A1.
PD 13-DEC-2001.
PA (WEIM/) WEI M.
PA (GUEG/) GUEGLER K.
PA (KETC/) KETCHUM K A.
PA (MERK/) MERKULOV G V.
PA (WOOD/) WOODAGE T.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 2.6%; Score 59; DB 6; Length 1878;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 598
ID ADG90363 standard; cDNA; 1878 BP.
DE Human kinase cDNA.
PN US2003166218-A1.
PD 04-SEP-2003.
PA (PEKE) PE CORP NY.
Query Match 2.6%; Score 59; DB 10; Length 1878;
Best Local Similarity 100.0%; Pred. No. 1e-10;

RESULT 599.
ID ADL45481 standard; DNA; 1885 BP.
DE Human ovarian cancer DNA marker #19371.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 1885;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 600
ID ABQ54288 standard; cDNA; 2054 BP.
DE Human ovarian antigen HSPSY43 cDNA, SEQ ID NO:168.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 6; Length 2054;
Best Local Similarity 100.0%; Pred. No. 9.8e-11;
RESULT 601
ID AAZ10670 standard; cDNA; 2083 BP.
DE cDNA encoding a human secreted protein.
PN WO9943693-A1.
PD 02-SEP-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 2; Length 2083;
Best Local Similarity 100.0%; Pred. No. 9.8e-11;
RESULT 602
ID ADL45474 standard; DNA; 2236 BP.
DE Human ovarian cancer DNA marker #19364.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 2236;
Best Local Similarity 100.0%; Pred. No. 9.6e-11;
RESULT 603
ID ADC38669 standard; cDNA; 2238 BP.
DE Human cDNA encoding a secreted protein #14.
PN US2002193567-A1.
PD 19-DEC-2002.
PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 59; DB 10; Length 2238;
Best Local Similarity 100.0%; Pred. No. 9.6e-11;
RESULT 604
ID ABV22595 standard; cDNA; 2242 BP.
DE Human prostate expression marker cDNA 22586.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 2242;
Best Local Similarity 100.0%; Pred. No. 9.6e-11;
RESULT 605
ID ABV28416 standard; cDNA; 2242 BP.
DE Human prostate expression marker cDNA 28407.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 2242;
Best Local Similarity 100.0%; Pred. No. 9.6e-11;
RESULT 606
ID AAC75666 standard; cDNA; 2244 BP.
DE Human ORFX ORF1221 polynucleotide sequence SEQ ID NO:2441.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 2.6%; Score 59; DB 3; Length 2244;
Best Local Similarity 100.0%; Pred. No. 9.6e-11;
RESULT 607
ID ABX92071 standard; cDNA; 2269 BP.
DE Lung specific nucleic acid (LSNA) #113.
PN WO200268633-A2.
PD 06-SEP-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 2.6%; Score 59; DB 6; Length 2269;
Best Local Similarity 100.0%; Pred. No. 9.6e-11;
RESULT 608

ID AAX99856 standard; DNA; 2504 BP.
DE Human secreted protein coding sequence clone bn69_15.
PN WO9938959-A1.
PD 05-AUG-1999.
PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 59; DB 2; Length 2504;
Best Local Similarity 100.0%; Pred. No. 9.4e-11;
RESULT 609
ID AAS59280 standard; cDNA; 2504 BP.
DE Human cDNA encoding a secreted protein bn69_15.
PN WO200175068-A2.
PD 11-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 59; DB 4; Length 2504;
Best Local Similarity 100.0%; Pred. No. 9.4e-11;
RESULT 610
ID ABA90949 standard; cDNA; 2504 BP.
DE Human polynucleotide SEQ ID NO 147.
PN US2001039335-A1.
PD 08-NOV-2001.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LAVA/) LAVALLIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (AGOS/) AGOSTINO M J.
PA (STEI/) STEININGER R J.
PA (SPAU/) SPAULDING V.
PA (WONG/) WONG G G.
PA (CLAR/) CLARK H.
PA (FECH/) FECHTEL K.
Query Match 2.6%; Score 59; DB 6; Length 2504;
Best Local Similarity 100.0%; Pred. No. 9.4e-11;
RESULT 611
ID ABQ55051 standard; cDNA; 3036 BP.
DE Human ovarian antigen HOCQ58 cDNA, SEQ ID NO:931.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 6; Length 3036;
Best Local Similarity 100.0%; Pred. No. 9e-11;
RESULT 612
ID AAF22384 standard; cDNA; 3268 BP.
DE Human secreted protein gene 12 SEQ ID NO:22.
PN WO2000061629-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 2.6%; Score 59; DB 3; Length 3268;
Best Local Similarity 100.0%; Pred. No. 8.8e-11;
RESULT 613
ID ADI36904 standard; cDNA; 3719 BP.
DE Human HLRRNS-3 cDNA.
PN US2003220263-A1.
PD 27-NOV-2003.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
Query Match 2.6%; Score 59; DB 12; Length 3719;
Best Local Similarity 100.0%; Pred. No. 8.6e-11;
RESULT 614
ID AAL38913 standard; cDNA; 3832 BP.
DE Human mitochondrial RNA polymerase cDNA.
PN WO200238759-A2.
PD 16-MAY-2002.
PA (MITO-) MITOTECH AB.
Query Match 2.6%; Score 59; DB 6; Length 3832;
Best Local Similarity 100.0%; Pred. No. 8.5e-11;
RESULT 615
ID ADQ24393 standard; DNA; 4522 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7213.

PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.6%; Score 59; DB 12; Length 4522;
Best Local Similarity 100.0%; Pred. No. 8.2e-11;
RESULT 616
ID ADQ24286 standard; DNA; 4522 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7106.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.6%; Score 59; DB 12; Length 4522;
Best Local Similarity 100.0%; Pred. No. 8.2e-11;
RESULT 617
ID ADQ24340 standard; DNA; 4696 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7160.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.6%; Score 59; DB 12; Length 4696;
Best Local Similarity 100.0%; Pred. No. 8.1e-11;
RESULT 618
ID ABK87749 standard; cDNA; 5344 BP.
DE Human cDNA encoding metalloprotease of the ADAMTS family 53014 #2.
PN WO200251995-A1.
PD 04-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.6%; Score 59; DB 6; Length 5344;
Best Local Similarity 100.0%; Pred. No. 7.9e-11;
RESULT 619
ID ABK87748 standard; cDNA; 5701 BP.
DE Human cDNA encoding metalloprotease of the ADAMTS family 53014 #1.
PN WO200251995-A1.
PD 04-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.6%; Score 59; DB 6; Length 5701;
Best Local Similarity 100.0%; Pred. No. 7.8e-11;
RESULT 620
ID ADQ22539 standard; DNA; 7047 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5359.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.6%; Score 59; DB 12; Length 7047;
Best Local Similarity 100.0%; Pred. No. 7.4e-11;
RESULT 621
ID AAS32492 standard; DNA; 32191 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 446.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 32191;
Best Local Similarity 100.0%; Pred. No. 5.2e-11;
RESULT 622
ID ABQ94562 standard; DNA; 101 BP.
DE Tumour suppression-related oligonucleotide #213.
PN FR2819824-A1.
PD 26-JUL-2002.
PA (MOLE-) MOLECULAR ENGINES LAB SA.
Query Match 2.6%; Score 58; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 4.3e-10;
RESULT 623
ID AAS07787 standard; DNA; 153 BP.
DE Cervical cancer pre-malignant condition DNA marker #86.
PN WO200142792-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
RESULT 624
ID AAS29047 standard; cDNA; 155 BP.
DE cDNA encoding for human DNA-binding protein #18.
PN WO200155162-A1.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 5; Length 155;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
RESULT 625
ID ABS68187 standard; cDNA; 155 BP.
DE cDNA encoding human DNA-binding protein #18.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.6%; Score 58; DB 6; Length 155;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
RESULT 626
ID ADC25181 standard; cDNA; 155 BP.
DE Human cDNA from extracellular matrix gene 18.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 10; Length 155;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
RESULT 627
ID ABX45893 standard; cDNA; 160 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11058.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 58; DB 8; Length 160;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
RESULT 628
ID ABV05796 standard; cDNA; 177 BP.
DE Human prostate expression marker cDNA 5787.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
RESULT 629
ID ABX49026 standard; cDNA; 179 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #14191.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 58; DB 8; Length 179;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
RESULT 630
ID ABX36136 standard; cDNA; 181 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #1301.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 58; DB 8; Length 181;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
RESULT 631
ID AAZ21523 standard; DNA; 196 BP.
DE Progression suppressed gene 28 (PSGen28).
PN WO9943844-A1.
PD 02-SEP-1999.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 2.6%; Score 58; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
RESULT 632
ID ABV58264 standard; cDNA; 201 BP.

DE Human prostate expression marker cDNA 58255.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 201;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
RESULT 633
ID ABV57413 standard; cDNA; 206 BP.
DE Human prostate expression marker cDNA 57404.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 206;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
RESULT 634
ID ABX38781 standard; cDNA; 207 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3946.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 58; DB 8; Length 207;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
RESULT 635
ID ABV57409 standard; cDNA; 234 BP.
DE Human prostate expression marker cDNA 57400.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 234;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
RESULT 636
ID ABX47018 standard; cDNA; 236 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12183.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 58; DB 8; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
RESULT 637
ID ABV56779 standard; cDNA; 247 BP.
DE Human prostate expression marker cDNA 56770.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 247;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
RESULT 638
ID ABV19470 standard; cDNA; 254 BP.
DE Human prostate expression marker cDNA 19461.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 254;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
RESULT 639
ID ABV49446 standard; cDNA; 254 BP.
DE Human prostate expression marker cDNA 49437.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 254;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
RESULT 640
ID AAV00423 standard; cDNA; 259 BP.
DE 3' fragment of clone H1075_1.
PN WO9740069-A2.
PD 30-OCT-1997.

PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 58; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
RESULT 641
ID AAT85891 standard; cDNA to mRNA; 263 BP.
DE Malassezia fungus MF-3 antigenic protein PCR amplification fragment.
PN WO9721817-A1.
PD 19-JUN-1997.
PA (TAKI) TAKARA SHUZO CO LTD.
Query Match 2.6%; Score 58; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
RESULT 642
ID AAS29061 standard; cDNA; 266 BP.
DE cDNA encoding for human DNA-binding protein #32.
PN WO200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 5; Length 266;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
RESULT 643
ID ABS68201 standard; cDNA; 266 BP.
DE cDNA encoding human DNA-binding protein #32.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.6%; Score 58; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
RESULT 644
ID ADC25195 standard; cDNA; 266 BP.
DE Human cDNA from extracellular matrix gene 32.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 10; Length 266;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
RESULT 645
ID ABV49955 standard; cDNA; 278 BP.
DE Human prostate expression marker cDNA 49946.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 278;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
RESULT 646
ID AAL20269 standard; cDNA; 282 BP.
DE Human breast cancer expressed polynucleotide 12726.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 4; Length 282;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
RESULT 647
ID AAS60667 standard; cDNA; 285 BP.
DE Human cancer agent-resistance marker #422.
PN WO200179556-A2.
PD 25-OCT-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
RESULT 648
ID ABL87534 standard; cDNA; 294 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:10512.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 6; Length 294;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
RESULT 649
ID ABX37743 standard; cDNA; 316 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2908.
PN US2002137139-A1.

PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 58; DB 8; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
RESULT 650
ID ABL93053 standard; cDNA; 321 BP.
DE Rat metastatic tumour cell related cDNA SEQ ID NO 107.
PN WO200208456-A2.
PD 31-JAN-2002.
PA (GESL) FORSCHUNGSZENTRUM KARLSRUHE GMBH.
Query Match 2.6%; Score 58; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
RESULT 651
ID ADN07844 standard; cDNA; 321 BP.
DE Human mammary carcinoma MLSSH cDNA library sequence #107.
PN DE10229391-A1.
PD 29-JAN-2004.
PA (GESL) FORSCHUNGSZENTRUM KARLSRUHE GMBH.
Query Match 2.6%; Score 58; DB 12; Length 321;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
RESULT 652
ID ABV59017 standard; cDNA; 325 BP.
DE Human prostate expression marker cDNA 59008.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 325;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
RESULT 653
ID ABX47256 standard; cDNA; 329 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12421.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 58; DB 8; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
RESULT 654
ID ABK54903 standard; cDNA; 342 BP.
DE Human colon cancer-associated cDNA, SEQ ID No 373.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 6; Length 342;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
RESULT 655
ID AAI88527 standard; cDNA; 352 BP.
DE Human polynucleotide SEQ ID NO 8587.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 656
ID AAC77649 standard; cDNA; 353 BP.
DE Human cancer associated gene sequence SEQ ID NO:43.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 3; Length 353;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 657
ID ABX43971 standard; cDNA; 357 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #9136.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.

PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 58; DB 8; Length 357;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 658
ID ABV14871 standard; cDNA; 360 BP.
DE Human prostate expression marker cDNA 14862.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 659
ID AAI88707 standard; cDNA; 363 BP.
DE Human polynucleotide SEQ ID NO 8767.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 363;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 660
ID AAI84802 standard; cDNA; 364 BP.
DE Human polynucleotide SEQ ID NO 4862.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 364;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 661
ID AAI84912 standard; cDNA; 364 BP.
DE Human polynucleotide SEQ ID NO 4972.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 364;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 662
ID AAI84900 standard; cDNA; 364 BP.
DE Human polynucleotide SEQ ID NO 4960.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 364;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 663
ID ACH30766 standard; cDNA; 364 BP.
DE Human bone marrow cDNA #57.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.6%; Score 58; DB 9; Length 364;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 664
ID AAI87540 standard; cDNA; 366 BP.
DE Human polynucleotide SEQ ID NO 7600.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 366;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 665
ID ABV55687 standard; cDNA; 367 BP.
DE Human prostate expression marker cDNA 55678.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 367;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 666

ID ABX37863 standard; cDNA; 369 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3028.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 58; DB 8; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 667
ID ABV58076 standard; cDNA; 373 BP.
DE Human prostate expression marker cDNA 58067.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 668
ID AAI87907 standard; cDNA; 374 BP.
DE Human polynucleotide SEQ ID NO 7967.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 669
ID ABV49242 standard; cDNA; 377 BP.
DE Human prostate expression marker cDNA 49233.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 377;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 670
ID ABQ56755 standard; cDNA; 377 BP.
DE Human colon cancer related nucleotide sequence SEQ ID NO:450.
PN WO200229086-A2.
PD 11-APR-2002.
PA (FARB) BAYER CORP.
Query Match 2.6%; Score 58; DB 6; Length 377;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 671
ID AAI82118 standard; cDNA; 385 BP.
DE Human polynucleotide SEQ ID NO 2178.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 385;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 672
ID AAI84785 standard; cDNA; 388 BP.
DE Human polynucleotide SEQ ID NO 4845.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 388;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 673
ID AAI88514 standard; cDNA; 389 BP.
DE Human polynucleotide SEQ ID NO 8574.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 389;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 674
ID AAI85202 standard; cDNA; 390 BP.
DE Human polynucleotide SEQ ID NO 5262.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 390;

Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 675
ID ABV39048 standard; cDNA; 392 BP.
DE Human prostate expression marker cDNA 39039.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 392;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 676
ID AAI83459 standard; cDNA; 394 BP.
DE Human polynucleotide SEQ ID NO 3519.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 677
ID ABZ53884 standard; cDNA; 394 BP.
DE Aspergillus oryzae polynucleotide SEQ ID NO 2997.
PN WO200279476-A1.
PD 10-OCT-2002.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (NARE-) NAT RES INST BREWING.
PA (NORQ) NAT FOOD RES INST MIN AGRIC.
Query Match 2.6%; Score 58; DB 8; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 678
ID ABV57596 standard; cDNA; 396 BP.
DE Human prostate expression marker cDNA 57587.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 679
ID ABV14965 standard; cDNA; 400 BP.
DE Human prostate expression marker cDNA 14956.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 400;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 680
ID ADF50926 standard; cDNA; 400 BP.
DE Human cysteine rich intestinal protein 1 cDNA (SeqID 25).
PN WO2003060164-A1.
PD 24-JUL-2003.
PA (ARCT-) ARCTURUS ENG INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 2.6%; Score 58; DB 10; Length 400;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 681
ID ABV38958 standard; cDNA; 404 BP.
DE Human prostate expression marker cDNA 38949.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 404;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 682
ID AAI83837 standard; cDNA; 405 BP.
DE Human polynucleotide SEQ ID NO 3897.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 683
ID AAI88562 standard; cDNA; 406 BP.
DE Human polynucleotide SEQ ID NO 8622.
PN WO200164835-A2.
PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 406;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 684
ID ADG32960 standard; DNA; 406 BP.
DE Human DNA differentially expressed in patients with SLE SeqID284.
PN WO2003090694-A2.
PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 2.6%; Score 58; DB 10; Length 406;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 685
ID AAI84733 standard; cDNA; 407 BP.
DE Human polynucleotide SEQ ID NO 4793.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 407;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 686
ID AAI88682 standard; cDNA; 407 BP.
DE Human polynucleotide SEQ ID NO 8742.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 407;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 687
ID ABK34899 standard; cDNA; 409 BP.
DE Human cDNA encoding secreted protein #37.
PN WO200177288-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 58; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 688
ID AAI84650 standard; cDNA; 410 BP.
DE Human polynucleotide SEQ ID NO 4710.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 410;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 689
ID AAI81190 standard; cDNA; 410 BP.
DE Human polynucleotide SEQ ID NO 1250.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 410;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 690
ID AAI80427 standard; cDNA; 412 BP.
DE Human polynucleotide SEQ ID NO 487.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 412;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 691
ID AAL19684 standard; cDNA; 413 BP.
DE Human breast cancer expressed polynucleotide 12141.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 4; Length 413;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 692
ID AAI85194 standard; cDNA; 414 BP.
DE Human polynucleotide SEQ ID NO 5254.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.

Query Match
Best Local Similarity 2.6%; Score 58; DB 4; Length 414;
RESULT 693
ID ABX40997 standard; cDNA; 414 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6162.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 414;
RESULT 694
ID ABX41704 standard; cDNA; 415 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6869.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 415;
RESULT 695
ID AAI89032 standard; cDNA; 416 BP.
DE Human polynucleotide SEQ ID NO 9092.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 4; Length 416;
RESULT 696
ID AAI83898 standard; cDNA; 417 BP.
DE Human polynucleotide SEQ ID NO 3958.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 4; Length 417;
RESULT 697
ID ACH19280 standard; cDNA; 419 BP.
DE Human adult lung cDNA #283.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 419;
RESULT 698
ID AAI88586 standard; cDNA; 420 BP.
DE Human polynucleotide SEQ ID NO 8646.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 4; Length 420;
RESULT 699
ID AAI89084 standard; cDNA; 421 BP.
DE Human polynucleotide SEQ ID NO 9144.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 4; Length 421;
RESULT 700
ID ABX62208 standard; DNA; 422 BP.
DE Arabidopsis thaliana expressed sequence related polynucleotide #323.
PN US2002040490-A1.
PD 04-APR-2002.

PA (GORL/) GORLACH J.
PA (ANYY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYU/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHIEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 422;
RESULT 701
ID ABV57952 standard; cDNA; 423 BP.
DE Human prostate expression marker cDNA 57943.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 5; Length 423;
RESULT 702
ID ADL45796 standard; DNA; 423 BP.
DE Human ovarian cancer DNA marker #19686.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 5; Length 423;
RESULT 703
ID ACH24941 standard; cDNA; 424 BP.
DE Human adult ovary cDNA #3321.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 424;
RESULT 704
ID ABV05669 standard; cDNA; 429 BP.
DE Human prostate expression marker cDNA 5660.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 5; Length 429;
RESULT 705
ID ABX38360 standard; cDNA; 434 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3525.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 434;
RESULT 706
ID AAI93088 standard; cDNA; 438 BP.
DE Human polynucleotide SEQ ID NO 13148.
PN WO200164835-A2.
PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 438;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 707
ID AAZ09474 standard; DNA; 441 BP.
DE p135-NT3 construct DNA.
PN WO9941390-A2.
PD 19-AUG-1999.
PA (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
Query Match 2.6%; Score 58; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 708
ID ABL94108 standard; cDNA; 442 BP.
DE Arabidopsis thaliana nucleic acid sequence Ref:2027873 SEQ ID NO:873.
PN US2002023280-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANYY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYU/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDE/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 2.6%; Score 58; DB 6; Length 442;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 709
ID AAA75749 standard; cDNA; 443 BP.
DE cDNA encoding a dermaseptin precursor polypeptide.
PN WO200055337-A1.
PD 21-SEP-2000.
PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
Query Match 2.6%; Score 58; DB 3; Length 443;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 710
ID ABV19606 standard; cDNA; 446 BP.
DE Human prostate expression marker cDNA 19597.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 446;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 711
ID AAI82904 standard; cDNA; 448 BP.
DE Human polynucleotide SEQ ID NO 2964.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 712
ID ABV56778 standard; cDNA; 451 BP.
DE Human prostate expression marker cDNA 56769.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 451;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 713
ID ABV49374 standard; cDNA; 453 BP.
DE Human prostate expression marker cDNA 49365.
PN WO200160860-A2.

PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 453;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 714
ID AAK87910 standard; cDNA; 456 BP.
DE Human digestive system antigen coding sequence SEQ ID NO: 226.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 715
ID AAS60044 standard; cDNA; 461 BP.
DE Human cancer agent-sensitive marker #45.
PN WO200179556-A2.
PD 25-OCT-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 716
ID ACH24394 standard; cDNA; 461 BP.
DE Human adult ovary cDNA #2774.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.6%; Score 58; DB 9; Length 461;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 717
ID AAV58579 standard; cDNA; 470 BP.
DE Prostate tumour specific gene clone 1D-4288.
PN WO9837418-A2.
PD 27-AUG-1998.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 2; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 718
ID AAV61312 standard; cDNA; 470 BP.
DE cDNA sequence of prostate tumour clone 1D-4288.
PN WO9837093-A2.
PD 27-AUG-1998.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 2; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 719
ID AAA06342 standard; cDNA; 470 BP.
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:102.
PN WO200004149-A2.
PD 27-JAN-2000.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 3; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 720
ID ABS71247 standard; cDNA; 470 BP.
DE Human prostate tumour protein partial DNA sequence #102.
PN US2002090372-A1.
PD 11-JUL-2002.
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
Query Match 2.6%; Score 58; DB 3; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 721
ID AAH93458 standard; cDNA; 470 BP.
DE Human prostate-specific cDNA sequence 1D-4288.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 4; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;

RESULT 722
ID AAS63550 standard; cDNA; 470 BP.
DE Human prostate cDNA sequence #102.
PN WO200173032-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 4; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 723
ID AAH02523 standard; cDNA; 470 BP.
DE Prostate tumour antigen determined cDNA sequence for 1D-4288.
PN WO200125272-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 4; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 724
ID AAH84772 standard; cDNA; 470 BP.
DE Human prostate-specific cDNA sequence 1D-4288.
PN WO200134802-A2.
PD 17-MAY-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 4; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 725
ID ACA59359 standard; cDNA; 470 BP.
DE Prostate cancer therapy associated cDNA #102.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (FOYT/) FOY T M.
Query Match 2.6%; Score 58; DB 5; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 726
ID AAS10101 standard; cDNA; 470 BP.
DE Human prostate tumour cDNA 1D-4288.
PN US6262245-B1.
PD 17-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 5; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 727
ID ABL94922 standard; cDNA; 470 BP.
DE Human 1D-4288 cDNA sequence SEQ ID NO 102.
PN US2002022248-A1.
PD 21-FEB-2002.
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.

PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
Query Match 2.6%; Score 58; DB 6; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 728
ID ABS58631 standard; cDNA; 470 BP.
DE Prostate tumour cDNA #102.
PN US2002081580-A1.
PD 27-JUN-2002.
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
Query Match 2.6%; Score 58; DB 6; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 729
ID ACC95086 standard; cDNA; 470 BP.
DE Prostate tumour specific cDNA sequence SEQ ID 102.
PN WO200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 8; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 730
ID ADB13552 standard; cDNA; 470 BP.
DE Human prostate specific cDNA 1D-4288.
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 10; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 731
ID ADG26968 standard; cDNA; 470 BP.
DE Human prostate-specific cDNA #102.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 10; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 732
ID ABV47755 standard; cDNA; 471 BP.
DE Human prostate expression marker cDNA 47746.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 471;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 733
ID ABX41242 standard; cDNA; 473 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6407.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 58; DB 8; Length 473;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 734
ID AA183554 standard; cDNA; 480 BP.
DE Human polynucleotide SEQ ID NO 3614.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 480;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 735


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ID ACH16280 standard; cDNA; 480 BP.
DE Human adult heart cDNA #594.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.6%; Score 58; DB 9; Length 480;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 736
ID ACH40652 standard; cDNA; 480 BP.
DE Human foetal brain cDNA #2019.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.6%; Score 58; DB 9; Length 480;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 737
ID ABV48907 standard; cDNA; 483 BP.
DE Human prostate expression marker cDNA 48898.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 483;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 738
ID AAZ65037 standard; cDNA; 485 BP.
DE Membrane-bound protein PRO1003 encoding cDNA.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 739
ID AAS46017 standard; cDNA; 485 BP.
DE Human DNA encoding PRO polypeptide sequence #93.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 740
ID AAF92079 standard; cDNA; 485 BP.
DE Human PRO1003 cDNA.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 741
ID AAF44183 standard; cDNA; 485 BP.
DE Human PRO1003 (UNQ487) nucleotide sequence SEQ ID NO:245.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 5; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 742
ID ABS74399 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 6; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 743
ID ACA89467 standard; cDNA; 485 BP.
DE CDNA encoding human PRO polypeptide #93.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 744
ID ACA73477 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 745
ID ACA05792 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 746
ID ACA66626 standard; cDNA; 485 BP.
DE CDNA encoding human PRO protein #93.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 747
ID ACA64328 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 748
ID ACA91185 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 749
ID ACD81562 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 750
ID ACF20201 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 751
ID ACF19587 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 752
ID ACD21875 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
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Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 753
ID ACF13040 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 754
ID ACD25143 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 755
ID ACF00192 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 756
ID ACA60384 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 757
ID ACA72249 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 758
ID ACD04773 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 759
ID ACD18234 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 760
ID ACD08241 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 761
ID ACA88675 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 762
ID ACA70117 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;

RESULT 763
ID ACD12339 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 764
ID ACC74254 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 765
ID ACD15882 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 766
ID ACD25450 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 767
ID ACD17927 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 768
ID ACC88214 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 769
ID ACD21568 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 770
ID ACD18635 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 771
ID ACA58831 standard; cDNA; 485 BP.
DE cDNA encoding human secreted polypeptide PRO1003.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 772
ID ABX98245 standard; cDNA; 485 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 185.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 773

ID ACD13996 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 774
ID ACD09776 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 775
ID ACC88521 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 776
ID ACD21261 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 777
ID ABX75633 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1003.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 778
ID ACA64007 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #22.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 779
ID ABX97836 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 780
ID ACA97312 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 781
ID ACA57775 standard; cDNA; 485 BP.
DE Human PRO1003 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 782
ID ACD14303 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 783
ID ACC91086 standard; cDNA; 485 BP.

DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 784
ID ACC88828 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 785
ID ACD07025 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 786
ID ACA67476 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 787
ID ACC81531 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 788
ID ACA91271 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #22.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 789
ID ACC89135 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 790
ID ACC86491 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 791
ID ACC89749 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 792
ID ACC92928 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 793

ID ABX80787 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein cDNA, #97.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 794
ID ACA72556 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 795
ID ACA89074 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 796
ID ACA69810 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 797
ID ACA96953 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 798
ID ACA90949 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 799
ID ACA70731 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 800
ID ACA95241 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 801
ID ACD44296 standard; cDNA; 485 BP.
DE cDNA encoding human PRO1003 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 802
ID ACC86184 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 803
ID ACD45170 standard; cDNA; 485 BP.

DE Human secreted/transmembrane polypeptide PRO1003 cDNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 804
ID ACC90056 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 805
ID ACD12664 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 806
ID ACF19894 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 807
ID ABX76838 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 808
ID ACA73170 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 809
ID ACA68713 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 810
ID ACA74557 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 811
ID ACA70424 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 812
ID ACD14610 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 813
ID ACA93718 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.

PD 06-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 8; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 814
ID ACA68282 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 815
ID ABX98747 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 816
ID ACA67292 standard; cDNA; 485 BP.
DE cDNA encoding human secreted polypeptide PRO1003.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 8; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 817
ID ACC81224 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 818
ID ACA95548 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 819
ID ACD04466 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 820
ID ACC87907 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 8; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 821
ID ACF12569 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 822
ID ACH66265 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 8; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 823
ID ABX79467 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein cDNA, #97.

PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 8; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 824
ID ACA96284 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 825
ID ACA65058 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 826
ID ACA73784 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 827
ID ACA74196 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 828
ID ACA96591 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 829
ID ACD10697 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 830
ID ACC91393 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 831
ID ACA93488 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 832
ID ACD02728 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 833
ID ACC87293 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036165-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 834
ID ACC85877 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 835
ID ABX81170 standard; DNA; 485 BP.
DE Novel human secreted or transmembrane protein PRO1108 DNA.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 836
ID ACA65365 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 837
ID ACA94182 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 838
ID ACA97926 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003036145-A1.
PD 20-FEB-2003..
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 839
ID ACA91428 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 840
ID ACA90642 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 841
ID ACD16189 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 842
ID ACD17350 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 843
ID ACC92007 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;

RESULT 844
ID ACD02319 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 845
ID ACA74864 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 846
ID ACA91735 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 847
ID ACA89310 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 848
ID ACA71379 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 849
ID ACC90779 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 850
ID ACA65789 standard; cDNA; 485 BP.
DE cDNA encoding human PRO protein #93.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 851
ID ACA68947 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 852
ID ACA92986 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 853
ID ACA94934 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;

RESULT 854
ID ACD16496 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 855
ID ACD15575 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 856
ID ACA98469 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 857
ID ABX17070 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 858
ID ABX16678 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein #93.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 859
ID ACA67925 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 860
ID ACA63394 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #22.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 861
ID ACA97619 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 862
ID ACA99068 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 863
ID ACC91700 standard; cDNA; 485 BP.
DE Human secreted polypeptidePRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040076-A1.
PD 27-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 864
ID ACD11111 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 865
ID ACD14961 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 866
ID ACA88374 standard; cDNA; 485 BP.
DE Human secreted and transmembrane polypeptide PRO1003 cDNA.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 867
ID ACD81881 standard; cDNA; 485 BP.
DE cDNA encoding human PRO1003 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 868
ID ACD11725 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 869
ID ACC95854 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 870
ID ACF16417 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 871
ID ACF02535 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 872
ID ACF02842 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 873
ID ACF21429 standard; cDNA; 485 BP.

DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 874
ID ACF10113 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 875
ID ACF78006 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 876
ID ACD46711 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 877
ID ACD49474 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 878
ID ACF28241 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 879
ID ACD88931 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 880
ID ACD84326 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 881
ID ACD99100 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 882
ID ADA77937 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.

PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 883
ID ACF48842 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 884
ID ACD09162 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 885
ID ACF11955 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 886
ID ACF41189 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 887
ID ACF15803 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 888
ID ACF16110 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 889
ID ADB17100 standard; cDNA; 485 BP.
DE Human cDNA clone (SeqID 43) encoding the transmembrane PRO protein.
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 890
ID ACD31937 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 891
ID ACF18745 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;

RESULT 892
ID ACF09192 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 893
ID ACF78313 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 894
ID ACF51912 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 895
ID ACF26399 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 896
ID ACF24192 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 897
ID ACF63503 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 898
ID ACF50377 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 899
ID ACH07848 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 900
ID ACF13654 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 901
ID ACD41580 standard; cDNA; 485 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 902
ID ADA37756 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 903
ID ACF31993 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 904
ID ACF23271 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 905
ID ACF39961 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 906
ID ACD45483 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 907
ID ACF53140 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 908
ID ACF27320 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 909
ID ACF45158 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 910
ID ACF29776 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.

PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 911
ID ACD89852 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 912
ID ACD84633 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 913
ID ACD98793 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 914
ID ACF77085 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 915
ID ACF76778 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 916
ID ACF49763 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 917
ID ACF50070 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 918
ID ADA21442 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1003.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 919
ID ACD09469 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 920

ID ACD08548 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 921
ID ACH03597 standard; cDNA; 485 BP.
DE Human secreted/transmembrane polypeptide PRO 1003 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 922
ID ACF12262 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 923
ID ACC94770 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 924
ID ACD22489 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 925
ID ACF15189 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 926
ID ACC97284 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 927
ID ACC92314 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 928
ID ACF13961 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 929
ID ACF14268 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 930
ID ADA10229 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1003.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 931
ID ACF09499 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 932
ID ACD45790 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 933
ID ACD47939 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 934
ID ACD67670 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93:
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 935
ID ACF25478 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 936
ID ACF29162 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 937
ID ACD84940 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 938
ID ACD84019 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;

RESULT 939
ID ACD88010 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 940
ID ACF30697 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 941
ID ACF32300 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 942
ID ACH11960 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 943
ID ACH12267 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 944
ID ADA19905 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 945
ID ACD40659 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 946
ID ADB17288 standard; cDNA; 485 BP.
DE Human cDNA clone (SeqID 43) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 947
ID ADA17773 standard; cDNA; 485 BP.
DE cDNA encoding human PRO1003 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 948
ID ACF18131 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.

PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 949
ID ACF08578 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 950
ID ACF31379 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 951
ID ACF52219 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 952
ID ACD50088 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 953
ID ACF38791 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 954
ID ACF26706 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 955
ID ACF24806 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 956
ID ACF46386 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 957
ID ACF27934 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068751-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 958
ID ACD89238 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 959
ID ACF63810 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 960
ID ACF60450 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 961
ID ACH12574 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 962
ID ACH09997 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 963
ID ACD03852 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 964
ID ACD10390 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 965
ID ACD12032 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 966
ID ACF42417 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 967

ID ADA27881 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 968
ID ACF18438 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 969
ID ACF02228 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 970
ID ACF21736 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 971
ID ACF10420 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 972
ID ACF33872 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 973
ID ACF44834 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 974
ID ACD90466 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 975
ID ACD91079 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 976
ID ACF30390 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003067478-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 977
ID ACD87089 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 978
ID ACF60143 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 979
ID ACF46693 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 980
ID ACF75550 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 981
ID ADA79729 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 982
ID ACF17210 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 983
ID ACF22964 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 984
ID ACF07964 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 985
ID ACF08271 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 986
ID ACF30390 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003067478-A1.

ID ACF40575 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 987
ID ACF53754 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 988
ID ACD47018 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 989
ID ACF47921 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 990
ID ACF47307 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 991
ID ACF46079 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 992
ID ACD86168 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 993
ID ACF52526 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 994
ID ACF52833 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 995
ID ACF64826 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068737-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 996
ID ACF76471 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 997
ID ACF61371 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 998
ID ACF61678 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 999
ID ACD30709 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1000
ID ACD31630 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1001
ID ACD32551 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1002
ID ADA20077 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1003
ID ACD82111 standard; cDNA; 485 BP.
DE Human secreted/transmembrane polypeptide PRO 1003 cDNA.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1004
ID ACF17517 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1005

Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1005
ID ADA94461 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1006
ID ACF07350 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1007
ID ACF20508 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1008
ID ACF21122 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1009
ID ACF20815 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1010
ID ACD47632 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1011
ID ACF47614 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1012
ID ACF53447 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1013
ID ACD86782 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1014
ID ACH05030 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.

PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1015
ID ACF44527 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1016
ID ADA81456 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1017
ID ACD22182 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1018
ID ACD24529 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1019
ID ACD39732 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1020
ID ACD40039 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1021
ID ACF13347 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1022
ID ACF03149 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1023
ID ACF78620 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;

Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1024
ID ACF11341 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1025
ID ACF50684 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1026
ID ACF34179 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1027
ID ACD46404 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1028
ID ACD48246 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1029
ID ACF27627 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1030
ID ACF24499 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1031
ID ACD8554 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1032
ID ACD90159 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1033
ID ACD83712 standard; cDNA; 485 BP.

DE Human PRO polynucleotide #93.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1034
ID ACF49149 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1035
ID ACH07234 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1036
ID ACH07541 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1037
ID ACH08155 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1038
ID ACH11346 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1039
ID ACH11653 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1040
ID ACH10304 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1041
ID ACF01307 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1042
ID ACF40882 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040078-A1.
PD 27-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1043
ID ACD24222 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1044
ID ACD31323 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1045
ID ACF17824 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1046
ID ADA38686 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1047
ID ACF32607 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1048
ID ACF40268 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1049
ID ACF48228 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1050
ID ACF38177 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1051
ID ACF25113 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1052
ID ACF27013 standard; cDNA; 485 BP.

DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1053
ID ACF29469 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1054
ID ACD87703 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1055
ID ACF76164 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1056
ID ACF49456 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1057
ID ACF43913 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1058
ID ACH06258 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1059
ID ACH06565 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1060
ID ADA83254 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1061
ID ACC92621 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032133-A1.
PD 13-FEB-2003.

Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1062
ID ACC93235 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1063
ID ACF19280 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1064
ID ACD12971 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1065
ID ACF06429 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1066
ID ACC94463 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1067
ID ACC97891 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1068
ID ACC94156 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1069
ID ACF42110 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1070
ID ACD31016 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1071
ID ACD43045 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1072
ID ACD43352 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1073
ID ACF14882 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1074
ID ADA92807 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1075
ID ACF01614 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1076
ID ACF31686 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1077
ID ACD67363 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1078
ID ACD48553 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1079
ID ACD48860 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1080
ID ACF51298 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1081

ID ACF54061 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1082
ID ACF25785 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1083
ID ACF39098 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1084
ID ACF28855 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1085
ID ACD90772 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1086
ID ACD86475 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1087
ID ACH05337 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1088
ID ACF65133 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1089
ID ADB20297 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1090
ID ACF43606 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.

PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1091
ID ACH09076 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1092
ID ACH09383 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1093
ID ADA78549 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1094
ID ACF09806 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1095
ID ADA00374 standard; cDNA; 485 BP.
DE Human secreted/transmembrane polypeptide PRO 1003 cDNA.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1096
ID ACF50991 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1097
ID ACF23885 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1098
ID ACD88317 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1099
ID ACH09690 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049776-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1100
ID ACH10611 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1101
ID ACD11418 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1102
ID ACC96468 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1103
ID ACC98498 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1104
ID ACF41803 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1105
ID ACF16724 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1106
ID ACD32244 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1107
ID ACD30402 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1108
ID ACD41273 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1109
ID ACF07657 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.

PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1110
ID ACF31072 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1111
ID ACF77392 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1112
ID ACF11034 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1113
ID ACF32914 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1114
ID ACF26092 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1115
ID ACD83405 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1116
ID ACF23578 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1117
ID ACF42992 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1118
ID ACF43299 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104551-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1119
ID ACH05951 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1120
ID ACH08769 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1121
ID ACC90363 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1122
ID ACF10727 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1123
ID ACC93542 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1124
ID ACC96161 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1125
ID ACD24836 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1126
ID ACF01921 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1127
ID ACF22043 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1128
ID ACF22657 standard; cDNA; 485 BP.

DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1129
ID ACF08885 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1130
ID ACF33221 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1131
ID ACF54675 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1132
ID ACF48535 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1133
ID ACD47325 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1134
ID ACD49167 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1135
ID ACF37870 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1136
ID ACF30083 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1137
ID ACD87396 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.

PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1138
ID ACF61985 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1139
ID ACH10918 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1140
ID ACD10083 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1141
ID ACD16808 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1142
ID ACH65442 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1143
ID ACC99105 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1144
ID ACF00499 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1145
ID ACD40966 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1146
ID ACF14575 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1147
ID ACF22350 standard; cDNA; 485 BP.

DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1148
ID ACF78927 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1149
ID ACF11648 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1150
ID ADA22368 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1003.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1151
ID ACF51605 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1152
ID ACF33528 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1153
ID ACD49781 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1154
ID ACF37563 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1155
ID ACF28548 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1156
ID ACD88624 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068681-A1.
PD 10-APR-2003.

Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1157
ID ACF75243 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1158
ID ACF61064 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1159
ID ACF44220 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1160
ID ACH08462 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1161
ID ACD39432 standard; cDNA; 485 BP.
DE Human cDNA encoding PRO1108.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1162
ID ACC93849 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036122-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1163
ID ACD20954 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1164
ID ACF06736 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040065-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1165
ID ACD20647 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044919-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1166
ID ACD22796 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.

PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1167
ID ACF41496 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003044928-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1168
ID ADA06534 standard; cDNA; 485 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #68.
PN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1169
ID ADA39227 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003059782-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1170
ID ACF07043 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1171
ID ACF77699 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1172
ID ACD46097 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1173
ID ACF47000 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1174
ID ACF54368 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1175
ID ACF45772 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;

RESULT 1176
ID ACF45465 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1177
ID ACF38484 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1178
ID ACD89545 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1179
ID ACD85247 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1180
ID ACD85861 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1181
ID ACF75857 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1182
ID ACF60757 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1183
ID ACH05644 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1184
ID ADA82620 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1185

ID ADB85616 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1186
ID ADB96253 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1187
ID ACF55903 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1188
ID ACF55289 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1189
ID ADB85928 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1190
ID ACF56210 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1191
ID ACF56517 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1192
ID ADB68295 standard; cDNA; 485 BP.
DE Human PRO1003 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1193
ID ADB68102 standard; cDNA; 485 BP.
DE Human PRO1003 cDNA.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1194
ID ACF55596 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068761-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1195
ID ACF54982 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1196
ID ADB90919 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1197
ID ADC57725 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1198
ID ADC55089 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1199
ID ADC11956 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1200
ID ADC06999 standard; cDNA; 485 BP.
DE Human PRO1003 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1201
ID ADC56378 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1202
ID ADC17178 standard; cDNA; 485 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 43).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1203
ID ADC07433 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1204
ID ADC11423 standard; cDNA; 485 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1205
ID ADC14876 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1206
ID ADC52371 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1207
ID ADC14545 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1208
ID ADD08077 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1209
ID ADC81902 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1210
ID ADD07544 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1211
ID ADC82435 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1212
ID ADD05658 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1213
ID ADD08615 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
RESULT 1214

ID ADD06864 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1215
ID ADC83111 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1216
ID ADD55218 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1217
ID ADD36047 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1218
ID ADD56176 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1219
ID ADD54614 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1220
ID ADE26768 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1221
ID ADE26235 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1222
ID ADF67172 standard; cDNA; 485 BP.
DE Human PRO1003 nucleotide sequence SEQ ID NO:245.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1223
ID ADG01048 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1224

Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1224
ID ADG08601 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1225
ID ADG02653 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1226
ID ADG01360 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1227
ID ADF95535 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1228
ID ADF95222 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1229
ID ADG12350 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1230
ID ADH24075 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1231
ID ADH34101 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1232
ID ADH29934 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1233

ID ADH23905 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1234
ID ADH09010 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1235
ID ADG85309 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1236
ID ADH24585 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1237
ID ADH37441 standard; cDNA; 485 BP.
DE Human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1238
ID ADH02030 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1239
ID ADH37611 standard; cDNA; 485 BP.
DE Human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1240
ID ADG85649 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1241
ID ADH24245 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1242
ID ADH38539 standard; cDNA; 485 BP.

DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1243
ID ADG83660 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1244
ID ADH29468 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1245
ID ADH27584 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1246
ID ADH37781 standard; cDNA; 485 BP.
DE Human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1247
ID ADH37958 standard; cDNA; 485 BP.
DE Human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1248
ID ADH57378 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1249
ID ADH53520 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1250
ID ADH53690 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1251
ID ADH52026 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.

PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1252
ID ADH49881 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1253
ID ADI25391 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1254
ID ADH90184 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1255
ID ADI25561 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181659-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1256
ID ADH97735 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1257
ID ADI35426 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1258
ID ADI03583 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1259
ID ADI11940 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1260
ID ADH90014 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181697-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1261
ID ADH99918 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1262
ID ADH98415 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1263
ID ADI11090 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1264
ID ADI11600 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1265
ID ADH98245 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1266
ID ADH98585 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1267
ID ADH98075 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1268
ID ABX78620 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1269
ID ACA75592 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1270

ID ACA71072 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032112-A1.
PD 13-FEB-2003. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1271
ID ACC87600 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027278-A1.
PD 06-FEB-2003. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1272
ID ACC86986 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036159-A1.
PD 20-FEB-2003. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1273
ID ACD04159 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003040070-A1.
PD 27-FEB-2003. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1274
ID ABX77871 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003027163-A1.
PD 06-FEB-2003. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1275
ID ABX80283 standard; DNA; 485 BP.
DE Novel human secreted or transmembrane protein PRO1108 DNA.
PN US2002132252-A1.
PD 19-SEP-2002. 2.6%; Score 58; DB 10; Length 485;
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1276
ID ACA69189 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003032023-A1.
PD 13-FEB-2003. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1277
ID ACA69490 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003032113-A1.
PD 13-FEB-2003. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1278
ID ACA90335 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1279
ID ACC89442 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027264-A1.
PD 06-FEB-2003. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1280
ID ABX90260 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein cDNA, #97.

PN US2002160384-A1.
PD 31-OCT-2002. 2.6%; Score 58; DB 10; Length 485;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1281
ID ACA98233 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1282
ID ACA93875 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036149-A1.
PD 20-FEB-2003. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1283
ID ACD15268 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044923-A1.
PD 06-MAR-2003. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1284
ID ACD08855 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003040062-A1.
PD 27-FEB-2003. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1285
ID ACC96775 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040056-A1.
PD 27-FEB-2003. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1286
ID ACF15496 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003044926-A1.
PD 06-MAR-2003. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1287
ID ABX64106 standard; cDNA; 485 BP.
DE cDNA encoding human PRO1003 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002. 2.6%; Score 58; DB 10; Length 485;
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1288
ID ACA72863 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003036140-A1.
PD 20-FEB-2003. 2.6%; Score 58; DB 10; Length 485;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1289
ID ACD03035 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003013153-A1.
PD 16-JAN-2003. 2.6%; Score 58; DB 10; Length 485;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity
RESULT 1290
ID ACD01850 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.

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PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1291
ID ACA92042 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1292
ID ADI05063 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1293
ID ADI03413 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1294
ID ADI04808 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1295
ID ADH78262 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1296
ID ADI19606 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1297
ID ADH90354 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1298
ID ADI03073 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1299
ID ADH77922 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.

Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1300
ID ADH97905 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1301
ID ADI01290 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1302
ID ADI01985 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1303
ID ADI03243 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1304
ID ADI11430 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1305
ID ADI02332 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1306
ID ADI11770 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1307
ID ADI05407 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1308
ID ADH79479 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
RESULT 1309
ID ADH77922 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1309
ID ADI19436 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1310
ID ADI05237 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1311
ID ADH79649 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1312
ID ADI01475 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1313
ID ADI01645 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1314
ID ADI01815 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1315
ID ADH79819 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1316
ID ADI04637 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1317
ID ADI02773 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;

RESULT 1318
ID ADH78092 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1319
ID ADI25731 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1320
ID ADI25901 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1321
ID ADK65413 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1322
ID ADH98755 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1323
ID ADH79996 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1324
ID ADL32791 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 11; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1325
ID ADM30325 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 11; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1326
ID ADL93727 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 11; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1327
ID ADL93727 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 11; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;

ID ADC52181 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1328
ID ADE74322 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1329
ID ADE74934 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1330
ID ADF35371 standard; cDNA; 485 BP.
DE cDNA encoding human PRO1003 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1331
ID ADG11621 standard; cDNA; 485 BP.
DE cDNA encoding human PRO1003 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1332
ID ADF96147 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1333
ID ADG04418 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1334
ID ADG00578 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1335
ID ADH06613 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1336
ID ADH06443 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1337
ID ADG68864 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1338
ID ADH27754 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1339
ID ADH25095 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1340
ID ADH33727 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1341
ID ADG82834 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1342
ID ADH02370 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1343
ID ADH07977 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1344
ID ADG69374 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1345
ID ADH39195 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;

Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1346
ID ADH26115 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1347
ID ADG83935 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1348
ID ADH19491 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1349
ID ADG85479 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1350
ID ADH06273 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1351
ID ADH30103 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1352
ID ADH24415 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1353
ID ADH33084 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1354
ID ADG69544 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;

RESULT 1355
ID ADH07807 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1356
ID ADG85819 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1357
ID ADH39365 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1358
ID ADH33557 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1359
ID ADH33897 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1360
ID ADH01107 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1361
ID ADG69714 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1362
ID ADH20984 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1363
ID ADH02200 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1364
ID ADG69204 standard; cDNA; 485 BP.

DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1365
ID ADG85989 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1366
ID ADH24925 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1367
ID ADH39542 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1368
ID ADH20024 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1369
ID ADH02540 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1370
ID ADG69034 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1371
ID ADH07637 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1372
ID ADG86159 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1373
ID ADH24755 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.

PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1374
ID ADH25803 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1375
ID ADH38369 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1376
ID ADH57208 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1377
ID ADH52196 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1378
ID ADH49562 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1379
ID ADH90524 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1380
ID ADI11260 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1381
ID ADH98925 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1382
ID ADI02155 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003190699-A1.

PD 09-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1383
ID ADH90694 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1384
ID ADJ54823 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1385
ID ADJ98569 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1386
ID ADJ98739 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1387
ID ADH78898 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1388
ID ADJ99132 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1389
ID ADJ99302 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1390
ID ADJ98920 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1391
ID ADH79068 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181702-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1392
ID ADK00928 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1393
ID ADK14449 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1394
ID ADJ64594 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1395
ID ADM31490 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1396
ID ADM36537 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1397
ID ADM40342 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1398
ID ADM80898 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1399
ID ADN37950 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1400
ID ABV57059 standard; cDNA; 490 BP.
DE Human prostate expression marker cDNA 57050.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 2.6%; Score 58; DB 5; Length 490;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1401
ID AAV58672 standard; cDNA; 509 BP.
DE Prostate tumour specific gene clone 1D-4288.
PN WO9837418-A2.
PD 27-AUG-1998.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1402
ID AAV61342 standard; cDNA; 509 BP.
DE Extended cDNA sequence of prostate tumour clone 1D-4288.
PN WO9837093-A2.
PD 27-AUG-1998.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1403
ID AAA06435 standard; cDNA; 509 BP.
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:202.
PN WO200004149-A2.
PD 27-JAN-2000.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 3; Length 509;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1404
ID ABS71340 standard; cDNA; 509 BP.
DE Human prostate tumour protein partial DNA sequence #188.
PN US2002090372-A1.
PD 11-JUL-2002.
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
Query Match 2.6%; Score 58; DB 3; Length 509;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1405
ID AAH93551 standard; cDNA; 509 BP.
DE Human prostate-specific extended cDNA sequence 1D-4288.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1406
ID AAS63643 standard; cDNA; 509 BP.
DE Human prostate cDNA sequence #195.
PN WO200173032-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1407
ID AAH02616 standard; cDNA; 509 BP.
DE Prostate tumour antigen determined extended cDNA for 1D-4288.
PN WO200125272-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1408
ID AAH84865 standard; cDNA; 509 BP.
DE Human prostate-specific extended cDNA sequence 1D-4288.
PN WO200134802-A2.
PD 17-MAY-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1409
ID ACA59452 standard; cDNA; 509 BP.
DE Prostate cancer therapy associated cDNA #195.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJJ/) XU J.

PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match 2.6%; Score 58; DB 5; Length 509;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1410
ID AAS10194 standard; cDNA; 509 BP.
DE Human prostate tumour cDNA 1D-4288 #2.
PN US6262245-B1.
PD 17-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 5; Length 509;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1411
ID ABL95015 standard; cDNA; 509 BP.
DE Human 1D-4288 cDNA sequence SEQ ID NO 202.
PN US2002022248-A1.
PD 21-FEB-2002.
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
Query Match 2.6%; Score 58; DB 6; Length 509;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1412
ID ABS58724 standard; cDNA; 509 BP.
DE Prostate tumour cDNA #195.
PN US2002081580-A1.
PD 27-JUN-2002.
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
Query Match 2.6%; Score 58; DB 6; Length 509;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1413
ID ACC95179 standard; cDNA; 509 BP.
DE Prostate tumour specific cDNA sequence SEQ ID 202.
PN WO200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 8; Length 509;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1414

ID ADB13652 standard; cDNA; 509 BP.
DE Human prostate specific extended cDNA 1D-4288.
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP. 2.6%; Score 58; DB 10; Length 509;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1415
ID ADG26068 standard; cDNA; 509 BP.
DE Human prostate-specific cDNA #195.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP. 2.6%; Score 58; DB 10; Length 509;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1416
ID ADQ21075 standard; DNA; 513 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3895.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC. 2.6%; Score 58; DB 12; Length 513;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1417
ID AAK63327 standard; cDNA; 519 BP.
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:8387.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC. 2.6%; Score 58; DB 4; Length 519;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1418
ID AAS29134 standard; cDNA; 519 BP.
DE cDNA encoding for human DNA-binding protein #105.
PN WO200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC. 2.6%; Score 58; DB 5; Length 519;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1419
ID ABS68274 standard; cDNA; 519 BP.
DE cDNA encoding human DNA-binding protein #105.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A. 2.6%; Score 58; DB 6; Length 519;
PA (RUBE/) RUBEN S M. 100.0%; Pred. No. 3e-10;
PA (BARA/) BARASH S C. 2.6%; Score 58; DB 6; Length 519;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1420
ID ADC25268 standard; cDNA; 519 BP.
DE Human cDNA from extracellular matrix gene 105.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC. 2.6%; Score 58; DB 10; Length 519;
Query Match 100.0%; Pred. No. 3e-10;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1421
ID ABV59169 standard; cDNA; 530 BP.
DE Human prostate expression marker cDNA 59160.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. 2.6%; Score 58; DB 5; Length 530;
Query Match 100.0%; Pred. No. 2.9e-10;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1422
ID ABV54230 standard; cDNA; 540 BP.
DE Human prostate expression marker cDNA 54221.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. 2.6%; Score 58; DB 5; Length 540;
Query Match 100.0%; Pred. No. 2.9e-10;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;

RESULT 1423
ID ACH43937 standard; cDNA; 550 BP.
DE Human foetal brain cDNA #4662.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T. 2.6%; Score 58; DB 9; Length 550;
PA (LABA/) LABAT I. 100.0%; Pred. No. 2.9e-10;
PA (STAC/) STACHE-CRAIN B. 2.6%; Score 58; DB 9; Length 550;
PA (DICK/) DICKSON M C. 100.0%; Pred. No. 2.9e-10;
PA (JONE/) JONES L W. 2.6%; Score 58; DB 9; Length 550;
Query Match 100.0%; Pred. No. 2.9e-10;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1424
ID ABX57018 standard; DNA; 564 BP.
DE Arabidopsis thaliana polynucleotide #370.
PN US2002040489-A1.
PD 04-APR-2002.
PA (GORL/) GORLACH J. 2.6%; Score 58; DB 10; Length 564;
PA (ANYV/) AN Y. 100.0%; Pred. No. 2.9e-10;
PA (HAMI/) HAMILTON C M. 2.6%; Score 58; DB 10; Length 564;
PA (PRIC/) PRICE J L. 100.0%; Pred. No. 2.9e-10;
PA (RAIN/) RAINES T M. 2.6%; Score 58; DB 10; Length 564;
PA (YUYV/) YU Y. 100.0%; Pred. No. 2.9e-10;
PA (RAME/) RAMEAKA J G. 2.6%; Score 58; DB 10; Length 564;
PA (PAGE/) PAGE A. 100.0%; Pred. No. 2.9e-10;
PA (MATH/) MATHW A V. 2.6%; Score 58; DB 10; Length 564;
PA (LEDF/) LEDFORD B L. 100.0%; Pred. No. 2.9e-10;
PA (WOES/) WOESSNER J P. 2.6%; Score 58; DB 10; Length 564;
PA (HAAS/) HAAS W D. 100.0%; Pred. No. 2.9e-10;
PA (GARC/) GARCIA C A. 2.6%; Score 58; DB 10; Length 564;
PA (KRIC/) KRICKER M. 100.0%; Pred. No. 2.9e-10;
PA (SLAT/) SLATER T. 2.6%; Score 58; DB 10; Length 564;
PA (DAVI/) DAVIS K R. 2.6%; Score 58; DB 10; Length 564;
PA (ALLE/) ALLEN K. 100.0%; Pred. No. 2.9e-10;
PA (HOFF/) HOFFMAN N. 2.6%; Score 58; DB 10; Length 564;
PA (HURB/) HURBAN P. 100.0%; Pred. No. 2.9e-10;
Query Match 100.0%; Pred. No. 2.9e-10;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1425
ID AAZ97052 standard; cDNA; 569 BP.
DE Human secreted protein gene 34 cDNA clone HCHPF68, SEQ ID NO:44.
PN WO9966041-A1.
PD 23-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC. 2.6%; Score 58; DB 3; Length 569;
Query Match 100.0%; Pred. No. 2.9e-10;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1426
ID ACH66681 standard; cDNA; 569 BP.
DE Novel human secreted protein #34 cDNA.
PN US2003065151-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC. 2.6%; Score 58; DB 9; Length 569;
Query Match 100.0%; Pred. No. 2.9e-10;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1427
ID ADP12881 standard; DNA; 575 BP.
DE Reference mRNA sequence #95.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC. 2.6%; Score 58; DB 12; Length 575;
Query Match 100.0%; Pred. No. 2.9e-10;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1428
ID ABL86809 standard; cDNA; 581 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:9787.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP. 2.6%; Score 58; DB 6; Length 581;
Query Match 100.0%; Pred. No. 2.9e-10;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1429
ID ABV56190 standard; cDNA; 585 BP.
DE Human prostate expression marker cDNA 56181.

PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1430
ID ABK55402 standard; cDNA; 586 BP.
DE Human colon cancer-associated cDNA, SEQ ID NO 872.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1431
ID AAV84464 standard; DNA; 588 BP.
DE Human secreted protein gene 54 clone HE2AY71.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 2; Length 588;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1432
ID ABA83247 standard; cDNA; 588 BP.
DE Human secreted protein gene 54 SEQ ID NO:64.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 4; Length 588;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1433
ID ACH04748 standard; cDNA; 588 BP.
DE Novel human secreted protein #54 cDNA.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 9; Length 588;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1434
ID ACD44558 standard; cDNA; 588 BP.
DE Human cDNA from novel secreted protein gene 54.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 9; Length 588;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1435
ID AAS25987 standard; cDNA; 600 BP.
DE Human cDNA encoding a novel secreted protein, Seq ID 166.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1436
ID ABX73328 standard; DNA; 600 BP.
DE Human novel polynucleotide #156.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.6%; Score 58; DB 8; Length 600;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1437
ID AAC59787 standard; cDNA; 604 BP.
DE Human secreted protein gene 50 SEQ ID NO:60.
PN WO200056751-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 3; Length 604;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1438
ID ABV43916 standard; cDNA; 606 BP.

DE Human prostate expression marker cDNA 43907.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 606;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1439
ID ABV35070 standard; cDNA; 609 BP.
DE Human prostate expression marker cDNA 35061.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 609;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1440
ID AAZ06238 standard; DNA; 620 BP.
DE Human secreted protein gene No. 20.
PN WO9935158-A1.
PD 15-JUL-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1441
ID AAQ75445 standard; DNA; 635 BP.
DE Murine glycosylation inhibition factor (GIF).
PN WO9426923-A1.
PD 24-NOV-1994.
PA (LJOL-) LA JOLLA INST ALLERGY & IMMUNOLOGY.
PA (KIRI) KIRIN BEER KK.
Query Match 2.6%; Score 58; DB 2; Length 635;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1442
ID AAT38390 standard; cDNA; 635 BP.
DE Murine glycosylation inhibiting factor cDNA.
PN WO9631617-A1.
PD 10-OCT-1996.
PA (LJOL-) LA JOLLA INST ALLERGY & IMMUNOLOGY.
Query Match 2.6%; Score 58; DB 2; Length 635;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1443
ID AAA60768 standard; cDNA; 638 BP.
DE Pig SENR ligand nucleotide sequence SEQ ID NO:15.
PN WO200032627-A1.
PD 08-JUN-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 2.6%; Score 58; DB 3; Length 638;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1444
ID ABK50021 standard; cDNA; 638 BP.
DE Pig sensory epithelium neuro peptide-like receptor (SENR) cDNA #1.
PN WO200214513-A1.
PD 21-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 2.6%; Score 58; DB 6; Length 638;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1445
ID AAX30410 standard; DNA; 687 BP.
DE DNA encoding a human secreted protein.
PN WO9907891-A1.
PD 18-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 2; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1446
ID ADB47824 standard; cDNA; 687 BP.
DE Novel human secreted protein cDNA #97.
PN US2003054443-A1.
PD 20-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (SOPP/) SOPPET D R.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (YOUN/) YOUNG P E.

Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1462
ID ACA03852 standard; cDNA; 693 BP.
DE CDNA encoding human PRO polypeptide #250.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1463
ID ABX89390 standard; cDNA; 693 BP.
DE DNA encoding novel secreted and transmembrane protein PRO1286.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1464
ID ACD42044 standard; cDNA; 693 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #250.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1465
ID ACA68584 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1466
ID ACA04273 standard; cDNA; 693 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 499.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1467
ID ADA76449 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1468
ID ADA76449 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1469
ID ABT44313 standard; cDNA; 693 BP.
DE Human PRO1286 cDNA.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1470
ID ADA19099 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;

RESULT 1471
ID ADA61722 standard; cDNA; 693 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1472
ID ADB19507 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1473
ID ADB28048 standard; cDNA; 693 BP.
DE cDNA encoding human PRO polypeptide #250.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1474
ID ADA86527 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1475
ID ADB16091 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1476
ID ADA47877 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1477
ID ACD68338 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1478
ID ADA67672 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1479
ID ADB30679 standard; cDNA; 693 BP.
DE cDNA encoding human PRO polypeptide #250.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1480

ID ADA85975 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1481
ID ADA97187 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1482
ID ADA79491 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1483
ID ADA87630 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1484
ID ADB16832 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1485
ID ADA91924 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1486
ID ADB14987 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1487
ID ADB18948 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1488
ID ADA94163 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1489
ID ADB20059 standard; cDNA; 693 BP.

DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1490
ID ADB13371 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1491
ID ACD98673 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1492
ID ADA74625 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1493
ID ADB24858 standard; cDNA; 693 BP.
DE Human PRO polynucleotide SEQ ID NO 499.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1494
ID ADA82382 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1495
ID ADA75345 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1496
ID ADA85423 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1497
ID ADA84871 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1498
ID ADB30127 standard; cDNA; 693 BP.
DE cDNA encoding human PRO polypeptide #250.

PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1499
ID ADA80655 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1500
ID ADA75897 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 15:43:38 ; Search time 6337 Seconds
(without alignments)
12892.201 Million cell updates/sec

Title: US-10-036-342-56
Perfect score: 2242
Sequence: 1 gaatgaataacctccgaagcc.....aaaaaaaaaaaaaaaaaaaa 2242

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 6
Total number of hits satisfying chosen parameters: 65638880

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1901	84.8	2105	3	CR610360 full-leng
2	1425	63.6	1528	3	BC004271 Homo sapi
3	688	30.7	913	5	BX453730 BX453730
4	687	30.6	928	5	BX432016 BX432016
5	679	30.3	799	4	BI754224 603025522
6	670	29.9	1006	5	BX422768 BX422768
7	625	27.9	730	4	BI667149 603291543
8	592	26.4	674	4	BI598229 603245407
9	577	25.7	702	4	BM691429 UI-E-C11-
10	577	25.7	772	4	BI489508 603032068
11	576	25.7	742	1	AI939620 tm64d04.x
12	570	25.4	630	4	BM669584 UI-E-DX1-
13	567	25.3	567	5	BX110726 BX110726
14	563	25.1	887	4	BI600248 603245955
15	553	24.7	748	4	BI597871 603245353
16	548	24.4	666	4	BI604126 603244067
17	548	24.4	675	4	BG201754 RST21096
18	542	24.2	684	4	BG202268 RST21623
19	535	23.9	710	2	BE386438 601273641
20	529	23.6	807	4	BG708811 602673107
21	523	23.3	632	2	AW300620 xs68h03.x
22	517	23.1	600	1	AI589129 tf81d02.x
23	501	22.3	882	4	BI489822 603031554
24	485	21.6	668	1	AI480056 tm71f08.x

C	98	61	2.7	213	1	AI251458	AI251458	qu74hl12.x	C	171	61	2.7	801	7	CK020485	CK020485	AGENCOURT
	99	61	2.7	222	7	CO180267	CO180267	EC01329.5		172	61	2.7	816	5	BU564811	BU564811	AGENCOURT
	100	61	2.7	223	4	BM561325	BM561325	AGENCOURT	C	173	61	2.7	818	2	BE964743	BE964743	601658288
	101	61	2.7	225	1	AA597154	AA597154	VO35G03.f		174	61	2.7	824	7	CN157645	CN157645	946365 MA
C	102	61	2.7	244	6	CB972639	CB972639	CAB30001	C	175	61	2.7	843	7	CK194951	CK194951	FGAS00338
C	103	61	2.7	250	6	CD671248	CD671248	fg02f02.x		176	61	2.7	865	7	CK396515	CK396515	AGENCOURT
	104	61	2.7	255	7	CO194180	CO194180	EC37566.5		177	61	2.7	876	5	BU534311	BU534311	AGENCOURT
	105	61	2.7	274	5	BP432150	BP432150		C	178	61	2.7	893	4	BI523117	BI523117	603175824
C	106	61	2.7	293	4	BI491319	BI491319	df07b02.w		179	61	2.7	909	3	CR707691	CR707691	Tetraodon
C	107	61	2.7	294	6	CB345423	CB345423	CA48EN000		180	61	2.7	909	7	CK195964	CK195964	FGAS00441
	108	61	2.7	295	4	BG508371	BG508371	sac95g05.	C	181	61	2.7	946	7	CF580919	CF580919	AGENCOURT
	109	61	2.7	298	2	AW960594	AW960594	EST372665	C	182	61	2.7	977	5	BQ926818	BQ926818	AGENCOURT
C	110	61	2.7	307	4	BM496458	BM496458	IpCGBr2.1		183	61	2.7	1041	6	CD051043	CD051043	AGENCOURT
	111	61	2.7	307	6	CD809585	CD809585	250_Lingu	C	184	61	2.7	1378	4	BI490467	BI490467	603032288
C	112	61	2.7	313	2	AW190242	AW190242	xl60g08.x		185	61	2.7	4319	3	BC069040	BC069040	Mus muscu
	113	61	2.7	317	2	AW021588	AW021588	df25f03.y		186	60	2.7	78	6	CF327666	CF327666	NACL--02-
C	114	61	2.7	319	2	AW170731	AW170731	xi97ci11.x		187	60	2.7	80	1	AA785747	AA785747	h1h02al.f
C	115	61	2.7	322	1	AI613523	AI613523	tw22g07.x	C	188	60	2.7	85	1	AI539707	AI539707	tp77b02.x
C	116	61	2.7	323	1	AI395113	AI395113	MA002449.		189	60	2.7	87	1	AI539781	AI539781	tp77f12.x
C	117	61	2.7	328	6	CF298861	CF298861	7LEAF--02	C	190	60	2.7	89	2	AW081383	AW081383	xc41f06.x
	118	61	2.7	328	7	F36859	F36859	HSPD34763 H		191	60	2.7	98	6	CF315597	CF315597	HD--04-J0
C	119	61	2.7	335	1	AI285431	AI285431	qt83b11.x	C	192	60	2.7	101	1	AJ500653	AJ500653	
	120	61	2.7	342	1	AV689723	AV689723			193	60	2.7	101	7	CK119050	CK119050	214119.p1
C	121	61	2.7	350	7	CO256376	CO256376	WS0082.B2		194	60	2.7	102	4	BI496873	BI496873	df128h09.
	122	61	2.7	355	7	CF804954	CF804954	lad59b03.	C	195	60	2.7	105	2	BF572734	BF572734	602079377
C	123	61	2.7	356	2	AW105455	AW105455	xd53a01.x		196	60	2.7	106	6	CB075468	CB075468	hz46d07.b
C	124	61	2.7	359	7	CO184089	CO184089	EC27086.5		197	60	2.7	107	1	AI589428	AI589428	tr75h03.x
C	125	61	2.7	361	5	BQ385855	BQ385855	NISC mn14	C	198	60	2.7	109	6	CF215082	CF215082	CAST0001
C	126	61	2.7	363	4	BM554614	BM554614	AGENCOURT		199	60	2.7	111	7	CK119188	CK119188	213m18.p1
C	127	61	2.7	368	6	CA722301	CA722301	wds1c.pk0	C	200	60	2.7	112	6	CD400416	CD400416	Gm CK2227
C	128	61	2.7	376	1	AI558302	AI558302	fb78d10.x		201	60	2.7	112	6	CF328795	CF328795	NACL--03-
C	129	61	2.7	376	1	AI647063	AI647063	ub74ci11.x	C	202	60	2.7	114	2	AW191844	AW191844	xl176b03.x
	130	61	2.7	376	6	CB079487	CB079487	hp72a03.b		203	60	2.7	114	4	BI491270	BI491270	df06d01.w
	131	61	2.7	378	1	AV681682	AV681682		C	204	60	2.7	114	6	CF214394	CF214394	CGF100081
	132	61	2.7	383	7	CF520808	CF520808	AGENCOURT	C	205	60	2.7	115	6	CF311750	CF311750	ABF--07-C
C	133	61	2.7	387	1	AI697177	AI697177	tq06f04.x		206	60	2.7	116	4	BI491375	BI491375	df08a04.w
	134	61	2.7	388	6	CF123150	CF123150	UI-HF-CH0	C	207	60	2.7	121	2	BE325423	BE325423	NF088GL1S
C	135	61	2.7	391	1	AI887211	AI887211	wm37d11.x		208	60	2.7	127	7	CR558711	CR558711	DKFZp468D
	136	61	2.7	394	1	AJ788571	AJ788571			209	60	2.7	129	1	AI345677	AI345677	tb78h05.x
	137	61	2.7	403	2	BF191104	BF191104	237824 MA	C	210	60	2.7	134	4	BI015375	BI015375	MR4-ET024
	138	61	2.7	405	6	CA852848	CA852848	E12F12.K1	C	211	60	2.7	134	7	CF667178	CF667178	RTCNT1.28
C	139	61	2.7	410	7	CF405497	CF405497	CSEC8054E	C	212	60	2.7	137	7	CN546325	CN546325	EST 18277
C	140	61	2.7	411	1	AT001678	AT001678			213	60	2.7	138	1	AL836657	AL836657	AL836657
	141	61	2.7	413	6	CB073120	CB073120	taa28el0.		214	60	2.7	139	1	AA123279	AA123279	mn23c05.f
C	142	61	2.7	415	1	AI361586	AI361586	qy48f10.x	C	215	60	2.7	139	2	BE907440	BE907440	601500177
C	143	61	2.7	426	6	CA722842	CA722842	wds1c.pk0	C	216	60	2.7	139	6	CB973884	CB973884	CAB30003
	144	61	2.7	431	7	CO191531	CO191531	EC31328.5	C	217	60	2.7	142	1	AI249877	AI249877	qx03e04.x
	145	61	2.7	432	7	CO191324	CO191324	EC30708.5	C	218	60	2.7	142	7	CK616330	CK616330	ou16e12.y
C	146	61	2.7	436	6	CD996103	CD996103	P	C	219	60	2.7	143	7	CN546305	CN546305	EST 18257
C	147	61	2.7	456	6	CB045766	CB045766	NISC_gc12	C	220	60	2.7	144	6	CF318389	CF318389	HD--08-H2
C	148	61	2.7	462	5	BQ524998	BQ524998	NISC_m008		221	60	2.7	144	7	CK360784	CK360784	AGENCOURT
C	149	61	2.7	488	5	BQ395463	BQ395463	NISC_ng15		222	60	2.7	144	7	CN272400	CN272400	170006000
	150	61	2.7	498	7	CO182279	CO182279	EC22369.5	C	223	60	2.7	147	6	CB977208	CB977208	CAB40003
C	151	61	2.7	502	9	CC853416	CC853416	NDL.21E21	C	224	60	2.7	147	7	CN527893	CN527893	UI-M-HQ0-
C	152	61	2.7	510	6	CB052268	CB052268	NISC_g106		225	60	2.7	148	4	BJ681098	BJ681098	BJ681098
C	153	61	2.7	528	6	CB348563	CB348563	CAB2S000	C	226	60	2.7	148	5	BQ384842	BQ384842	NISC_mn09
	154	61	2.7	534	1	AA615853	AA615853	vo94f04.f	C	227	60	2.7	149	1	AJ499525	AJ499525	AJ499525
C	155	61	2.7	548	1	AI571049	AI571049	to26b06.x	C	228	60	2.7	150	2	BE964700	BE964700	601658238
C	156	61	2.7	552	6	CB247053	CB247053	UI-M-F10-	C	229	60	2.7	150	6	CF336864	CF336864	JMT--07-B
C	157	61	2.7	574	5	BU688209	BU688209	UI-CF-EC1	C	230	60	2.7	151	1	AI537643	AI537643	tp10h01.x
C	158	61	2.7	590	6	CA347558	CA347558	678700 NC		231	60	2.7	152	6	CB455595	CB455595	712748 MA
C	159	61	2.7	594	5	BQ400399	BQ400399	NISC_mp09		232	60	2.7	152	7	CK384839	CK384839	lah55a12.
C	160	61	2.7	594	6	CD416515	CD416515	Gm ck891	C	233	60	2.7	152	7	CK617056	CK617056	ou32g06.y
	161	61	2.7	601	7	CN786814	CN786814	4120863 B		234	60	2.7	154	6	CF313028	CF313028	HD--01-A0
	162	61	2.7	625	7	CN984035	CN984035	52752.126	C	235	60	2.7	154	7	CF510746	CF510746	CABud0001
	163	61	2.7	680	3	CR702672	CR702672	Tetraodon	C	236	60	2.7	155	1	AI953765	AI953765	wx69b02.x
	164	61	2.7	699	7	CR842027	CR842027	AGENCOURT		237	60	2.7	156	7	CR547142	CR547142	DKFZp468A
	165	61	2.7	703	3	CR689517	CR689517	Tetraodon		238	60	2.7	158	7	CR630352	CR630352	DKFZp469J
C	166	61	2.7	716	6	CB342493	CB342493	CA32EN000		239	60	2.7	160	4	BM496442	BM496442	IpCGBr2.1
	167	61	2.7	728	4	BG572322	BG572322	602594547	C	240	60	2.7	160	6	CA670655	CA670655	w1su1.pk0
	168	61	2.7	734	9	CG848156	CG848156	ZMMBB031	C	241	60	2.7	160	6	CB977957	CB977957	CAB40005
	169	61	2.7	763	7	CN802656	CN802656	ILLUMIGEN	C	242	60	2.7	160	7	CK817434	CK817434	hags009xc
	170	61	2.7	767	5	BX490481	BX490481	DKFZp686K	C	243	60	2.7	161	6	CF330162	CF330162	NACL--05-

C 244 60 2.7 162 1 AI886594
C 245 60 2.7 162 1 AI925404
246 60 2.7 163 7 CR559263
247 60 2.7 165 2 BE543089
C 248 60 2.7 168 6 CF322022
C 249 60 2.7 170 2 AW081255
250 60 2.7 171 7 CR559476
251 60 2.7 172 2 BE059635
252 60 2.7 175 4 BI945748
253 60 2.7 175 5 BX953641
254 60 2.7 178 2 AW786766
255 60 2.7 178 2 BE022664
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AL509380 AL509380
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C 420	60	2.7	286	1	AI283914	qt66b04.x	
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C 448	60	2.7	306	4	BM495074	IpcGBr1_4	
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AI282376	qv03g10.x						
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CB519742	UI-M-GH0-						
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AI813913	wk61g10.x						
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AW172878	xj05a12.x						
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C 572	60	2.7	388	6	CF276248	CF276248 14ETL--01
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C 578	60	2.7	391	5	BQ526631	BQ526631 NISC_nol7
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C 582	60	2.7	392	5	BQ396364	BQ396364 NISC_ng20
C 583	60	2.7	392	5	BQ523600	BQ523600 NISC_n123
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C 606	60	2.7	405	6	CF316565	CF316565 HD--05-O0
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C 612	60	2.7	410	2	BF475206	BF475206
613	60	2.7	410	6	BY668300	BY668300
C 614	60	2.7	412	1	AI886016	AI886016
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C 618	60	2.7	414	1	AI921232	AI921232
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C 620	60	2.7	416	2	AW166975	AW166975
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C 631	60	2.7	424	2	AW262042	AW262042
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C 634	60	2.7	425	6	CF316656	CF316656
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C 934 60 CO385354 AGENCOURT
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C 937 60 CK197616 FGAS00609
C 938 60 CA453861 AGENCOURT
C 939 60 BU555935 AGENCOURT
C 940 60 CK198254 FGAS00673
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C 942 60 CK196840 FGAS00530
C 943 60 CK200159 FGAS00866
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C 966 60 CK156192 FGAS03711
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C 968 60 CK156041 FGAS03694
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BE965171 601658967
CK164886 FGAS04881
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CF311486 ABF--06-L
CF327983 NACL--02-
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CF338194 JMT--08-P
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AI211208 o0d11a1.f
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N34355 Yy12d04.s1
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BQ265370 NISC_ff05
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C 974	59	2.6	88	6	CD399147	CD399147 Gm_ck2060	c1047	59	2.6	112	1	AI249946	AI249946 qx47b01.x
C 975	59	2.6	88	7	N74355	N74355 za52b01.s1	c1048	59	2.6	112	6	CB410038	CB410038 NISC_rc09
C 976	59	2.6	90	1	AI828574	AI828574 w142d08.x	c1049	59	2.6	112	6	CF334957	CF334957 JMT--04-H
C 977	59	2.6	90	2	BF458032	BF458032 UI-M-BZ1-	c1050	59	2.6	112	6	CF337940	CF337940 JMT--08-J
C 978	59	2.6	90	6	CF291813	CF291813 14ROOT--0	c1051	59	2.6	113	4	BM495149	BM495149 IPCGBx1_6
C 979	59	2.6	90	6	CF298069	CF298069 7LEAF--01	c1052	59	2.6	114	7	CK616588	CK616588 ou22c01.y
C 980	59	2.6	91	2	BF633562	BF633562 NF058E07D	c1053	59	2.6	115	2	BE613727	BE613727 601504529
C 981	59	2.6	92	1	AI242736	AI242736 qt86d12.x	c1054	59	2.6	115	4	BG980787	BG980787 MR3-CN014
C 982	59	2.6	92	1	AA124213	AA124213 mn46c01.x	c1055	59	2.6	115	6	CB052012	CB052012 NISC_g105
C 983	59	2.6	92	2	BF643410	BF643410 NF003B05E	c1056	59	2.6	115	7	CO534692	CO534692 3530_1_22
C 984	59	2.6	92	7	CK616738	CK616738 ou25d01.y	c1057	59	2.6	116	1	AI583578	AI583578 ts15h09.x
C 985	59	2.6	93	6	CF302130	CF302130 7LEAF--07	c1058	59	2.6	116	5	BQ586431	BQ586431 S013307-0
C 986	59	2.6	93	6	CF333328	CF333328 JMT--02-A	c1059	59	2.6	116	6	CB817178	CB817178 d3b08pz.f
C 987	59	2.6	93	6	CF336292	CF336292 JMT--06-E	c1060	59	2.6	116	6	CF316173	CF316173 HD--05-F2
C 988	59	2.6	93	7	CK616543	CK616543 ou21d05.y	c1061	59	2.6	117	6	CF292121	CF292121 14ROOT--0
C 989	59	2.6	94	1	AI866786	AI866786 tz53b05.x	1062	59	2.6	118	2	AW347176	AW347176 30517 MAR
C 990	59	2.6	94	4	BG499656	BG499656 602545044	1063	59	2.6	118	6	CB089318	CB089318 gs07g02.b
C 991	59	2.6	94	6	CF281066	CF281066 14ETL--07	c1064	59	2.6	118	6	CB606769	CB606769 AMGNNUC:S
C 992	59	2.6	94	7	CK615940	CK615940 ou07h07.y	c1065	59	2.6	118	6	CB972851	CB972851 CAB30001
C 993	59	2.6	96	2	AW332994	AW332994 S15H10 AG	c1066	59	2.6	119	4	BG792385	BG792385 UTSW_H34F
C 994	59	2.6	96	6	CF316463	CF316463 HD--05-M0	c1067	59	2.6	119	4	BG817171	BG817171 UTSW_H18B
C 995	59	2.6	97	6	CB053740	CB053740 NISC_g116	c1068	59	2.6	119	4	BI014412	BI014412 MR3-ET025
C 996	59	2.6	98	6	CB054081	CB054081 NISC_gm02	c1069	59	2.6	119	4	BI015377	BI015377 MR4-ET024
C 997	59	2.6	99	1	AI452857	AI452857 tj26e03.x	c1070	59	2.6	119	6	CF326816	CF326816 NACL--01-
C 998	59	2.6	99	7	CN546690	CN546690 EST_18461	c1071	59	2.6	120	1	AI550318	AI550318 vx03h11.x
C 999	59	2.6	100	1	AI446124	AI446124 tj07b06.x	c1072	59	2.6	120	1	CF326816	CF326816 NACL--01-
C1000	59	2.6	100	1	AI623736	AI623736 ts38f07.x	c1073	59	2.6	120	2	AW858254	AW858254 CM1-CT033
C1001	59	2.6	100	6	CF307943	CF307943 ABE--01-J	c1074	59	2.6	120	4	BG991132	BG991132 MR2-HT118
C1002	59	2.6	100	7	CK617039	CK617039 ou32d08.y	c1075	59	2.6	121	1	AA514684	AA514684 nf58f05.s
C1003	59	2.6	101	1	AI619370	AI619370 486093D07	c1076	59	2.6	122	1	AI677797	AI677797 wc80e03.x
1004	59	2.6	101	6	CB079792	CB079792 hp76f07.b	c1077	59	2.6	122	2	AW082600	AW082600 xc20b10.x
C1005	59	2.6	101	7	CK616022	CK616022 ou09g07.y	c1078	59	2.6	122	5	BQ524894	BQ524894 NISC_rc07
C1006	59	2.6	102	1	AL045630	AL045630 DKFZp434P	c1079	59	2.6	122	6	CF321272	CF321272 HD--12-H1
C1007	59	2.6	102	5	BQ385719	BQ385719 NISC_mml3	c1080	59	2.6	122	6	CF328903	CF328903 NACL--04-
C1008	59	2.6	102	6	CB977914	CB977914 CAB40004	c1081	59	2.6	123	1	AI472536	AI472536 t177g07.x
C1009	59	2.6	102	6	CD538640	CD538640 B0205C04-	c1082	59	2.6	123	6	CF337275	CF337275 JMT--07-K
1010	59	2.6	103	5	BU068740	BU068740 2567_B08	c1083	59	2.6	124	1	AI886055	AI886055 wn08h03.x
1011	59	2.6	103	6	CA336726	CA336726 NISC_lv04	c1084	59	2.6	124	1	AL045324	AL045324 DKFZp434A
C1012	59	2.6	103	6	CD390858	CD390858 Gm_ck0255	c1085	59	2.6	125	2	BF817746	BF817746 MR2-C1012
C1013	59	2.6	103	6	CF202825	CF202825 RR890915N	c1086	59	2.6	125	6	CA778959	CA778959 MPL384_11
C1014	59	2.6	103	7	CN640199	CN640199 264F07_55	c1087	59	2.6	125	6	CF327201	CF327201 NACL--01-
C1015	59	2.6	104	2	BE172499	BE172499 MR0-HT055	c1088	59	2.6	125	7	CK894586	CK894586 SGP160194
C1016	59	2.6	104	6	CD403321	CD403321 Gm_ck2604	c1089	59	2.6	126	6	CB088871	CB088871 if06h08.b
C1017	59	2.6	104	6	CD405413	CD405413 Gm_ck2879	c1090	59	2.6	126	7	CK615858	CK615858 ou05h09.y
C1018	59	2.6	104	7	CF519095	CF519095 CAP0006_I	c1091	59	2.6	127	2	AW265004	AW265004 qx59d11.x
C1019	59	2.6	105	6	CB346432	CB346432 CAB2SG000	c1092	59	2.6	127	2	AW999906	AW999906 MR0-BN007
C1020	59	2.6	105	6	CB975252	CB975252 CAB300006	c1093	59	2.6	127	2	BE393551	BE393551 601310247
C1021	59	2.6	105	6	CF313736	CF313736 HD--01-P1	c1094	59	2.6	127	4	BI041322	BI041322 MR4-NT014
C1022	59	2.6	105	6	CF314459	CF314459 HD--02-P1	c1095	59	2.6	127	4	BI496442	BI496442 df125d01.
1023	59	2.6	105	6	CF330299	CF330299 NACL--05-	1096	59	2.6	127	4	BM030766	BM030766 495270 MA
C1024	59	2.6	106	1	AI434242	AI434242 ti33c05.x	c1097	59	2.6	127	6	CB085026	CB085026 hq26b02.b
C1025	59	2.6	106	1	AI805769	AI805769 tx89h05.x	c1098	59	2.6	127	6	CB977737	CB977737 CAB40004
C1026	59	2.6	106	2	BF641709	BF641709 NF057F081	c1099	59	2.6	128	1	AI250627	AI250627 qx46b05.x
C1027	59	2.6	106	2	BE238676	BE238676 946006F11	c1100	59	2.6	128	2	BF814449	BF814449 MR2-C1018
C1028	59	2.6	106	5	BQ393762	BQ393762 NISC_ng05	c1101	59	2.6	128	2	BE538466	BE538466 601068105
C1029	59	2.6	106	6	CB051709	CB051709 NISC_g102	c1102	59	2.6	128	2	AW085786	AW085786 xc55g11.x
1030	59	2.6	106	6	CB094428	CB094428 hz69h08.b	c1103	59	2.6	129	4	BG956236	BG956236 QV1-CT075
1031	59	2.6	106	6	CF299320	CF299320 7LEAF--03	c1104	59	2.6	129	6	CB286160	CB286160 CMD31_F12
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C1033	59	2.6	107	1	AI553669	AI553669 tq46f09.x	c1106	59	2.6	130	5	BQ525571	BQ525571 NISC_rc011
C1034	59	2.6	107	4	BG942081	BG942081 ax20h05.x	c1107	59	2.6	130	6	CF309778	CF309778 ABE--04-B
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C1039	59	2.6	108	4	BI024831	BI024831 MR3-MT033	c1112	59	2.6	131	6	CF971631	CF971631 CAB10005
C1040	59	2.6	109	2	AW331462	AW331462 707013G08	c1113	59	2.6	131	6	CF202166	CF202166 RR890915N
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C1042	59	2.6	110	6	CF315453	CF315453 HD--04-G0	c1115	59	2.6	132	4	BI001166	BI001166 MR3-HN012
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C1046	59	2.6	112	1	AI244380	AI244380 qj76d12.x	c1119	59	2.6	133	4	BI019339	BI019339 MR3-MT032

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c1126	59	2.6	134	7	CN806612	CN806612
c1127	59	2.6	135	1	AA848053	AA848053
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c1129	59	2.6	135	4	BI519352	BI519352
c1130	59	2.6	135	6	CA814292	CA814292
c1131	59	2.6	135	6	CB410429	CB410429
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c1153	59	2.6	140	2	AW083804	AW083804
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c1160	59	2.6	141	7	CO176589	CO176589
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1173	59	2.6	144	6	CB051042	CB051042
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c1175	59	2.6	145	1	AI805688	AI805688
1176	59	2.6	145	1	AU057087	AU057087
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c1181	59	2.6	146	2	AW633023	AW633023
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1185	59	2.6	147	6	CB075436	CB075436
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c1200	59	2.6	151	1	AI560679	AI560679
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1202	59	2.6	151	1	AL585970	AL585970
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c1210	59	2.6	152	4	BM612283	BM612283
1211	59	2.6	152	5	BU068781	BU068781
1212	59	2.6	152	7	CR630205	CR630205
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1218	59	2.6	153	6	CF305051	CF305051
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c1221	59	2.6	154	1	AI620093	AI620093
c1222	59	2.6	154	1	AI929108	AI929108
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c1227	59	2.6	154	4	CA672344	CA672344
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c1231	59	2.6	155	2	BG981972	BG981972
1232	59	2.6	155	4	BI041310	BI041310
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c1234	59	2.6	156	6	CB978449	CB978449
c1235	59	2.6	157	1	AI570966	AI570966
c1236	59	2.6	157	2	BE964767	BE964767
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c1238	59	2.6	157	4	BI015378	BI015378
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c1251	59	2.6	159	1	AI539153	AI539153
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c1254	59	2.6	159	6	CF330943	CF330943
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CF327124	NACL--01-	CF327124
AI866608	tz51h07.x	AI866608
BG991108	MR2-HT118	BG991108
BP869360	12 87-P18	BP869360
BU924529	7092-95 M	BU924529
CB047590	NISC_gg03	CB047590
CN000048	io93c01.b	CN000048
AI560679	tg55a06.x	AI560679
AI873638	wm27g11.x	AI873638
AL585970	AL585970	AL585970
AL598374	DKF2p313B	AL598374
AW632918	bl01906.x	AW632918
BM307176	sak37f12.	BM307176
AI573026	tn65d11.x	AI573026
AW500379	UI-HF-BN0	AW500379
BI015395	MR4-ET024	BI015395
BI492305	df22d10.w	BI492305
BM612283	170006871	BM612283
BU068781	2567_H04	BU068781
CR630205	DKF2p469G	CR630205
AL046463	DKF2p434A	AL046463
CA673454	wlsu2.pk0	CA673454
CA735721	wpils.pk0	CA735721
CB052185	NISC_g106	CB052185
CB052782	NISC_g110	CB052782
CB089286	q807C10.b	CB089286
CF305051	ABF1--06-	CF305051
CF329786	NACL--05-	CF329786
AI539771	tp77e11.x	AI539771
AI620093	tu92e01.x	AI620093
AI929108	au65b12.y	AI929108
AV669940	AV669940	AV669940
BG939829	cr63c03.x	BG939829
BG977627	MR2-CI018	BG977627
BI053610	MR3-GN046	BI053610
CA672344	wlsu2.pk0	CA672344
CF312541	ABF--08-F	CF312541
CK635614	UI-M-HN0-	CK635614
BF904180	MR3-MT033	BF904180
BG981972	MR3-CN014	BG981972
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CA673486	wlsu2.pk0	CA673486
CB978449	CAB40005	CB978449
AI570966	to24f08.x	AI570966
BE964767	601658419	BE964767
BI001155	MR3-HN012	BI001155
BI015378	MR4-ET024	BI015378
BJ684383	BJ684383	BJ684383
CA674135	wlsu2.pk0	CA674135
CB970689	CAB10004	CB970689
CF314238	HD--02-K2	CF314238
AI419440	tf28f05.x	AI419440
BG287559	602384586	BG287559
BI002556	MR3-HN014	BI002556
CA598443	wyrlc.pk0	CA598443
CF215202	CAST0001	CF215202
CK615927	ou07f07.y	CK615927
CN472181	hh_Ab_Bra	CN472181
AI470293	tj41g11.x	AI470293
AI539153	tp73c08.x	AI539153
BG996109	MR4-HT119	BG996109
CA672755	wlsu2.pk0	CA672755
CF330943	NACL--06-	CF330943
CN546646	EST 18417	CN546646</

C1266	59	2.6	161	4	BG991140	BG991140	MR2-HT118	C1339	59	2.6	173	6	CB973491	CB973491	CAB30003
1267	59	2.6	161	5	BX955084	BX955084	DKFZp781H	1340	59	2.6	173	7	CR559321	CR559321	DKFZp468G
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C1269	59	2.6	161	6	CA672056	CA672056	wlsu2.pk0	1342	59	2.6	174	5	BX503608	BX503608	DKFZp686B
C1270	59	2.6	161	6	CF334139	CF334139	JMT--03-F	C1343	59	2.6	174	6	CA667523	CA667523	wlsul.pk0
C1271	59	2.6	162	1	AI545030	AI545030	fb73g11.x	C1344	59	2.6	174	6	CF291867	CF291867	14ROOF--0
C1272	59	2.6	162	1	AI805638	AI805638	tx97f05.x	C1345	59	2.6	175	1	AI698401	AI698401	tx64e10.x
C1273	59	2.6	162	4	BG991087	BG991087	MR2-HT118	C1346	59	2.6	175	1	AI802240	AI802240	tj36e02.x
C1274	59	2.6	162	4	BI015391	BI015391	MR4-ET024	C1347	59	2.6	175	1	AI922577	AI922577	wm89h02.x
C1275	59	2.6	162	4	BM537512	BM537512	ha83c10.g	C1348	59	2.6	175	2	AW129230	AW129230	xf21h03.x
1276	59	2.6	162	6	CA337690	CA337690	NISC_lw05	C1349	59	2.6	175	2	AW130863	AW130863	xe66b06.x
1277	59	2.6	162	6	CB082953	CB082953	hn64f09.b	C1350	59	2.6	175	4	BG993627	BG993627	MR3-HT127
1278	59	2.6	163	2	AW156320	AW156320	se22e08.y	C1351	59	2.6	175	4	BG996281	BG996281	MR4-HT119
C1279	59	2.6	163	2	AW227512	AW227512	up10a05.x	1352	59	2.6	175	4	BI002835	BI002835	MR3-HN016
C1280	59	2.6	163	2	BE072233	BE072233	QV4-BT053	1353	59	2.6	175	4	BM532325	BM532325	fy06e08.y
C1281	59	2.6	164	1	AI643690	AI643690	vi04f05.x	C1354	59	2.6	175	6	CF302180	CF302180	7LEAF--07
C1282	59	2.6	164	2	AW088899	AW088899	xd31g10.x	C1355	59	2.6	176	1	AL719759	AL719759	AL719759
C1283	59	2.6	164	2	AW409775	AW409775	fh02c10.y	1356	59	2.6	176	2	BF337479	BF337479	602035215
C1284	59	2.6	164	2	BE963918	BE963918	601657690	C1357	59	2.6	176	4	BI002842	BI002842	MR3-HN016
C1285	59	2.6	164	6	CB083541	CB083541	hp99c04.b	1358	59	2.6	176	6	CD679051	CD679051	hq03h07.y
C1286	59	2.6	164	6	CF209989	CF209989	CAB20005	1359	59	2.6	177	1	AI364788	AI364788	qu18f06.x
C1287	59	2.6	164	6	CF211607	CF211607	CGF100066	C1360	59	2.6	177	1	AI919345	AI919345	tu57c07.x
C1288	59	2.6	164	7	CN269469	CN269469	170005999	C1361	59	2.6	177	2	AW088903	AW088903	xd31h03.x
C1289	59	2.6	165	2	AW088944	AW088944	xd32f02.x	C1362	59	2.6	177	2	AW151714	AW151714	xf68c08.x
C1290	59	2.6	165	2	AW089006	AW089006	xd34b08.x	C1363	59	2.6	177	4	BG027628	BG027628	602296211
1291	59	2.6	165	5	BU778029	BU778029	SJEDQF06	1364	59	2.6	177	5	BQ894953	BQ894953	AGENCOURT
C1292	59	2.6	165	6	CA669317	CA669317	wlsul.pk0	C1365	59	2.6	177	6	CA668992	CA668992	wlsul.pk0
C1293	59	2.6	165	6	CB258462	CB258462	05-E01084	C1366	59	2.6	177	6	CB978729	CB978729	CAB40006
1294	59	2.6	166	2	BE666175	BE666175	149455 MA	C1367	59	2.6	177	6	CF313976	CF313976	HD--02-F0
1295	59	2.6	166	5	BU770824	BU770824	SJEDAC12	C1368	59	2.6	178	1	AI537617	AI537617	tp05d10.x
1296	59	2.6	166	6	CA598254	CA598254	wyr1c.pk0	C1369	59	2.6	178	1	AI680498	AI680498	tw63f03.x
C1297	59	2.6	166	6	CD394052	CD394052	Gm_ck1368	C1370	59	2.6	178	6	CF215957	CF215957	CAST0002
C1298	59	2.6	166	6	CF315606	CF315606	HD--04-J1	C1371	59	2.6	179	1	AI004911	AI004911	ou59f04.x
C1299	59	2.6	167	1	AI679550	AI679550	tu64e06.x	C1372	59	2.6	179	2	AW193203	AW193203	xl71g07.x
C1300	59	2.6	167	6	CB970037	CB970037	CAB10003	C1373	59	2.6	179	4	BG995885	BG995885	MR4-HT127
C1301	59	2.6	168	1	AI642413	AI642413	vt01g03.x	1374	59	2.6	179	5	BX956705	BX956705	DKFZp781M
C1302	59	2.6	168	1	AL589450	AL589450	DKFZp451A	C1375	59	2.6	179	7	CO732676	CO732676	SL1L01b03
C1303	59	2.6	168	2	AW681728	AW681728	EST00446	C1376	59	2.6	180	1	AI499974	AI499974	tn69a11.x
C1304	59	2.6	168	6	CA672154	CA672154	wlsu2.pk0	C1377	59	2.6	180	1	AI698427	AI698427	tx65b10.x
C1305	59	2.6	168	6	CA672564	CA672564	wlsu2.pk0	C1378	59	2.6	180	1	AI699011	AI699011	wc62f07.x
C1306	59	2.6	168	6	CB977323	CB977323	CAB40003	C1379	59	2.6	180	1	AJ465885	AJ465885	AJ465885
C1307	59	2.6	168	6	CD453325	CD453325	WHE1837 H	C1380	59	2.6	180	1	AJ484750	AJ484750	MR3-MT032
C1308	59	2.6	168	6	CF319725	CF319725	HD--10-F0	C1381	59	2.6	180	4	BI019323	BI019323	603394458
C1309	59	2.6	168	6	CF320327	CF320327	HD--11-C2	C1382	59	2.6	180	4	BI870913	BI870913	603394458
C1310	59	2.6	168	7	CK996023	CK996023	ip45d06.b	1383	59	2.6	180	4	BJ365372	BJ365372	BJ365372
C1311	59	2.6	169	2	AW834355	AW834355	MR2-TT001	C1384	59	2.6	180	6	CF291836	CF291836	14ROOF--0
C1312	59	2.6	169	4	BI019332	BI019332	PM0-GN040	C1385	59	2.6	180	7	CF511415	CF511415	CABud0002
C1313	59	2.6	169	4	BI054915	BI054915	PM0-GN040	C1386	59	2.6	180	7	CN281024	CN281024	170004182
C1314	59	2.6	169	6	CB083355	CB083355	hp96d06.b	C1387	59	2.6	181	1	AI567637	AI567637	tp62d02.x
C1315	59	2.6	170	1	AI471361	AI471361	tm10b02.x	C1388	59	2.6	181	1	AI569328	AI569328	tx79g08.x
C1316	59	2.6	170	4	BG956250	BG956250	QV1-CT075	C1389	59	2.6	181	1	AL715700	AL715700	AL715700
1317	59	2.6	170	4	BI840126	BI840126	fs69g08.y	C1390	59	2.6	181	1	AL728768	AL728768	AL728768
C1318	59	2.6	170	6	CA672361	CA672361	wlsu2.pk0	C1391	59	2.6	181	2	BF814541	BF814541	MR2-CI018
C1319	59	2.6	170	6	CA673140	CA673140	wlsu2.pk0	C1392	59	2.6	181	2	BF819891	BF819891	MR1-RT002
C1320	59	2.6	170	7	CN166093	CN166093	996952 MA	1393	59	2.6	181	4	BI322405	BI322405	kx20g08.y
1321	59	2.6	171	1	AL110306	AL110306	DKFZp564J	C1394	59	2.6	181	6	CA673433	CA673433	wlsu2.pk0
C1322	59	2.6	171	4	BG983789	BG983789	MR4-CN014	C1395	59	2.6	182	1	AI280661	AI280661	qu04d06.x
1323	59	2.6	171	4	BM806184	BM806184	AGENCOURT	C1396	59	2.6	182	2	BE061389	BE061389	QV0-BT022
C1324	59	2.6	171	6	CA673933	CA673933	wlsu2.pk0	1397	59	2.6	182	4	BI945309	BI945309	sb55a03.y
C1325	59	2.6	171	6	CA814433	CA814433	CA48LN09I	C1398	59	2.6	182	5	BX498199	BX498199	DKFZp779A
C1326	59	2.6	172	1	AI874151	AI874151	wm47h04.x	C1399	59	2.6	183	2	AW655696	AW655696	106893 MA
C1327	59	2.6	172	4	BI001560	BI001560	MR3-HN015	C1400	59	2.6	183	4	BGI13493	BGI13493	602283943
C1328	59	2.6	172	4	BI024603	BI024603	CM3-MT035	C1401	59	2.6	183	4	BI002841	BI002841	MR3-HN016
C1329	59	2.6	172	6	CA672333	CA672333	wlsu2.pk0	1402	59	2.6	183	4	BM532520	BM532520	fy09b06.y
C1330	59	2.6	172	6	CB080221	CB080221	hp83b10.b	C1403	59	2.6	183	6	CA674841	CA674841	wlsu2.pk0
1331	59	2.6	172	7	CN833173	CN833173	AGENCOURT	C1404	59	2.6	183	6	CB982353	CB982353	CAB70006
C1332	59	2.6	173	2	BF915537	BF915537	MR3-UT012	C1405	59	2.6	183	6	CF213724	CF213724	CGF100080
C1333	59	2.6	173	2	AW078729	AW078729	xb33b08.x	C1406	59	2.6	183	6	CF299110	CF299110	7LEAF--02
1334	59	2.6	173	2	AW478711	AW478711	21056 MAR	C1407	59	2.6	184	1	AI254727	AI254727	qt89c08.x
C1335	59	2.6	173	4	BG294062	BG294062	602390924	C1408	59	2.6	184	1	AI783861	AI783861	tr29c08.x
C1336	59	2.6	173	4	BG991159	BG991159	MR2-HT118	C1409	59	2.6	184	4	BG260144	BG260144	602371240
C1337	59	2.6	173	6	CA673926	CA673926	wlsu2.pk0	1410	59	2.6	184	5	BQ918566	BQ918566	AGENCOURT
1338	59	2.6	173	6	CB084519	CB084519	hq16f08.b	C1411	59	2.6	184	6	CA751858	CA751858	UI-M-FD0-

c1412	59	2.6	184	6	CD976164	CD976164	QAF13f04.
c1413	59	2.6	184	6	CF278819	CF278819	14ETL--04
c1414	59	2.6	184	6	CF291719	CF291719	14ROOT--0
1415	59	2.6	184	7	CK654106	CK654106	AGENCOURT
c1416	59	2.6	185	1	AI269580	AI269580	qv88h06.x
c1417	59	2.6	185	1	AI661538	AI661538	va52e04.x
c1418	59	2.6	185	2	BF913616	BF913616	NR3-UT012
c1419	59	2.6	185	2	AW091413	AW091413	583023E06
1420	59	2.6	185	5	BU777475	BU777475	SJEDKH02
c1421	59	2.6	186	1	AA807088	AA807088	OC31b05.s
c1422	59	2.6	186	1	AI784028	AI784028	to29c02.x
1423	59	2.6	186	4	BG058039	BG058039	nah19g05.
c1424	59	2.6	186	6	CA672968	CA672968	wlsu2.pk0
c1425	59	2.6	186	6	CA721881	CA721881	wdslc.pk0
c1426	59	2.6	186	6	CF213954	CF213954	CGF100081
c1427	59	2.6	186	7	CF511816	CF511816	CABud0002
c1428	59	2.6	187	1	AI566630	AI566630	tr77e03.x
c1429	59	2.6	187	1	AI633300	AI633300	ts66c07.x
c1430	59	2.6	187	2	AW085373	AW085373	wy62h02.x
c1431	59	2.6	187	2	AW633150	AW633150	bl04c12.x
c1432	59	2.6	187	4	BG981718	BG981718	MR3-CN014
c1433	59	2.6	187	4	BI001562	BI001562	MR3-HN015
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c1435	59	2.6	187	6	CA305591	CA305591	hasp015xp
c1436	59	2.6	187	6	CA674872	CA674872	wlsu2.pk0
c1437	59	2.6	187	6	CB044804	CB044804	NISC_gc06
1438	59	2.6	187	6	CB079501	CB079501	hp72C05.b
c1439	59	2.6	187	6	CB981961	CB981961	CAB70005
c1440	59	2.6	188	1	AI696819	AI696819	wc74c12.x
c1441	59	2.6	188	1	AI865334	AI865334	wn1ld11.x
c1442	59	2.6	188	1	AI867042	AI867042	wn14h02.x
c1443	59	2.6	188	2	BF816455	BF816455	MR2-CI012
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1445	59	2.6	188	2	AW317368	AW317368	sg48e01.y
c1446	59	2.6	188	6	CA673383	CA673383	wlsu2.pk0
c1447	59	2.6	188	7	CF516171	CF516171	CAP0002.I
c1448	59	2.6	189	1	AI610645	AI610645	tp20c10.x
c1449	59	2.6	189	1	AJ798430	AJ798430	AJ798430
c1450	59	2.6	189	1	AL719240	AL719240	AL719240
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c1452	59	2.6	189	2	BF816785	BF816785	MR2-CI012
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c1454	59	2.6	189	6	CB973436	CB973436	CAB30003
c1455	59	2.6	189	6	CB978351	CB978351	CAB40005
c1456	59	2.6	190	1	AI607808	AI607808	ub58e05.x
c1457	59	2.6	190	1	AI698437	AI698437	tx65c12.x
c1458	59	2.6	190	1	AI952302	AI952302	wx50h02.x
1459	59	2.6	190	2	AW308312	AW308312	3777 MARC
c1460	59	2.6	190	2	AW983822	AW983822	RC3-HN000
1461	59	2.6	190	4	BI941977	BI941977	se21g07.y
1462	59	2.6	190	4	BM091602	BM091602	sag99a06.
c1463	59	2.6	190	5	BX484808	BX484808	DKF2p686I
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c1481	59	2.6	192	6	CA722022	CA722022	wdslc.pk0
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c1483	59	2.6	193	1	AI648684	AI648684	tx64g10.x
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c1489	59	2.6	194	2	AW168031	AW168031	xg58h09.x
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ALIGNMENTS							
2105 bp mRNA linear HTC 21-JUL-2004							
CR610360 full-length cDNA clone CS0DN001YK12 of Adult brain of Homo sapiens (human).							
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LOCUS							
DEFINITION							
ACCESSION							
VERSION							
KEYWORDS							
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ORGANISM							
REFERENCE							
AUTHORS							
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AUTHORS							
TITLE							
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FEATURES							
source							
ORIGIN							
Query Match							
Best Local Similarity							
Matches 2101; Conservative							
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QY 160 GAGGTTGGAAAGTTGCTAGAGGCTTCAGAACTCCAGCCCTAATGGATCCCAAACTCGGGA 219
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QY 400 TGCCTCGCTTCAGACAAAGAGCTCTTCAGAATGATGGCCGTGGCTGCGGACACGCTGCAGC 459
Db 361 TGCCTCGCTTCAGACAAAGAGCTCTTCAGAATGATGGCCGTGGCTGCGGACACGCTGCAGC 420
QY 460 GCCTGGGGGCCCTGTGGCCTCGGTGGACATGGGTCTCAGCAGTGCCTCCGATGGTTCAGA 519
Db 421 GCCTGGGGGCCCTGTGGCCTCGGTGGACATGGGTCTCAGCAGTGCCTCCGATGGTTCAGA 480
QY 520 GTCTTCCAAATACCTCCCATCATCCTGGCCGAACTGGGAGCGATCCACGAAAGGCACCG 579
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QY 580 TGTGCTTCTACGGCCACTTGGACGTGCAGCCTGCTGACCCGGGGCGATGGGTGGCTCACGG 639
Db 541 TGTGCTTCTACGGCCACTTGGACGTGCAGCCTGCTGACCCGGGGCGATGGGTGGCTCACGG 600
QY 640 ACCCCTATGTCTGACGAGGTAGACGGGAACTTTATGGACGAGGAGCGACCGACAACA 699
Db 601 ACCCCTATGTCTGACGAGGTAGACGGGAACTTTATGGACGAGGAGCGACCGACAACA 660
QY 700 AAGGCCCTGTCTTGGCTGGATCAATGCTGTGAGCGCCTTCAGAGCCCTGGAGCAAGATC 759
Db 661 AAGGCCCTGTCTTGGCTGGATCAATGCTGTGAGCGCCTTCAGAGCCCTGGAGCAAGATC 720
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QY 1660 GGAACTACATAGAGGGAACCAAAATATTGTTGCTGCTTTTCTTAGAGATGGCCCCAGCTCC 1719
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QY 1960 GCAACTTGATTTCCCAAGTCTGTGCAATAGCCCCAGGATTGGATTCCCTTCCAACTTT 2019
Db 1921 GCAACTTGATTTCCCAAGTCTGTGCAATAGCCCCAGGATTGGATTCCCTTCCAACTTT 1980
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QY 2080 CTCAAGTGTCTGTGACACATATCATTCATCCAATGATCGCCTTTGCTTTACCACTCTT 2139
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QY 2140 TCCTT 2144
Db 2101 TCCTT 2105

RESULT 2
BC004271
LOCUS
DEFINITION
BC004271
Homo sapiens carnosine dipeptidase 1 (metallopeptidase M20 family),
mRNA (cdna clone IMAGE:3614507), with apparent retained intron.
ACCESSION
BC004271
VERSION
BC004271.1
KEYWORDS
HTC.
Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1528)
REFERENCE
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaby,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalusz,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1528)
Strausberg,R.
Direct Submission
Submitted (01-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angélique Schnerch, Ursula Skalska,
Duane Smalusz, Jeff Stott, Miranda Tsai, George Yang, Jacques
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 13 Row: f Column: 3
This clone has the following problem: retained intron.
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Matches 1425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 756 GATCTTCGTGAATCAAAATTCATCATTTAGGGGATGGAAGAGGCTGCTGTGGCC 815
|||||

Db 80 GATCTTCGTGAATATCAAAATTCATCATTTAGGGGATGGAAGAGGCTGCTGTGGCC 139
QY 816 CTGGAGGAACCTTGTGGAAAAAGAAAAGGACCGAATCTTCTCTGGTGTGGACTACATTGTA 875
|||||
Db 140 CTGGAGGAACCTTGTGGAAAAAGAAAAGGACCGAATCTTCTCTGGTGTGGACTACATTGTA 199
QY 876 ATTTTCAGATAACCTGTGGATCAGCCAAAAGGAAGCCAGCAATCACCTTATGGAACCCGGGG 935
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QY 996 GGTGGCATCCTTCATGAACCAATGGCTGATCTGGTTGCTCTTCTCGGTAGCCTGGTAGAC 1055
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Db 380 TCGTCTGGTCATATCCTCGTGGTCCCTGGAATCTATGATGAAGTGGTTCCTCTTACAGAAAGAG 439
QY 1116 GAAATAAATACATACAAAAGCCATCCATCTAGACCTAGAAAGAAATACCGGAATAGCAGCCGG 1175
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Db	1280	TGCAGCAACTTGATTTCCCCAAGTCCTGTGCAATAGCCCCAGGATTGGATTCCTTCCAAC	1339
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QY	2136	TCTTTCCCTTTTATCTTATTAATAAAAAATGTTGGTCTCCACCACTG	2180
Db	1460	TCTTTCCCTTTTATCTTATTAATAAAAAATGTTGGTCTCCACCACTG	1504
RESULT 3			
BX453730/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
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AUTHORS			
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JOURNAL			
COMMENT			
FEATURES			
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Query Match			
Best Local Similarity			
Matches			
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Query			
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AAGGCACCGTGTGCTTCTACGGCCACTTTGGACGTCGACGCCTGTGACCCGGGCGGATGGGT			
606			
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607			
AAGGCACCGTGTGCTTCTACGGCCACTTTGGACGTCGACGCCTGTGACCCGGGCGGATGGGT			
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TCTTCTCTGTTGGACTACA			
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TCTTCTCTGTTGGACTACA			
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620			
TCTTCTCTGTTGGACTACA			
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AAGGCACCGTGTGCTTCTACGGCCACTTTGGACGTCGACGCCTGTGACCCGGGCGGATGGGT			
622			
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623			
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634			
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635			
AAGGCACCGTGTGCTTCTACGGCCACTTTGGACGTCGACGCCTGTGACCCGGGCGGATGGGT			
636			
TCTTCTCTGTTGGACTACA			
637			
AAGGCACCGTGTGCTTCTACGGCCACTTTGGACGTCGACGCCTGTGACCCGGGCGGATGGGT			
638			
TCTTCTCTGTTGGACTACA			
639			
AAGGCACCGTGTGCTTCTACGGCCACTTTGGACGTCGACGCCTGTGACCCGGGCGGATGGGT			
640			
TCTTCTCTGTTGGACTACA			
641			
AAGGCACCGTGTGCTTCTACGGCCACTTTGGACGTCGACGCCTGTGACCCGGGCGGATGGGT			
642			
TCTTCTCTGTTGGACTACA			
643			
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644			
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AAGGCACCGTGTGCTTCTACGGCCACTTTGGACGTCGACGCCTGTGACCCGGGCGGATGGGT			
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651			
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652			
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653			
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655			
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657			
AAGGCACCGTGTGCTTCTACGGCCACTTTGGACGTCGACGCCTGTGACCCGGGCGGATGGGT			
658			
TCTTCTCTGTTGGACTACA			
659			

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
This sequence belongs to sequence cluster 9111.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BA069ZA11_CS06609_1&c=9111.f

FEATURES

source
Location/Qualifiers
1. .928
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN001YK12"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 30.6%; Score 687; DB 5; Length 928;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 924 GGAACCCGGGGAAACAGCTACTTTCATGGTGGAGGTGAAATGCAGAGACCAGGATTTTCAC 983
|||||
Db 76 GGAACCCGGGGAAACAGCTACTTTCATGGTGGAGGTGAAATGCAGAGACCAGGATTTTCAC 135
|||||

QY 984 TCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGGCTGATCTGGTTGCTCTCTCGGT 1043
|||||
Db 136 TCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGGCTGATCTGGTTGCTCTCTCGGT 195
|||||

QY 1044 AGCCTGGTAGACTCGTCTGGTCATATCCTGGTCCCTGGAATCTATGATGAAGTGTTCCT 1103
|||||
Db 196 AGCCTGGTAGACTCGTCTGGTCATATCCTGGTCCCTGGAATCTATGATGAAGTGTTCCT 255
|||||

QY 1104 CTTACAGAAGAGGAAATAAATACATACAAAGCCATCCATCTAGACCTAGAGAATACCGG 1163
|||||
Db 256 CTTACAGAAGAGGAAATAAATACATACAAAGCCATCCATCTAGACCTAGAGAATACCGG 315
|||||

QY 1164 AATAGCAGCCGGTTGAGAAATTTCTGTTTCGATACTAAGGAGGAGATTCTAATGCACCTC 1223
|||||
Db 316 AATAGCAGCCGGTTGAGAAATTTCTGTTTCGATACTAAGGAGGAGATTCTAATGCACCTC 375
|||||

QY 1224 TGGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGGCGCGTGTGATGAGCCTGGAAC 1283
|||||
Db 376 TGGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGGCGCGTGTGATGAGCCTGGAAC 435
|||||

QY 1284 AAAACAGTCATACCTGGCGGAGTTATAGGAAAAATTTCAATCCGTCTAGTCCCTCACATG 1343
|||||
Db 436 AAAACAGTCATACCTGGCGGAGTTATAGGAAAAATTTCAATCCGTCTAGTCCCTCACATG 495
|||||

QY 1344 AATGTGTCTGCGGTGAAAAACAGGTGACACGACATCTTGAAGATGTGTTCTCCAAAAGA 1403
|||||
Db 496 AATGTGTCTGCGGTGAAAAACAGGTGACACGACATCTTGAAGATGTGTTCTCCAAAAGA 555
|||||

QY 1404 AATAGTTCCAAACAGATGGTTGTTTCCATGACTTAGGACTACACCCGTTGGAATGCAA 1463
|||||
Db 556 AATAGTTCCAAACAGATGGTTGTTTCCATGACTTAGGACTACACCCGTTGGAATGCAA 615
|||||

QY 1464 ATTGATGACACCCAGTATCTCGCAGCAAAAAGCGCATCAGAACAGTGTGGAACAGAA 1523
|||||
Db 616 ATTGATGACACCCAGTATCTCGCAGCAAAAAGCGCATCAGAACAGTGTGGAACAGAA 675
|||||

QY 1524 CCAGATATGATCCGGATGGATCCACCATTCCAATTGCCAAAATGTTCCAGGAGATCGTC 1583
|||||
Db 676 CCAGATATGATCCGGATGGATCCACCATTCCAATTGCCAAAATGTTCCAGGAGATCGTC 735
|||||

QY 1584 CACAAGAGCGTGGTCTAATTCGCTG 1610
|||||

Db 736 CACAAGAGCGTGTGCTAATTCCGCTG 762

RESULT 5
BI754224
LOCUS
DEFINITION BI754224 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5196053 5', mRNA linear EST 25-SEP-2001
mRNA sequence.
ACCESSION BI754224 GI:15745802
VERSION BI754224.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 799)
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
http://image.llnl.gov
Plate: LLAM11490 row: 1 column: 06
High quality sequence stop: 797.

FEATURES
Location/Qualifiers
1. .799
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5196053"
/lab_host="DH10B"
/clone_lib="NIH_MGC_114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 30.3%; Score 679; DB 4; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 TGCTGCTGCTGCTGGAGCGGCGCATGTTCTCCTCACCCCTCCCCCGCCCGCGCTGT 303
|||||
Db 94 TGCTGCTGCTGCTGGAGCGGCGCATGTTCTCCTCACCCCTCCCCCGCCCGCGCTGT 153
|||||

QY 304 TAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAG 363
|||||

Db 154 TAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAG 213
|||||

QY 364 AGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCCTGTGCCTCGCTTCAGACAAGAGCTCT 423
|||||

Db 214 AGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCCTGTGCCTCGCTTCAGACAAGAGCTCT 273
|||||

QY 424 TCAGAAATGATGCGCGTGGCTGCGGACACGCTGCAGCGCCTGGGGGCCCGTGTGGCCTCGG 483
|||||

Db 274 TCAGAAATGATGCGCGTGGCTGCGGACACGCTGCAGCGCCTGGGGGCCCGTGTGGCCTCGG 333
|||||

QY 484 TGGACATGGTCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCATCC 543
|||||

Db 334 TGGACATGGTCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCATCC 393
|||||

Db 152 CTTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTTTTGGAGGTTGGAAAGTTGCTAGA 211

Qy 181 GGCTTCAGAACTCCAGCCCTAATGGATCCCAAACTCGGAGAAATGGTGCCTCGCTGG 240

Db 212 GGCTTCAGAACTCCAGCCCTAATGGATCCCAAACTCAGGAAATGGTGCCTCGCTGG 271

Qy 241 CTGTGCTGTGCTGTGCTGGAGCGGGCATGTTCTCCCTCACCCCTCCCGCCCGCGCGC 300

Db 272 CTGTGCTGTGCTGTGCTGGAGCGGGCATGTTCTCCCTCACCCCTCCCGCCCGCGCGC 331

Qy 301 TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA 360

Db 332 TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA 391

Qy 361 AGGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAGAGC 420

Db 392 AGGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAGAGC 451

Qy 421 TCTTCAGAAATGATGGCCGTGGTGGGACACGCTGCAGCGCCTGGGGGCCCGTGTGGCCT 480

Db 452 TCTTCAGAAATGATGGCCGTGGTGGGACACGCTGCAGCGCCTGGGGGCCCGTGTGGCCT 511

Qy 481 CGGTGGACATGGTTCCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCA 540

Db 512 CGGTGGACATGGTTCCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCA 571

Qy 541 TCCTGGCCGAACCTGGGGAGCGATCCCACGAAAGGCACCGTGTGCTTACGGCCACTTGG 600

Db 572 TCCTGGCCGAACCTGGGGAGCGATCCCACGAAAGGCACCGTGTGCTTACGGCCACTTGG 631

Qy 601 ACGTGCAGCCTGCTGACCGGGCGGATGGGTGGCTCACGGACCC 643

Db 632 ACGTGCAGCCTGCTGACCGGGCGGATGGGTGGCTCACGGACCC 674

RESULT 9

BM691429

LOCUS

DEFINITION

UI-E-C11-abe-d-05-0-UI.r1 UI-E-C11 Homo sapiens cDNA clone

UI-E-C11-abe-d-05-0-UI 5', mRNA sequence.

ACCESSION

BM691429

VERSION

BM691429.1 GI:19004687

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 602)

BONALDO,M.F., LENNON,G. and SOARES,M.B.

Normalization and subtraction: two approaches to facilitate gene discovery

AUTHORS

Genome Res. 6 (9), 791-806 (1996)

TITLE

Genome Res. 6 (9), 791-806 (1996)

JOURNAL

97044477

MEDLINE

8889548

PUBMED

CONTACT: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).

Seq primer: M13 Reverse.

Location/Qualifiers

1. .602

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

FEATURES

source

/clone="UI-E-C11-abe-d-05-0-UI"

/tissue_type="RPE and Choroid"

/dev_stage="adult"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-E-C11"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-C11 is a normalized cDNA library containing the following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Query Match 25.7%; Score 577; DB 4; Length 602;

Best Local Similarity 100.0%; Pred. No. 1e-270;

Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1554 CCAATTGCCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTCTAATTCGCTGGGA 1613

Db 8 CCAATTGCCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTCTAATTCGCTGGGA 67

Qy 1614 GCTGTTGATGATGGAGAACATTCCGAGAAATGAGAAAATCAACAGGTGGAACTACATAGAG 1673

Db 68 GCTGTTGATGATGGAGAACATTCCGAGAAATGAGAAAATCAACAGGTGGAACTACATAGAG 127

Qy 1674 GGAACCAAATATTGCTGCCTTTTCTTAGAGATGGCCCAGCTCCATTATCACAAGAA 1733

Db 128 GGAACCAAATATTGCTGCCTTTTCTTAGAGATGGCCCAGCTCCATTATCACAAGAA 187

Qy 1734 CCTTCTAGTCTGATCTGATCCACTGACAGATTCACTCCCCCACATCCCTAGACAGGGAT 1793

Db 188 CCTTCTAGTCTGATCTGATCCACTGACAGATTCACTCCCCCACATCCCTAGACAGGGAT 247

Qy 1794 GGAATGTAAAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTCCCTTCCATTAAAA 1853

Db 248 GGAATGTAAAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTCCCTTCCATTAAAA 307

Qy 1854 TGTCTTGGGATATCTGGATCAGTAATAAAATATTTCAAAGGCACAGATGTTGGAATGGT 1913

Db 308 TGTCTTGGGATATCTGGATCAGTAATAAAATATTTCAAAGGCACAGATGTTGGAATGGT 367

Qy 1914 TTAAGGTCCCCCACTGCACACCTTCTCAAGTCATAGTGTGCTGCAGCAACTTGATTTC 1973

Db 368 TTAAGGTCCCCCACTGCACACCTTCTCAAGTCATAGTGTGCTGCAGCAACTTGATTTC 427

Qy 1974 CCAAGTCTGTGCAATAGCCCCCAGGATTTGGATTCTTCCAACTTTTAGCATATCTCCAA 2033

Db 428 CCAAGTCTGTGCAATAGCCCCCAGGATTTGGATTCTTCCAACTTTTAGCATATCTCCAA 487

Qy 2034 CTTTGCAATTGATTGGCATAATCACTCCGGTTTGTCTTCTAGGTCCTCAAGTGTCTG 2093

Db 488 CTTTGCAATTGATTGGCATAATCACTCCGGTTTGTCTTCTAGGTCCTCAAGTGTCTG 547

Qy 2094 ACACATAATCATTCATCCATCCAATGATCGCCTTTTGCTTT 2130

Db 548 ACACATAATCATTCATCCATCCAATGATCGCCTTTTGCTTT 584

RESULT 10

BI489508

LOCUS

DEFINITION

603032068F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173289 5', mRNA sequence.

Query Match 25.7%; Score 576; DB 1; Length 742;
Best Local Similarity 100.0%; Pred. No. 3.1e-270; Mismatches 0; Indels 0; Gaps 0;
Matches 576; Conservative 0;

QY 1288 CAGTCATACCTGGCCGAGTTATAGGAAAAATTTTCAATCCGCTCTAGTCCCTCACAATG 1347
|||||
Db 609 CAGTCATACCTGGCCGAGTTATAGGAAAAATTTTCAATCCGCTCTAGTCCCTCACAATG 550
|||||

QY 1348 TGTCTGCGGTGGAAAAACAGGTGACACGACATCTTGAAGATGTGTTCTCCAAAAAGAAATA 1407
|||||
Db 549 TGTCTGCGGTGGAAAAACAGGTGACACGACATCTTGAAGATGTGTTCTCCAAAAAGAAATA 490
|||||

QY 1408 GTTCCAAACAAGATGGTTGTTTCCATGACTCTAGGACTACACCCGTGGATTGCAATATTG 1467
|||||
Db 489 GTTCCAAACAAGATGGTTGTTTCCATGACTCTAGGACTACACCCGTGGATTGCAATATTG 430
|||||

QY 1468 ATGACACCCAGTATCTCGCAGCAAAAAGACCGATCAGAACAGTGTGTTGGAACAGAACCCAG 1527
|||||
Db 429 ATGACACCCAGTATCTCGCAGCAAAAAGACCGATCAGAACAGTGTGTTGGAACAGAACCCAG 370
|||||

QY 1528 ATATGATCCGGATGGATCCACCAATTCCAATTGCCAAATGTTCCAGGAGATCGTCCACA 1587
|||||
Db 369 ATATGATCCGGATGGATCCACCAATTCCAATTGCCAAATGTTCCAGGAGATCGTCCACA 310
|||||

QY 1588 AGAGCGTGGTCTTAATTCGCTGGGAGCTGTTGATGATGGAGAACATTCGCAGAATGAGA 1647
|||||
Db 309 AGAGCGTGGTCTTAATTCGCTGGGAGCTGTTGATGATGGAGAACATTCGCAGAATGAGA 250
|||||

QY 1648 AAATCAACAGGTGGAACACTACATAGAGGGAACCAAAATTAATTTGCTGCTTTTCTTAGAGA 1707
|||||
Db 249 AAATCAACAGGTGGAACACTACATAGAGGGAACCAAAATTAATTTGCTGCTTTTCTTAGAGA 190
|||||

QY 1708 TGGCCAGCTCCATTAATCACAAGAACCTTCTAGTCTGATCTGATCCACTGACAGATTCA 1767
|||||
Db 189 TGGCCAGCTCCATTAATCACAAGAACCTTCTAGTCTGATCTGATCCACTGACAGATTCA 130
|||||

QY 1768 CCTCCCCACATCCTTAGACAGGGATGGAATGTAAATATCCAGAGAAATTTGGGTCTAGTA 1827
|||||
Db 129 CCTCCCCACATCCTTAGACAGGGATGGAATGTAAATATCCAGAGAAATTTGGGTCTAGTA 70
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QY 1828 TAGTACATTTTCCCTCCATTTAAAAATGCTTTGGGA 1863
|||||
Db 69 TAGTACATTTTCCCTCCATTTAAAAATGCTTTGGGA 34
|||||

RESULT 12
BM669584/c
LOCUS
DEFINITION
UI-E-DX1-agw-i-19-0-UI.s1 UI-E-DX1 Homo sapiens cDNA clone
UI-E-DX1-agw-i-19-0-UI 3', mRNA sequence.
ACCESSION
BM669584
VERSION
BM669584.1 GI:18979481
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 630)
AUTHORS
Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
PUBMED
8889548
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman

cdNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cdNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
Location/Qualifiers
1. .630
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-DX1-agw-i-19-0-UI"
/tissue_type="fetal eyes"
/dev_stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-DX1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-DX1 is a normalized cdNA library containing the
following tissue(s): fetal eyes. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cdNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cdNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cdNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
AGAATCAAGA. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
Institute (NEI).
TAG_TISSUE=human fetal eyes
TAG_LIB=UI-E-DX1
TAG_SEQ=AGAATCAAGA"

ORIGIN

Query Match 25.4%; Score 570; DB 4; Length 630;
Best Local Similarity 100.0%; Pred. No. 2.7e-267; Mismatches 0; Indels 0; Gaps 0;
Matches 570; Conservative 0;

QY 1605 CCGCTGGGAGCTGTTGATGATGGAGAACATTCGCAGAATGAGAAAAATCAACAGGTGGAAC 1664
|||||
Db 587 CCGCTGGGAGCTGTTGATGATGGAGAACATTCGCAGAATGAGAAAAATCAACAGGTGGAAC 528
|||||

QY 1665 TACATAGAGGGAAACCAATTATTGCTGCCTTTTCTTAGAGATGGCCCAGTCCATTAA 1724
|||||
Db 527 TACATAGAGGGAAACCAATTATTGCTGCCTTTTCTTAGAGATGGCCCAGTCCATTAA 468
|||||

QY 1725 TCACAAGAACCTTCTAGTCTGATCTGATCCACTGACAGATTACACCTCCCCACATCCCTA 1784
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Db 467 TCACAAGAACCTTCTAGTCTGATCTGATCCACTGACAGATTACACCTCCCCACATCCCTA 408
|||||

QY 1785 GACAGGGATGGAATGTAAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTC 1844
|||||
Db 407 GACAGGGATGGAATGTAAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTC 348
|||||

QY 1845 CATTTAAAAATGCTTTGGGATATCTGGATCAGTAATAAATATTTCAAAGGCACAGATGTT 1904
|||||
Db 347 CATTTAAAAATGCTTTGGGATATCTGGATCAGTAATAAATATTTCAAAGGCACAGATGTT 288
|||||

QY 1905 GGAAATGGTTAAAGGTCCCCCACTGCACACCTTCTCAAGTCATAGCTGCTTGCAGCAAC 1964
|||||
Db 287 GGAAATGGTTAAAGGTCCCCCACTGCACACCTTCTCAAGTCATAGCTGCTTGCAGCAAC 228
|||||

QY 1965 TTGATTTCCCCAAGTCTGTGCAATAGCCCCCAGGATTGGATTCTTCCAACCTTTTAGCA 2024
|||||
Db 227 TTGATTTCCCCAAGTCTGTGCAATAGCCCCCAGGATTGGATTCTTCCAACCTTTTAGCA 168
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1 (bases 1 to 567)
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
TITLE Human Unigeneset - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998G204957.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGGAACAGCTATGAC.

FEATURES
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T 3']; double-stranded cDNA was ligated to Eco RI
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the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 8e-266;
Matches 567; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 (bases 1 to 887)
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AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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THI SHIP
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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SUMMARIES

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172	57	2.5	1248	4	US-09-489-847-101	Sequence 101, App	245	57	2.5	10660	3	US-09-041-886-16	Sequence 16, Appl
173	57	2.5	1297	4	US-09-800-729-80	Sequence 80, Appl	246	57	2.5	10660	3		

247	56	2.5	56	4	US-09-621-976-12139	Sequence 12139, A	C 320	56	2.5	91	4	US-09-338-933-201	Sequence 201, App
248	56	2.5	56	4	US-09-621-976-14556	Sequence 14556, A	C 321	56	2.5	91	4	US-09-215-681-201	Sequence 201, App
249	56	2.5	57	4	US-09-621-976-11970	Sequence 11970, A	C 322	56	2.5	91	4	US-09-621-976-14925	Sequence 14925, A
250	56	2.5	57	4	US-09-621-976-13937	Sequence 13937, A	C 323	56	2.5	91	4	US-09-216-003A-201	Sequence 201, App
251	56	2.5	58	4	US-09-621-976-14827	Sequence 14827, A	C 324	56	2.5	91	4	US-09-667-857-201	Sequence 201, App
252	56	2.5	59	4	US-09-621-976-13084	Sequence 13084, A	325	56	2.5	92	4	US-09-621-976-14689	Sequence 14689, A
253	56	2.5	59	4	US-09-621-976-13752	Sequence 13752, A	C 326	56	2.5	94	4	US-09-404-879A-261	Sequence 261, App
254	56	2.5	60	3	US-09-457-959-8	Sequence 8, Appli	C 327	56	2.5	94	4	US-09-338-933-261	Sequence 261, App
255	56	2.5	60	4	US-09-621-976-12480	Sequence 12480, A	C 328	56	2.5	94	4	US-09-215-681-261	Sequence 261, App
256	56	2.5	60	4	US-09-621-976-13761	Sequence 13761, A	C 329	56	2.5	94	4	US-09-216-003A-261	Sequence 261, App
257	56	2.5	60	4	US-09-621-976-14742	Sequence 14742, A	C 330	56	2.5	94	4	US-09-667-857-261	Sequence 261, App
258	56	2.5	60	4	US-09-621-976-14884	Sequence 14884, A	331	56	2.5	97	4	US-09-621-976-12430	Sequence 12430, A
259	56	2.5	60	4	US-10-079-178-8	Sequence 8, Appli	332	56	2.5	98	1	US-08-088-658-42	Sequence 42, Appli
260	56	2.5	61	4	US-09-621-976-14680	Sequence 14680, A	333	56	2.5	98	2	US-08-471-907A-42	Sequence 42, Appli
261	56	2.5	61	4	US-09-621-976-14681	Sequence 14681, A	334	56	2.5	98	4	US-09-621-976-11744	Sequence 11744, A
262	56	2.5	61	4	US-09-621-976-14799	Sequence 14799, A	335	56	2.5	98	4	US-09-621-976-12160	Sequence 12160, A
263	56	2.5	61	4	US-09-621-976-14834	Sequence 14834, A	336	56	2.5	98	4	US-09-621-976-15091	Sequence 15091, A
264	56	2.5	61	4	US-09-621-976-14948	Sequence 14948, A	337	56	2.5	100	4	US-09-621-976-12774	Sequence 12774, A
265	56	2.5	62	4	US-09-621-976-11091	Sequence 11091, A	C 338	56	2.5	101	4	US-09-404-879A-293	Sequence 293, App
266	56	2.5	62	4	US-09-621-976-14130	Sequence 14130, A	C 339	56	2.5	101	4	US-09-338-933-293	Sequence 293, App
267	56	2.5	62	4	US-09-621-976-14936	Sequence 14936, A	C 340	56	2.5	101	4	US-09-215-681-293	Sequence 293, App
268	56	2.5	63	4	US-09-621-976-13480	Sequence 13480, A	C 341	56	2.5	101	4	US-09-216-003A-293	Sequence 293, App
269	56	2.5	63	4	US-09-621-976-13842	Sequence 13842, A	C 342	56	2.5	101	4	US-09-667-857-293	Sequence 293, App
270	56	2.5	63	4	US-09-621-976-14756	Sequence 14756, A	343	56	2.5	102	4	US-09-621-976-11436	Sequence 11436, A
271	56	2.5	64	4	US-09-621-976-14858	Sequence 14858, A	344	56	2.5	102	4	US-09-621-976-14804	Sequence 14804, A
272	56	2.5	65	4	US-09-621-976-14743	Sequence 14743, A	C 345	56	2.5	105	3	US-09-284-627-23	Sequence 23, Appli
273	56	2.5	65	4	US-09-621-976-14853	Sequence 14853, A	346	56	2.5	105	4	US-09-621-976-13820	Sequence 13820, A
274	56	2.5	66	4	US-09-621-976-12404	Sequence 12404, A	347	56	2.5	111	3	US-09-297-535-23	Sequence 23, Appli
275	56	2.5	66	4	US-09-621-976-14819	Sequence 14819, A	348	56	2.5	111	4	US-09-621-976-14677	Sequence 14677, A
276	56	2.5	67	4	US-09-621-976-11909	Sequence 11909, A	349	56	2.5	117	1	US-08-702-344-3	Sequence 3, Appli
277	56	2.5	67	4	US-09-621-976-13917	Sequence 13917, A	350	56	2.5	121	3	US-09-297-535-20	Sequence 20, Appli
278	56	2.5	67	4	US-09-621-976-14753	Sequence 14753, A	351	56	2.5	123	4	US-09-621-976-12330	Sequence 12330, A
279	56	2.5	68	4	US-09-621-976-11613	Sequence 11613, A	352	56	2.5	130	4	US-09-621-976-12892	Sequence 12892, A
280	56	2.5	68	4	US-09-621-976-11912	Sequence 11912, A	353	56	2.5	138	4	US-09-621-976-9595	Sequence 9595, Ap
281	56	2.5	68	4	US-09-621-976-12005	Sequence 12005, A	354	56	2.5	140	1	US-08-628-417-5	Sequence 5, Appli
282	56	2.5	69	1	US-08-702-344-7	Sequence 7, Appli	C 355	56	2.5	141	3	US-08-737-078A-1	Sequence 1, Appli
283	56	2.5	69	4	US-09-621-976-12006	Sequence 12006, A	C 356	56	2.5	141	5	PCT-US94-04706-1	Sequence 1, Appli
284	56	2.5	69	4	US-09-621-976-14105	Sequence 14105, A	357	56	2.5	144	1	US-08-702-344-26	Sequence 26, Appli
285	56	2.5	69	4	US-09-621-976-14869	Sequence 14869, A	358	56	2.5	145	4	US-09-621-976-16688	Sequence 16688, A
286	56	2.5	70	4	US-09-621-976-13579	Sequence 13579, A	359	56	2.5	145	4	US-09-621-976-16691	Sequence 16691, A
287	56	2.5	70	4	US-09-621-976-14750	Sequence 14750, A	360	56	2.5	146	4	US-09-621-976-16115	Sequence 16115, A
288	56	2.5	71	4	US-09-621-976-14905	Sequence 14905, A	361	56	2.5	146	4	US-09-621-976-16686	Sequence 16686, A
289	56	2.5	72	4	US-09-621-976-9837	Sequence 9837, Ap	362	56	2.5	146	4	US-09-621-976-16695	Sequence 16695, A
290	56	2.5	72	4	US-09-621-976-10145	Sequence 10145, A	363	56	2.5	147	4	US-09-621-976-10383	Sequence 10383, A
291	56	2.5	72	4	US-09-621-976-14815	Sequence 14815, A	364	56	2.5	148	4	US-09-621-976-17447	Sequence 17447, A
292	56	2.5	72	4	US-09-621-976-14842	Sequence 14842, A	365	56	2.5	148	4	US-09-621-976-17450	Sequence 17450, A
293	56	2.5	72	4	US-09-621-976-15064	Sequence 15064, A	366	56	2.5	153	4	US-09-621-976-17451	Sequence 17451, A
294	56	2.5	73	4	US-09-621-976-14729	Sequence 14729, A	367	56	2.5	156	4	US-09-621-976-9095	Sequence 9095, Ap
295	56	2.5	73	4	US-09-621-976-14963	Sequence 14963, A	368	56	2.5	159	4	US-09-621-976-17448	Sequence 17448, A
296	56	2.5	75	4	US-09-621-976-12516	Sequence 12516, A	369	56	2.5	160	4	US-09-621-976-18071	Sequence 18071, A
297	56	2.5	75	4	US-09-621-976-14892	Sequence 14892, A	370	56	2.5	162	4	US-09-621-976-18068	Sequence 18068, A
298	56	2.5	76	4	US-09-621-976-12446	Sequence 12446, A	371	56	2.5	166	4	US-09-621-976-18390	Sequence 18390, A
299	56	2.5	76	4	US-09-621-976-14831	Sequence 14831, A	372	56	2.5	179	4	US-09-621-976-18054	Sequence 18054, A
300	56	2.5	76	4	US-09-621-976-14915	Sequence 14915, A	373	56	2.5	185	4	US-09-621-976-16779	Sequence 16779, A
C 301	56	2.5	77	4	US-08-956-171E-2883	Sequence 2883, Ap	374	56	2.5	188	4	US-09-621-976-10364	Sequence 10364, A
302	56	2.5	77	4	US-09-621-976-14176	Sequence 14176, A	375	56	2.5	189	4	US-09-621-976-14761	Sequence 14761, A
303	56	2.5	77	4	US-08-781-986A-2883	Sequence 2883, Ap	376	56	2.5	193	4	US-09-621-976-10543	Sequence 10543, A
304	56	2.5	78	4	US-09-621-976-14824	Sequence 14824, A	377	56	2.5	194	4	US-09-621-976-9596	Sequence 9596, Ap
305	56	2.5	78	4	US-09-621-976-15092	Sequence 15092, A	378	56	2.5	194	4	US-09-621-976-15317	Sequence 15317, A
306	56	2.5	79	4	US-09-621-976-15090	Sequence 15090, A	379	56	2.5	195	4	US-09-621-976-15314	Sequence 15314, A
307	56	2.5	81	4	US-09-621-976-13152	Sequence 13152, A	380	56	2.5	196	4	US-09-442-054A-42	Sequence 42, Appli
308	56	2.5	81	4	US-09-513-999C-17324	Sequence 17324, A	C 381	56	2.5	196	4	US-09-442-054A-42	Sequence 42, Appli
309	56	2.5	83	4	US-09-621-976-14751	Sequence 14751, A	382	56	2.5	204	4	US-09-621-976-1323	Sequence 1323, Ap
310	56	2.5	83	4	US-09-621-976-14959	Sequence 14959, A	383	56	2.5	213	4	US-09-621-976-16536	Sequence 16536, A
311	56	2.5	84	1	US-08-664-596B-3	Sequence 3, Appli	384	56	2.5	214	4	US-09-621-976-9843	Sequence 9843, Ap
312	56	2.5	84	1	US-08-738-367-3	Sequence 3, Appli	385	56	2.5	215	4	US-09-621-976-15321	Sequence 15321, A
313	56	2.5	84	4	US-09-621-976-14571	Sequence 14571, A	C 386	56	2.5	227	2	US-08-520-678A-28	Sequence 28, Appli
314	56	2.5	84	4	US-09-621-976-14577	Sequence 14577, A	C 387	56	2.5	227	3	US-08-897-126-28	Sequence 28, Appli
315	56	2.5	85	4	US-09-621-976-13395	Sequence 13395, A	388	56	2.5	231	4	US-09-621-976-16317	Sequence 16317, A
316	56	2.5	85	4	US-09-621-976-14949	Sequence 14949, A	389	56	2.5	231	4	US-09-621-976-16456	Sequence 16456, A
317	56	2.5	89	4	US-09-621-976-14749	Sequence 14749, A	390	56	2.5	232	4	US-09-621-976-17701	Sequence 17701, A
318	56	2.5	89	4	US-09-621-976-14974	Sequence 14974, A	391	56	2.5	233	4	US-09-621-976-16559	Sequence 16559, A
C 319	56	2.5	91	4	US-09-404-879A-201	Sequence 201, App	392	56	2.5	234	4	US-09-621-976-16557	Sequence 16557, A

393	56	2.5	235	4	US-09-621-976-16550	Sequence 16550, A	466	56	2.5	496	4	US-10-140-002-533	Sequence 533, App
394	56	2.5	240	1	US-08-628-417-6	Sequence 6, Appli	467	56	2.5	530	4	US-09-461-325-28	Sequence 28, Appl
395	56	2.5	240	4	US-09-621-976-1324	Sequence 1324, Ap	468	56	2.5	530	4	US-10-012-542-28	Sequence 28, Appl
396	56	2.5	242	4	US-09-621-976-16320	Sequence 16320, A	469	56	2.5	530	4	US-10-115-123-28	Sequence 28, Appl
397	56	2.5	242	4	US-09-621-976-16324	Sequence 16324, A	470	56	2.5	536	1	US-08-341-568-1	Sequence 1, Appli
398	56	2.5	246	4	US-09-621-976-13617	Sequence 13617, A	471	56	2.5	536	2	US-08-911-020-1	Sequence 1, Appli
399	56	2.5	246	4	US-09-621-976-16288	Sequence 16288, A	472	56	2.5	550	4	US-09-010-147B-5	Sequence 5, Appli
400	56	2.5	249	4	US-09-621-976-1322	Sequence 1322, Ap	473	56	2.5	552	4	US-09-461-325-111	Sequence 111, App
401	56	2.5	249	4	US-09-621-976-16291	Sequence 16291, A	474	56	2.5	552	4	US-10-012-542-111	Sequence 111, App
402	56	2.5	249	4	US-09-621-976-16292	Sequence 16292, A	475	56	2.5	552	4	US-10-115-123-111	Sequence 111, App
403	56	2.5	250	4	US-09-621-976-18893	Sequence 18893, A	476	56	2.5	554	4	US-09-696-169A-14	Sequence 14, Appl
C 404	56	2.5	253	2	US-08-520-678A-25	Sequence 25, Appl	477	56	2.5	570	1	US-07-885-970A-10	Sequence 10, Appl
C 405	56	2.5	253	3	US-08-897-126-25	Sequence 25, Appl	478	56	2.5	570	1	US-08-298-887A-10	Sequence 10, Appl
406	56	2.5	255	4	US-09-621-976-9406	Sequence 9406, Ap	479	56	2.5	570	1	US-08-298-829-10	Sequence 10, Appl
407	56	2.5	258	4	US-09-621-976-15353	Sequence 15353, A	480	56	2.5	572	3	US-09-342-653-5	Sequence 5, Appli
408	56	2.5	259	4	US-09-621-976-16294	Sequence 16294, A	C 481	56	2.5	609	1	US-08-530-797-9	Sequence 9, Appli
C 409	56	2.5	260	2	US-08-520-678A-29	Sequence 29, Appl	C 482	56	2.5	609	2	US-08-787-335-9	Sequence 9, Appli
C 410	56	2.5	266	3	US-08-897-126-29	Sequence 29, Appl	483	56	2.5	612	4	US-09-270-767-11643	Sequence 11643, A
411	56	2.5	266	4	US-09-621-976-16813	Sequence 16813, A	484	56	2.5	664	4	US-09-904-615-66	Sequence 66, Appl
412	56	2.5	269	4	US-09-621-976-16936	Sequence 16936, A	485	56	2.5	675	4	US-09-621-976-2461	Sequence 2461, Ap
C 413	56	2.5	270	2	US-08-520-678A-30	Sequence 30, Appl	486	56	2.5	711	4	US-09-621-976-17854	Sequence 17854, A
C 414	56	2.5	270	3	US-08-897-126-30	Sequence 30, Appl	487	56	2.5	730	4	US-09-270-767-14600	Sequence 14600, A
415	56	2.5	272	4	US-09-621-976-16932	Sequence 16932, A	488	56	2.5	746	3	US-09-013-810-1	Sequence 1, Appli
416	56	2.5	282	4	US-09-621-976-18648	Sequence 18648, A	489	56	2.5	748	1	US-08-361-467B-3	Sequence 3, Appli
417	56	2.5	283	4	US-09-621-976-16989	Sequence 16989, A	490	56	2.5	748	1	US-08-484-332C-3	Sequence 3, Appli
418	56	2.5	289	1	US-08-341-568-3	Sequence 3, Appli	491	56	2.5	755	4	US-10-140-002-153	Sequence 153, App
419	56	2.5	289	2	US-08-911-020-3	Sequence 3, Appli	492	56	2.5	763	4	US-09-743-207-3	Sequence 3, Appli
420	56	2.5	293	4	US-09-621-976-16965	Sequence 16965, A	493	56	2.5	773	4	US-09-149-476-20	Sequence 20, Appl
421	56	2.5	299	4	US-09-621-976-10211	Sequence 10211, A	494	56	2.5	783	4	US-10-140-002-321	Sequence 321, App
422	56	2.5	299	4	US-09-621-976-16226	Sequence 16226, A	C 495	56	2.5	789	3	US-09-020-956-32	Sequence 32, Appl
423	56	2.5	318	4	US-09-621-976-10247	Sequence 10247, A	C 496	56	2.5	789	3	US-09-030-607-32	Sequence 32, Appl
424	56	2.5	323	4	US-09-621-976-10374	Sequence 10374, A	C 497	56	2.5	789	3	US-09-439-313-32	Sequence 32, Appl
425	56	2.5	329	4	US-09-621-976-16012	Sequence 16012, A	C 498	56	2.5	789	3	US-09-352-616A-32	Sequence 32, Appl
426	56	2.5	332	4	US-09-621-976-16031	Sequence 16031, A	C 499	56	2.5	789	4	US-09-232-149A-32	Sequence 32, Appl
427	56	2.5	332	4	US-09-621-976-16050	Sequence 16050, A	C 500	56	2.5	789	4	US-09-159-812-32	Sequence 32, Appl
428	56	2.5	332	4	US-09-621-976-16053	Sequence 16053, A	C 501	56	2.5	789	4	US-09-636-215-32	Sequence 32, Appl
429	56	2.5	333	4	US-09-621-976-16032	Sequence 16032, A	C 502	56	2.5	789	4	US-09-685-166A-32	Sequence 32, Appl
430	56	2.5	333	4	US-09-621-976-16045	Sequence 16045, A	C 503	56	2.5	789	4	US-09-115-453-32	Sequence 32, Appl
431	56	2.5	334	4	US-09-621-976-16044	Sequence 16044, A	C 504	56	2.5	789	4	US-09-688-489-32	Sequence 32, Appl
432	56	2.5	335	4	US-09-621-976-16061	Sequence 16061, A	C 505	56	2.5	789	4	US-09-679-426-32	Sequence 32, Appl
433	56	2.5	336	4	US-09-621-976-16013	Sequence 16013, A	506	56	2.5	795	4	US-09-270-767-14068	Sequence 14068, A
434	56	2.5	338	4	US-09-621-976-16041	Sequence 16041, A	507	56	2.5	796	1	US-08-104-073-2	Sequence 2, Appli
435	56	2.5	341	4	US-09-621-976-16135	Sequence 16135, A	508	56	2.5	812	4	US-09-091-097-7	Sequence 7, Appli
436	56	2.5	347	4	US-09-621-976-16026	Sequence 16026, A	C 509	56	2.5	844	4	US-09-690-942-3	Sequence 3, Appli
437	56	2.5	351	4	US-09-621-976-15134	Sequence 15134, A	510	56	2.5	903	5	PCT-US95-06406A-21	Sequence 21, Appl
438	56	2.5	357	4	US-09-621-976-16058	Sequence 16058, A	511	56	2.5	941	4	US-09-205-258-186	Sequence 186, App
439	56	2.5	358	4	US-09-621-976-927	Sequence 927, App	512	56	2.5	958	2	US-08-757-046A-5	Sequence 5, Appli
440	56	2.5	359	4	US-09-621-976-16008	Sequence 16008, A	513	56	2.5	958	3	US-09-447-208-5	Sequence 5, Appli
441	56	2.5	359	4	US-09-621-976-16019	Sequence 16019, A	514	56	2.5	958	3	US-09-135-988-5	Sequence 5, Appli
442	56	2.5	362	4	US-09-621-976-16010	Sequence 16010, A	515	56	2.5	958	3	US-09-277-716-5	Sequence 5, Appli
443	56	2.5	365	4	US-09-621-976-16042	Sequence 16042, A	516	56	2.5	958	3	US-08-597-274A-5	Sequence 5, Appli
C 444	56	2.5	396	4	US-09-640-173-10	Sequence 10, Appl	517	56	2.5	958	4	US-08-908-909-5	Sequence 5, Appli
C 445	56	2.5	396	4	US-09-640-173-16	Sequence 16, Appl	518	56	2.5	958	4	US-09-609-161B-5	Sequence 5, Appli
C 446	56	2.5	396	4	US-09-640-173-33	Sequence 33, Appl	519	56	2.5	958	4	US-08-990-103-5	Sequence 5, Appli
C 447	56	2.5	396	4	US-09-640-173-42	Sequence 42, Appl	520	56	2.5	958	4	US-09-746-485A-5	Sequence 5, Appli
C 448	56	2.5	396	4	US-09-640-173-53	Sequence 53, Appl	521	56	2.5	958	4	US-10-126-139-5	Sequence 5, Appli
C 449	56	2.5	396	4	US-09-713-550-10	Sequence 10, Appl	522	56	2.5	958	4	US-10-126-798-5	Sequence 5, Appli
C 450	56	2.5	396	4	US-09-713-550-16	Sequence 16, Appl	523	56	2.5	958	4	US-10-126-777-5	Sequence 5, Appli
C 451	56	2.5	396	4	US-09-713-550-33	Sequence 33, Appl	524	56	2.5	966	1	US-08-514-014-7	Sequence 7, Appli
C 452	56	2.5	396	4	US-09-713-550-42	Sequence 42, Appl	525	56	2.5	966	2	US-08-833-823-7	Sequence 7, Appli
C 453	56	2.5	396	4	US-09-713-550-53	Sequence 53, Appl	526	56	2.5	976	2	US-08-504-459-9	Sequence 9, Appli
C 454	56	2.5	396	4	US-09-825-294-10	Sequence 10, Appl	527	56	2.5	981	4	US-09-780-717-4	Sequence 4, Appli
C 455	56	2.5	396	4	US-09-825-294-16	Sequence 16, Appl	528	56	2.5	990	4	US-09-800-729-79	Sequence 79, Appl
C 456	56	2.5	396	4	US-09-825-294-33	Sequence 33, Appl	529	56	2.5	991	3	US-08-924-747-25	Sequence 25, Appl
C 457	56	2.5	396	4	US-09-825-294-42	Sequence 42, Appl	530	56	2.5	991	3	US-09-247-373B-25	Sequence 25, Appl
C 458	56	2.5	396	4	US-09-825-294-53	Sequence 53, Appl	531	56	2.5	991	3	US-09-296-715-25	Sequence 25, Appl
C 459	56	2.5	396	4	US-09-970-966-10	Sequence 10, Appl	532	56	2.5	997	4	US-09-907-794A-376	Sequence 376, App
C 460	56	2.5	396	4	US-09-970-966-16	Sequence 16, Appl	533	56	2.5	997	4	US-09-905-125A-376	Sequence 376, App
C 461	56	2.5	396	4	US-09-970-966-33	Sequence 33, Appl	534	56	2.5	997	4	US-09-902-775A-376	Sequence 376, App
C 462	56	2.5	396	4	US-09-970-966-42	Sequence 42, Appl	535	56	2.5	997	4	US-09-906-700-376	Sequence 376, App
C 463	56	2.5	396	4	US-09-970-966-53	Sequence 53, Appl	536	56	2.5	997	4	US-09-903-603A-376	Sequence 376, App
C 464	56	2.5	467	2	US-08-841-349-18	Sequence 18, Appl	C 537	56	2.5	1020	4	US-09-328-475C-43	Sequence 43, Appl
C 465	56	2.5	467	4	US-09-431-184A-18	Sequence 18, Appl	538	56	2.5	1024	4	US-09-328-475C-50	Sequence 50, Appl

539	56	1034	4	US-09-311-021-105	Sequence 105, App	612	56	2.5	1503	4	US-09-906-700-220	Sequence 220, App
540	56	1037	4	US-09-489-847-112	Sequence 112, App	613	56	2.5	1503	4	US-10-140-002-363	Sequence 363, App
541	56	1039	4	US-09-464-535-23	Sequence 23, Appl	614	56	2.5	1503	4	US-09-903-603A-220	Sequence 220, App
542	56	1048	4	US-09-489-847-38	Sequence 38, Appl	615	56	2.5	1505	2	US-08-909-965C-13	Sequence 13, Appl
543	56	1051	3	US-09-245-041-10	Sequence 10, Appl	616	56	2.5	1507	4	US-09-453-323-1	Sequence 1, Appl
544	56	1051	4	US-09-358-055B-10	Sequence 10, Appl	617	56	2.5	1508	3	US-09-039-046-1	Sequence 1, Appl
545	56	1051	4	US-09-893-238-10	Sequence 10, Appl	618	56	2.5	1509	4	US-09-149-476-179	Sequence 179, App
546	56	1052	4	US-09-489-847-23	Sequence 23, Appl	619	56	2.5	1510	4	US-10-140-002-399	Sequence 399, App
547	56	1057	4	US-09-716-129-16	Sequence 16, Appl	620	56	2.5	1522	3	US-09-413-574-1	Sequence 1, Appl
548	56	1069	3	US-09-372-422A-7	Sequence 7, Appl	621	56	2.5	1534	1	US-08-300-903A-6	Sequence 6, Appl
549	56	1074	3	US-09-248-335-67	Sequence 67, Appl	622	56	2.5	1534	4	US-08-988-197-6	Sequence 6, Appl
550	56	1075	3	US-08-400-006B-6	Sequence 6, Appl	623	56	2.5	1534	4	US-10-385-072-6	Sequence 6, Appl
551	56	1091	4	US-09-328-965-1	Sequence 1, Appl	624	56	2.5	1540	3	US-08-977-001-2	Sequence 2, Appl
552	56	1100	3	US-07-861-458C-4	Sequence 4, Appl	625	56	2.5	1544	4	US-09-187-999-14	Sequence 14, Appl
553	56	1114	4	US-09-152-060-41	Sequence 41, Appl	626	56	2.5	1546	4	US-09-901-151-1	Sequence 1, Appl
554	56	1117	3	US-09-247-373B-33	Sequence 33, Appl	627	56	2.5	1578	3	US-09-416-050A-1	Sequence 1, Appl
555	56	1123	4	US-09-152-060-15	Sequence 15, Appl	628	56	2.5	1578	3	US-09-664-800-1	Sequence 1, Appl
556	56	1129	3	US-09-227-357-40	Sequence 40, Appl	629	56	2.5	1578	3	US-09-665-309-1	Sequence 1, Appl
557	56	1133	4	US-09-916-204-1	Sequence 1, Appl	630	56	2.5	1578	3	US-09-661-569-1	Sequence 1, Appl
558	56	1133	4	US-10-282-048-1	Sequence 1, Appl	631	56	2.5	1582	3	US-08-545-196B-10	Sequence 10, Appl
559	56	1138	4	US-09-800-729-44	Sequence 44, Appl	632	56	2.5	1582	3	US-08-545-196B-12	Sequence 12, Appl
560	56	1141	4	US-09-800-729-78	Sequence 78, Appl	633	56	2.5	1604	1	US-08-665-966-9	Sequence 9, Appl
561	56	1147	1	US-08-665-716-1	Sequence 1, Appl	634	56	2.5	1604	3	US-09-041-780-9	Sequence 1, Appl
562	56	1153	4	US-09-149-476-41	Sequence 41, Appl	635	56	2.5	1606	4	US-09-820-004-1	Sequence 1, Appl
563	56	1154	3	US-08-651-136C-7	Sequence 7, Appl	636	56	2.5	1618	4	US-09-800-729-29	Sequence 29, Appl
564	56	1154	3	US-09-229-911A-7	Sequence 7, Appl	637	56	2.5	1633	4	US-10-140-002-217	Sequence 217, App
565	56	1166	5	PCT-US96-12129B-1	Sequence 1, Appl	638	56	2.5	1641	1	US-08-300-903A-8	Sequence 8, Appl
566	56	1172	1	US-07-945-288-9	Sequence 9, Appl	639	56	2.5	1641	4	US-08-988-197-8	Sequence 8, Appl
567	56	1172	1	US-08-462-831-9	Sequence 9, Appl	640	56	2.5	1641	4	US-10-385-072-8	Sequence 8, Appl
568	56	1172	1	US-08-461-809-9	Sequence 9, Appl	641	56	2.5	1660	4	US-09-722-971-9	Sequence 9, Appl
569	56	1172	1	US-08-461-441-9	Sequence 9, Appl	642	56	2.5	1662	4	US-09-668-097A-13	Sequence 13, Appl
570	56	1172	5	PCT-US93-08518-9	Sequence 1, Appl	643	56	2.5	1696	4	US-09-835-811-1	Sequence 1, Appl
571	56	1174	2	US-08-872-437-1	Sequence 1, Appl	644	56	2.5	1700	2	US-08-897-340-4	Sequence 4, Appl
572	56	1174	3	US-08-651-136C-11	Sequence 11, Appl	645	56	2.5	1700	3	US-09-252-329-4	Sequence 4, Appl
573	56	1174	3	US-09-229-911A-11	Sequence 11, Appl	646	56	2.5	1736	3	US-09-182-816-22	Sequence 22, Appl
574	56	1190	4	US-09-390-207-1	Sequence 1, Appl	647	56	2.5	1736	3	US-09-182-816-24	Sequence 24, Appl
575	56	1193	3	US-09-372-422A-23	Sequence 23, Appl	648	56	2.5	1736	3	US-09-471-528-22	Sequence 22, Appl
576	56	1198	3	US-09-248-335-27	Sequence 27, Appl	649	56	2.5	1736	3	US-09-471-528-24	Sequence 24, Appl
577	56	1201	4	US-09-461-325-36	Sequence 36, Appl	650	56	2.5	1736	3	US-09-634-530-22	Sequence 22, Appl
578	56	1201	4	US-10-012-542-36	Sequence 36, Appl	651	56	2.5	1736	3	US-09-634-530-24	Sequence 24, Appl
579	56	1201	4	US-10-115-123-36	Sequence 36, Appl	652	56	2.5	1738	2	US-08-379-482A-2	Sequence 2, Appl
580	56	1210	4	US-09-443-041A-29	Sequence 29, Appl	653	56	2.5	1738	4	US-09-918-909A-27	Sequence 27, Appl
581	56	1273	4	US-09-270-767-14731	Sequence 14731, A	654	56	2.5	1740	4	US-09-709-103-45	Sequence 45, Appl
582	56	1279	3	US-09-248-335-25	Sequence 25, Appl	655	56	2.5	1740	4	US-09-439-410A-45	Sequence 45, Appl
583	56	1296	4	US-09-461-325-29	Sequence 29, Appl	656	56	2.5	1746	4	US-09-485-529-57	Sequence 57, Appl
584	56	1296	4	US-10-012-542-29	Sequence 29, Appl	657	56	2.5	1768	4	US-09-485-529-13	Sequence 13, Appl
585	56	1296	4	US-10-115-123-29	Sequence 29, Appl	658	56	2.5	1771	4	US-09-907-794A-158	Sequence 158, App
586	56	1315	3	US-09-164-193-1	Sequence 1, Appl	659	56	2.5	1771	4	US-09-866-028-36	Sequence 36, Appl
587	56	1315	4	US-09-221-448A-1	Sequence 1, Appl	660	56	2.5	1771	4	US-09-905-125A-158	Sequence 158, App
588	56	1325	1	US-08-306-691B-51	Sequence 51, Appl	661	56	2.5	1771	4	US-09-902-775A-158	Sequence 158, App
589	56	1325	2	US-08-464-517-1	Sequence 1, Appl	662	56	2.5	1771	4	US-09-906-700-158	Sequence 158, App
590	56	1325	2	US-08-246-361A-1	Sequence 1, Appl	663	56	2.5	1771	4	US-09-944-457-36	Sequence 36, Appl
591	56	1325	3	US-08-463-772-1	Sequence 1, Appl	664	56	2.5	1771	4	US-09-903-603A-158	Sequence 158, App
592	56	1325	5	PCT-US93-05000-1	Sequence 1, Appl	665	56	2.5	1780	3	US-09-202-548B-5	Sequence 5, Appl
593	56	1361	4	US-09-489-847-64	Sequence 64, Appl	666	56	2.5	1780	4	US-09-942-858-5	Sequence 5, Appl
594	56	1378	4	US-09-149-476-208	Sequence 208, App	667	56	2.5	1781	4	US-09-818-512-1	Sequence 1, Appl
595	56	1383	4	US-09-735-846-1	Sequence 1, Appl	668	56	2.5	1798	3	US-09-797-906-1	Sequence 1, Appl
596	56	1406	4	US-10-000-489-81	Sequence 81, Appl	669	56	2.5	1801	4	US-09-709-103-3	Sequence 3, Appl
597	56	1411	3	US-08-964-127-5	Sequence 5, Appl	670	56	2.5	1801	4	US-09-439-410A-3	Sequence 3, Appl
598	56	1411	3	US-09-496-692-5	Sequence 5, Appl	671	56	2.5	1804	2	US-08-504-459-5	Sequence 5, Appl
599	56	1411	4	US-10-000-273-5	Sequence 5, Appl	672	56	2.5	1813	5	PCT-US94-12883-3	Sequence 3, Appl
600	56	1414	4	US-09-501-115-5	Sequence 5, Appl	673	56	2.5	1817	1	US-08-473-981A-5	Sequence 5, Appl
601	56	1447	4	US-09-443-041A-27	Sequence 27, Appl	674	56	2.5	1817	2	US-08-474-087-5	Sequence 5, Appl
602	56	1454	3	US-09-372-422A-19	Sequence 19, Appl	675	56	2.5	1835	3	US-09-485-549-1	Sequence 1, Appl
603	56	1454	4	US-09-614-912-63	Sequence 63, Appl	676	56	2.5	1842	4	US-09-482-273-90	Sequence 90, Appl
604	56	1461	3	US-08-722-126A-4	Sequence 4, Appl	677	56	2.5	1844	4	US-10-003-392-7	Sequence 7, Appl
605	56	1461	5	PCT-US95-04258-4	Sequence 4, Appl	678	56	2.5	1864	4	US-09-149-476-130	Sequence 130, App
606	56	1474	3	US-08-821-994-64	Sequence 64, Appl	679	56	2.5	1872	3	US-09-801-052-1	Sequence 1, Appl
607	56	1485	3	US-09-372-422A-39	Sequence 39, Appl	680	56	2.5	1872	4	US-10-020-121-1	Sequence 1, Appl
608	56	1492	4	US-09-369-247-23	Sequence 23, Appl	681	56	2.5	1878	4	US-09-465-558-39	Sequence 39, Appl
609	56	1503	4	US-09-907-794A-220	Sequence 220, App	682	56	2.5	1898	1	US-08-342-411A-1	Sequence 1, Appl
610	56	1503	4	US-09-905-125A-220	Sequence 220, App	683	56	2.5	1925	4	US-09-148-545-128	Sequence 128, App
611	56	1503	4	US-09-902-775A-220	Sequence 220, App	684	56	2.5	1927	4	US-09-336-536-66	Sequence 66, Appl

685	56	2.5	1958	4	US-08-665-034A-3	Sequence 3, Appli	758	56	2.5	2481	2	US-08-838-399-1	Sequence 1, Appli
686	56	2.5	1963	4	US-09-482-273-91	Sequence 91, Appl	759	56	2.5	2481	3	US-09-235-839-1	Sequence 1, Appli
687	56	2.5	1965	4	US-09-482-273-27	Sequence 27, Appl	760	56	2.5	2481	3	US-09-327-035-1	Sequence 1, Appli
688	56	2.5	1981	4	US-09-720-317A-3	Sequence 3, Appli	761	56	2.5	2483	4	US-09-205-258-68	Sequence 68, Appl
689	56	2.5	1985	4	US-10-140-002-143	Sequence 143, App	762	56	2.5	2485	4	US-09-889-463A-9	Sequence 9, Appli
690	56	2.5	2010	1	US-07-864-475A-4	Sequence 4, Appli	763	56	2.5	2527	4	US-09-244-805-29	Sequence 29, Appl
691	56	2.5	2010	2	US-08-468-249A-4	Sequence 4, Appli	764	56	2.5	2550	6	5258287-23	Patent No. 5258287
692	56	2.5	2026	2	US-08-993-228-3	Sequence 3, Appli	765	56	2.5	2589	3	US-08-569-749-1	Sequence 1, Appli
693	56	2.5	2065	3	US-09-370-473-5	Sequence 5, Appli	766	56	2.5	2589	5	PCT-US96-12860-1	Sequence 1, Appli
694	56	2.5	2091	4	US-09-813-818-1	Sequence 1, Appli	767	56	2.5	2604	2	US-08-630-118A-3	Sequence 3, Appli
695	56	2.5	2096	3	US-09-008-481A-10	Sequence 10, Appl	768	56	2.5	2604	2	US-08-838-399-3	Sequence 3, Appli
696	56	2.5	2096	3	US-09-195-666A-16	Sequence 16, Appl	769	56	2.5	2604	3	US-09-235-839-3	Sequence 3, Appli
697	56	2.5	2096	3	US-09-309-592-10	Sequence 10, Appl	770	56	2.5	2604	3	US-09-327-035-3	Sequence 3, Appli
698	56	2.5	2096	3	US-09-635-705-16	Sequence 16, Appl	771	56	2.5	2608	4	US-09-904-615-16	Sequence 16, Appl
699	56	2.5	2096	4	US-09-634-858A-16	Sequence 16, Appl	772	56	2.5	2625	4	US-09-270-767-10080	Sequence 10080, A
700	56	2.5	2096	4	US-08-869-927C-16	Sequence 16, Appl	773	56	2.5	2665	4	US-08-971-089-5	Sequence 5, Appli
701	56	2.5	2146	4	US-10-003-392-3	Sequence 3, Appli	774	56	2.5	2668	4	US-10-140-002-511	Sequence 511, App
702	56	2.5	2184	3	US-08-955-918C-1	Sequence 1, Appli	775	56	2.5	2671	6	5168051-9	Patent No. 5168051
703	56	2.5	2184	3	US-08-697-766A-1	Sequence 1, Appli	776	56	2.5	2674	3	US-09-817-180-1	Sequence 1, Appli
704	56	2.5	2187	3	US-09-127-219B-2	Sequence 2, Appli	777	56	2.5	2674	4	US-10-003-295-1	Sequence 1, Appli
705	56	2.5	2202	4	US-09-465-558-59	Sequence 59, Appl	778	56	2.5	2710	3	US-09-232-200-44	Sequence 44, Appl
706	56	2.5	2203	4	US-09-801-861-1	Sequence 1, Appli	779	56	2.5	2710	3	US-09-232-200-70	Sequence 70, Appl
707	56	2.5	2203	4	US-10-224-562-1	Sequence 1, Appli	780	56	2.5	2710	3	US-09-232-197-44	Sequence 44, Appl
708	56	2.5	2205	3	US-08-888-077A-41	Sequence 41, Appl	781	56	2.5	2710	3	US-09-232-197-70	Sequence 70, Appl
709	56	2.5	2218	4	US-09-016-434-1157	Sequence 1157, Ap	782	56	2.5	2710	3	US-09-232-201-44	Sequence 44, Appl
710	56	2.5	2218	4	US-09-205-258-103	Sequence 103, App	783	56	2.5	2710	3	US-09-232-201-70	Sequence 70, Appl
711	56	2.5	2218	4	US-10-329-668-7	Sequence 7, Appli	784	56	2.5	2710	4	US-09-232-195-44	Sequence 44, Appl
712	56	2.5	2230	3	US-08-378-313-24	Sequence 24, Appl	785	56	2.5	2710	4	US-09-232-195-70	Sequence 70, Appl
713	56	2.5	2233	1	US-08-496-631-1	Sequence 1, Appli	786	56	2.5	2744	3	US-09-071-101-1	Sequence 1, Appli
714	56	2.5	2239	3	US-09-196-390-1	Sequence 1, Appli	787	56	2.5	2744	3	US-09-369-617-1	Sequence 1, Appli
715	56	2.5	2239	4	US-09-952-677-1	Sequence 1, Appli	788	56	2.5	2744	3	US-09-369-617-1	Sequence 1, Appli
716	56	2.5	2262	4	US-09-311-021-171	Sequence 171, App	789	56	2.5	2790	3	US-08-800-291B-1	Sequence 1, Appli
717	56	2.5	2269	3	US-09-394-645-1	Sequence 1, Appli	790	56	2.5	2808	4	US-09-917-254-27	Sequence 27, Appl
718	56	2.5	2269	3	US-09-243-560B-1	Sequence 1, Appli	791	56	2.5	2808	4	US-09-917-254-27	Sequence 27, Appl
719	56	2.5	2271	4	US-09-205-258-243	Sequence 243, App	792	56	2.5	2845	4	US-10-140-002-207	Sequence 207, App
720	56	2.5	2276	4	US-09-205-258-183	Sequence 183, App	793	56	2.5	2908	4	US-09-904-615-35	Sequence 35, Appl
721	56	2.5	2280	3	US-08-813-150-1	Sequence 1, Appli	794	56	2.5	2968	3	US-09-813-819-1	Sequence 1, Appli
722	56	2.5	2280	4	US-09-546-553-1	Sequence 1, Appli	795	56	2.5	2968	3	US-09-813-819-1	Sequence 1, Appli
723	56	2.5	2285	2	US-08-967-101-136	Sequence 136, App	796	56	2.5	3200	1	US-08-444-405-1	Sequence 1, Appli
724	56	2.5	2285	2	US-08-592-541-136	Sequence 136, App	797	56	2.5	3200	1	US-08-384-850-1	Sequence 1, Appli
725	56	2.5	2285	3	US-09-124-698-136	Sequence 136, App	798	56	2.5	3214	1	US-08-484-105-17	Sequence 17, Appl
726	56	2.5	2285	3	US-09-127-480-136	Sequence 136, App	799	56	2.5	3214	1	US-08-484-106-17	Sequence 17, Appl
727	56	2.5	2285	3	US-09-124-523-136	Sequence 136, App	800	56	2.5	3334	4	US-09-668-119-2	Sequence 12, Appl
728	56	2.5	2285	4	US-09-636-796A-136	Sequence 136, App	801	56	2.5	3501	2	US-08-909-965C-7	Sequence 7, Appli
729	56	2.5	2291	4	US-09-220-132-114	Sequence 114, App	802	56	2.5	3527	2	US-08-909-965C-7	Sequence 7, Appli
730	56	2.5	2291	4	US-09-814-915A-95	Sequence 95, Appl	803	56	2.5	3581	2	US-08-738-349-1	Sequence 1, Appli
731	56	2.5	2301	3	US-09-232-191-8	Sequence 8, Appli	804	56	2.5	3715	4	US-09-234-245-1	Sequence 1, Appli
732	56	2.5	2301	3	US-09-232-200-8	Sequence 8, Appli	805	56	2.5	3871	2	US-08-599-455B-3	Sequence 3, Appli
733	56	2.5	2301	3	US-09-232-197-8	Sequence 8, Appli	806	56	2.5	3871	3	US-09-069-781B-3	Sequence 3, Appli
734	56	2.5	2301	3	US-09-232-201-8	Sequence 8, Appli	807	56	2.5	3871	3	US-09-137-132-3	Sequence 3, Appli
735	56	2.5	2301	4	US-09-232-195-8	Sequence 8, Appli	808	56	2.5	3871	4	US-08-864-564A-3	Sequence 3, Appli
736	56	2.5	2311	4	US-09-720-317A-19	Sequence 19, Appl	809	56	2.5	3871	4	US-09-094-410-3	Sequence 3, Appli
737	56	2.5	2312	4	US-09-103-331-1	Sequence 1, Appli	810	56	2.5	3871	4	US-08-708-123D-3	Sequence 3, Appli
738	56	2.5	2312	4	US-09-631-594-45	Sequence 45, Appl	811	56	2.5	3871	4	US-08-583-153A-3	Sequence 3, Appli
739	56	2.5	2320	3	US-09-202-904A-13	Sequence 13, Appl	812	56	2.5	3871	4	US-08-570-142D-3	Sequence 3, Appli
740	56	2.5	2323	4	US-09-149-476-24	Sequence 24, Appl	813	56	2.5	3871	4	US-08-638-524B-3	Sequence 3, Appli
741	56	2.5	2329	4	US-09-800-729-11	Sequence 11, Appl	814	56	2.5	3975	4	US-09-270-767-3	Sequence 3, Appli
742	56	2.5	2378	3	US-08-802-805D-20	Sequence 20, Appl	815	56	2.5	3994	4	US-09-738-946-7	Sequence 7, Appli
743	56	2.5	2378	4	US-08-860-370-1	Sequence 1, Appli	c	56	2.5	4055	4	US-09-620-312D-706	Sequence 706, App
744	56	2.5	2389	4	US-09-799-875-7	Sequence 7, Appli	816	56	2.5	4064	4	US-09-873-737A-3	Sequence 3, Appli
745	56	2.5	2394	4	US-09-800-729-33	Sequence 33, Appl	817	56	2.5	4239	4	US-09-815-048-1	Sequence 1, Appli
746	56	2.5	2407	3	US-09-370-807-7	Sequence 7, Appli	818	56	2.5	4456	3	US-09-095-443-1	Sequence 1, Appli
747	56	2.5	2407	4	US-09-921-259-7	Sequence 7, Appli	819	56	2.5	4895	3	US-09-053-866-1	Sequence 1, Appli
748	56	2.5	2409	3	US-09-293-322C-8	Sequence 8, Appli	820	56	2.5	4895	4	US-09-479-130-1	Sequence 1, Appli
749	56	2.5	2409	4	US-09-839-497A-8	Sequence 8, Appli	821	56	2.5	4895	4	US-09-472-130A-1	Sequence 1, Appli
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751	56	2.5	2431	2	US-08-456-241-25	Sequence 25, Appl	823	56	2.5	5554	4	US-09-815-923-1	Sequence 1, Appli
752	56	2.5	2431	2	US-08-456-201-25	Sequence 25, Appl	824	56	2.5	6065	4	US-09-800-729-35	Sequence 35, Appl
753	56	2.5	2431	5	PCT-US92-04295A-25	Sequence 25, Appl	825	56	2.5	6200	4	US-09-439-923-1	Sequence 1, Appli
754	56	2.5	2434	4	US-09-489-847-67	Sequence 67, Appl	826	56	2.5	6200	4	US-09-711-202A-1	Sequence 1, Appli
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833	56	2.5	6671	5	PCT-US95-02275-1	Sequence 1, Appli	906	54	2.4	1013	1	US-08-314-586-30	Sequence 30, Appl
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836	56	2.5	7859	2	US-08-450-905B-15	Sequence 15, Appl	909	54	2.4	1302	4	US-09-322-409-91	Sequence 91, Appl
837	56	2.5	7859	3	US-07-982-759F-15	Sequence 15, Appl	c	910	2.4	1302	4	US-09-322-409-93	Sequence 93, Appl
838	56	2.5	8607	4	US-10-204-708-72	Sequence 72, Appl	911	54	2.4	1302	4	US-09-451-527-91	Sequence 91, Appl
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841	56	2.5	9472	4	US-08-150-204E-96	Sequence 96, Appl	914	54	2.4	1395	3	US-09-295-306-1	Sequence 1, Appli
842	56	2.5	9589	1	US-07-925-695-1	Sequence 1, Appli	915	54	2.4	1395	4	US-09-734-719-1	Sequence 1, Appli
843	56	2.5	9589	1	US-07-925-695-2	Sequence 2, Appli	916	54	2.4	1705	4	US-09-205-258-216	Sequence 216, App
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846	55	2.5	55	4	US-09-621-976-14535	Sequence 14535, A	919	54	2.4	2311	4	US-09-614-912-91	Sequence 91, Appl
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858	55	2.5	474	3	US-08-516-859A-97	Sequence 97, Appl	931	53	2.4	82	4	US-09-621-976-11864	Sequence 11864, A
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860	55	2.5	474	4	US-09-528-706-97	Sequence 97, Appl	933	53	2.4	82	4	US-09-621-976-11944	Sequence 11944, A
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863	55	2.5	1181	4	US-09-149-476-310	Sequence 310, App	936	53	2.4	82	4	US-09-621-976-12088	Sequence 12088, A
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874	55	2.5	1934	4	US-09-909-326-1	Sequence 1, Appli	947	53	2.4	140	4	US-09-621-976-17449	Sequence 17449, A
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876	55	2.5	2331	4	US-09-944-457-54	Sequence 54, Appl	949	53	2.4	235	4	US-09-621-976-9455	Sequence 9455, Ap
877	55	2.5	2349	4	US-09-805-455-1	Sequence 1, Appli	950	53	2.4	244	4	US-09-621-976-484	Sequence 484, App
878	55	2.5	2797	4	US-09-482-273-74	Sequence 74, Appl	951	53	2.4	351	4	US-09-621-976-16140	Sequence 16140, A
879	55	2.5	2821	4	US-09-702-705-1669	Sequence 1669, Ap	952	53	2.4	443	4	US-09-621-976-17631	Sequence 17631, A
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881	55	2.5	2821	4	US-09-671-325-1669	Sequence 1669, Ap	954	53	2.4	872	3	US-09-248-335-63	Sequence 63, Appl
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883	55	2.5	3047	4	US-09-873-737A-1	Sequence 1, Appli	956	53	2.4	1315	3	US-09-721-822A-10	Sequence 10, Appl
884	55	2.5	5503	2	US-08-726-012B-1	Sequence 1, Appli	957	53	2.4	1375	4	US-09-489-847-120	Sequence 120, App
885	55	2.5	5503	4	US-09-023-655-989	Sequence 989, App	958	53	2.4	1376	4	US-09-489-847-66	Sequence 66, Appl
886	55	2.5	15450	4	US-09-470-661A-1	Sequence 1, Appli	959	53	2.4	1619	4	US-09-522-714-11	Sequence 11, Appl
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895	54	2.4	257	2	US-08-520-678A-24	Sequence 24, Appl	968	53	2.4	2648	3	US-09-348-942-6	Sequence 6, Appli
896	54	2.4	257	3	US-08-897-126-24	Sequence 24, Appl	969	53	2.4	2648	4	US-09-457-626-6	Sequence 6, Appli
897	54	2.4	298	4	US-09-621-976-3871	Sequence 3871, Ap	970	53	2.4	2648	4	US-09-576-008-6	Sequence 6, Appli
898	54	2.4	334	4	US-09-513-999C-22131	Sequence 22131, A	971	53	2.4	2674	4	US-10-066-130-19	Sequence 19, Appl
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c 978	53	2.4	12980	3	US-09-034-756-5	Sequence 5, Appli	1051	51	2.3	1728	3	US-08-985-950-7	Sequence 7, Appli
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982	52	2.3	81	4	US-09-621-976-12198	Sequence 12198, A	1055	51	2.3	1865	3	US-09-370-253-5	Sequence 5, Appli
983	52	2.3	81	4	US-09-621-976-13601	Sequence 13601, A	1056	51	2.3	1933	4	US-09-920-759-3	Sequence 3, Appli
984	52	2.3	85	4	US-09-621-976-14741	Sequence 14741, A	1057	51	2.3	1976	4	US-09-920-759-10	Sequence 10, Appl
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987	52	2.3	164	4	US-09-621-976-8070	Sequence 8070, Ap	1060	51	2.3	1998	3	US-09-232-201-68	Sequence 68, Appl
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993	52	2.3	347	4	US-09-621-976-16136	Sequence 16136, A	1066	51	2.3	2087	3	US-09-232-200-6	Sequence 6, Appli
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998	52	2.3	756	4	US-10-140-002-171	Sequence 171, App	1071	51	2.3	2475	4	US-10-140-002-195	Sequence 195, App
999	52	2.3	1050	4	US-09-482-273-58	Sequence 58, Appl	1072	51	2.3	2581	4	US-09-369-247-51	Sequence 51, Appl
1000	52	2.3	1184	4	US-09-489-847-76	Sequence 76, Appl	1073	51	2.3	3238	3	US-08-123-934A-5	Sequence 5, Appli
1001	52	2.3	1525	4	US-09-461-325-110	Sequence 110, App	1074	51	2.3	3238	4	US-09-874-628-5	Sequence 5, Appli
1002	52	2.3	1525	4	US-10-012-542-110	Sequence 110, App	1075	51	2.3	3238	5	PCT-US94-10080-5	Sequence 5, Appli
1003	52	2.3	1525	4	US-10-115-123-110	Sequence 110, App	1076	51	2.3	3375	3	US-09-511-625B-67	Sequence 67, Appl
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1005	52	2.3	1558	1	US-08-455-550-7	Sequence 7, Appli	1078	51	2.3	3912	3	US-09-115-954-1	Sequence 1, Appli
1006	52	2.3	1810	4	US-09-369-247-11	Sequence 11, Appl	1079	51	2.3	9646	3	US-08-111-566-1	Sequence 1, Appli
1007	52	2.3	1810	4	US-09-800-729-73	Sequence 73, Appl	1080	51	2.3	9646	3	US-09-034-756-1	Sequence 1, Appli
1008	52	2.3	1811	4	US-09-800-729-77	Sequence 77, Appl	1081	51	2.3	13584	4	US-09-991-258-17	Sequence 17, Appl
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1010	52	2.3	2202	4	US-09-396-149-3	Sequence 3, Appli	1083	50	2.2	50	4	US-09-621-976-14715	Sequence 14715, A
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1012	52	2.3	2719	4	US-09-650-284B-1	Sequence 1, Appli	1085	50	2.2	61	4	US-10-079-178-7	Sequence 7, Appli
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c1014	52	2.3	2836	3	US-08-747-221B-26	Sequence 26, Appl	c1087	50	2.2	90	1	US-08-677-944-1	Sequence 1, Appli
1015	52	2.3	2836	3	US-09-005-051-24	Sequence 24, Appl	c1088	50	2.2	90	1	US-08-677-944-2	Sequence 2, Appli
c1016	52	2.3	2836	3	US-09-005-051-26	Sequence 26, Appl	c1089	50	2.2	90	3	US-09-254-048A-1	Sequence 1, Appli
1017	52	2.3	2836	4	US-09-403-942F-24	Sequence 24, Appl	c1090	50	2.2	90	4	US-09-921-203-1	Sequence 1, Appli
c1018	52	2.3	2836	4	US-09-403-942F-26	Sequence 26, Appl	c1091	50	2.2	90	4	US-09-816-089A-2	Sequence 2, Appli
1019	52	2.3	2837	2	US-08-993-228-11	Sequence 11, Appl	c1092	50	2.2	90	4	US-10-106-832-1	Sequence 1, Appli
1020	52	2.3	3136	4	US-09-680-728-1	Sequence 1, Appli	c1093	50	2.2	93	4	US-09-816-089A-8	Sequence 8, Appli
1021	51	2.3	57	4	US-09-621-976-12150	Sequence 12150, A	c1094	50	2.2	100	3	US-08-991-789A-30	Sequence 30, Appl
1022	51	2.3	61	4	US-09-621-976-14754	Sequence 14754, A	c1095	50	2.2	100	3	US-09-062-451-30	Sequence 30, Appl
1023	51	2.3	63	4	US-09-621-976-12231	Sequence 12231, A	c1096	50	2.2	100	4	US-09-598-326-30	Sequence 30, Appl
1024	51	2.3	75	4	US-09-621-976-15073	Sequence 15073, A	c1097	50	2.2	100	4	US-09-289-198-30	Sequence 30, Appl
c1025	51	2.3	90	3	US-09-065-058-16	Sequence 16, Appl	c1098	50	2.2	100	4	US-09-429-755-30	Sequence 30, Appl
1026	51	2.3	157	4	US-09-621-976-16781	Sequence 16781, A	1099	50	2.2	104	4	US-09-621-976-9392	Sequence 9392, Ap
1027	51	2.3	327	4	US-09-621-976-16141	Sequence 16141, A	1100	50	2.2	105	2	US-08-735-381-2	Sequence 2, Appli
1028	51	2.3	335	4	US-09-621-976-16038	Sequence 16038, A	1101	50	2.2	105	3	US-09-183-619-1	Sequence 1, Appli
c1029	51	2.3	356	2	US-08-520-678A-22	Sequence 22, Appl	1102	50	2.2	105	3	US-09-201-674-2	Sequence 2, Appli
c1030	51	2.3	356	2	US-08-897-126-22	Sequence 22, Appl	1103	50	2.2	184	4	US-09-621-976-12893	Sequence 12893, A
1031	51	2.3	371	4	US-09-621-976-16048	Sequence 16048, A	c1104	50	2.2	271	2	US-08-731-272A-29	Sequence 29, Appl
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1033	51	2.3	508	4	US-09-621-976-17886	Sequence 17886, A	c1106	50	2.2	351	4	US-09-270-767-11437	Sequence 11437, A
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1035	51	2.3	780	2	US-08-540-804-36	Sequence 36, Appl	1108	50	2.2	399	1	US-08-298-687A-13	Sequence 13, Appl
1036	51	2.3	780	3	US-08-590-399-36	Sequence 36, Appl	c1109	50	2.2	399	1	US-08-530-797-12	Sequence 12, Appl
1037	51	2.3	803	4	US-09-800-729-60	Sequence 60, Appl	1110	50	2.2	399	1	US-08-298-829-13	Sequence 13, Appl
1038	51	2.3	974	2	US-08-504-459-13	Sequence 13, Appl	c1111	50	2.2	399	2	US-08-787-335-12	Sequence 12, Appl
1039	51	2.3	1100	3	US-09-248-335-53	Sequence 53, Appl	1112	50	2.2	406	4	US-09-621-976-15107	Sequence 15107, A
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1043	51	2.3	1332	3	US-09-333-423-1	Sequence 1, Appli	1116	50	2.2	636	4	US-09-594-506-27	Sequence 27, Appl
1044	51	2.3	1375	3	US-09-372-422A-37	Sequence 37, Appl	1117	50	2.2	741	2	US-08-975-316-58	Sequence 58, Appl
1045	51	2.3	1386	2	US-08-897-340-1	Sequence 1, Appli	1118	50	2.2	741	4	US-09-615-192A-58	Sequence 58, Appl
1046	51	2.3	1386	3	US-09-252-329-1	Sequence 1, Appli	1119	50	2.2	741	4	US-09-169-789-58	Sequence 58, Appl
1047	51	2.3	1445	3	US-09-697-367-19	Sequence 19, Appl	1120	50	2.2	785	4	US-09-518-036-9	Sequence 9, Appli
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1049	51	2.3	1577	3	US-08-821-994-59	Sequence 59, Appl	1122	50	2.2	788	4	US-09-615-192A-96	Sequence 96, Appl

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1124	50	2.2	873	3	US-09-475-316A-20	Sequence 20, Appl	1197	49	2.2	568	1	US-08-582-257-20	Sequence 20, Appl
1125	50	2.2	873	4	US-09-704-640-20	Sequence 20, Appl	1198	49	2.2	568	2	US-08-582-298-20	Sequence 20, Appl
1126	50	2.2	888	3	US-09-188-930-13	Sequence 13, Appl	1199	49	2.2	619	4	US-09-489-847-58	Sequence 58, Appl
1127	50	2.2	888	4	US-09-312-283C-13	Sequence 13, Appl	1200	49	2.2	728	4	US-09-091-097-5	Sequence 5, Appli
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1141	50	2.2	1576	1	US-08-157-101A-6	Sequence 6, Appli	1214	49	2.2	1670	4	US-09-023-655-980	Sequence 980, App
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1168	50	2.2	3040	1	US-08-446-794A-1	Sequence 1, Appli	1241	49	2.2	1931	4	US-09-470-271-2	Sequence 2, Appli
1169	50	2.2	3040	1	US-08-750-007-2	Sequence 2, Appli	1242	49	2.2	1931	4	US-09-207-359B-1	Sequence 1, Appli
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1171	50	2.2	3299	4	US-09-800-729-68	Sequence 68, Appl	1244	49	2.2	1931	4	US-09-865-364-1	Sequence 1, Appli
1172	50	2.2	4704	2	US-08-476-062A-52	Sequence 52, Appl	1245	49	2.2	1931	4	US-09-748-537-2	Sequence 2, Appli
1173	50	2.2	4704	4	US-09-023-655-1358	Sequence 1358, Ap	1246	49	2.2	2025	4	US-09-149-476-316	Sequence 316, App
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1175	49	2.2	139	4	US-09-621-976-8632	Sequence 8632, Ap	1248	49	2.2	2182	4	US-09-555-820A-11	Sequence 11, Appl
1176	49	2.2	141	4	US-09-621-976-8705	Sequence 8705, Ap	1249	49	2.2	2311	4	US-09-800-729-66	Sequence 66, Appl
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1178	49	2.2	165	4	US-09-621-976-19195	Sequence 19195, A	1251	49	2.2	2625	4	US-09-358-055B-18	Sequence 18, Appl
1179	49	2.2	229	4	US-09-702-705-195	Sequence 19195, A	1252	49	2.2	2625	4	US-09-893-238-18	Sequence 18, Appl
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1181	49	2.2	229	4	US-09-614-124B-195	Sequence 195, App	c1254	49	2.2	2760	1	US-08-101-593-3	Sequence 3, Appli
1182	49	2.2	229	4	US-09-671-325-195	Sequence 195, App	c1255	49	2.2	3001	4	US-09-539-333D-153	Sequence 153, App
1183	49	2.2	229	4	US-09-589-184-195	Sequence 195, App	1256	49	2.2	3007	4	US-09-810-268-1	Sequence 1, Appli
1184	49	2.2	229	4	US-09-658-824-195	Sequence 195, App	1257	49	2.2	4137	3	US-09-499-964-2	Sequence 2, Appli
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c1189	49	2.2	396	4	US-09-640-173-57	Sequence 57, Appl	1262	49	2.2	5325	4	US-10-164-595-21	Sequence 21, Appl
c1190	49	2.2	396	4	US-09-713-550-18	Sequence 18, Appl	1263	49	2.2	5334	4	US-10-164-595-19	Sequence 19, Appl
c1191	49	2.2	396	4	US-09-713-550-57	Sequence 57, Appl	1264	49	2.2	5581	4	US-10-164-595-19	Sequence 19, Appl
c1192	49	2.2	396	4	US-09-825-294-18	Sequence 18, Appl	1265	49	2.2	9704	3	US-09-814-951A-3	Sequence 3, Appli
c1193	49	2.2	396	4	US-09-825-294-57	Sequence 57, Appl	1266	49	2.2	193303	4	US-09-497-855A-37	Sequence 37, Appl
c1194	49	2.2	396	4	US-09-970-966-18	Sequence 18, Appl	1267	49	2.2	193303	4	US-09-497-855A-44	Sequence 44, Appl
c1195	49	2.2	396	4	US-09-970-966-57	Sequence 57, Appl	1268	48	2.1	56	4	US-09-513-999C-17929	Sequence 17929, A

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1270	48	2.1	138	4	US-09-621-976-8112	Sequence 8112, Ap	Sequence 8112, Ap	1343	47	2.1	1277	4	US-10-012-542-20	Sequence 20, Appl
1271	48	2.1	191	4	US-09-621-976-18332	Sequence 18332, A	Sequence 18332, A	1344	47	2.1	1277	4	US-10-115-123-20	Sequence 20, Appl
1272	48	2.1	216	1	US-08-686-878A-34	Sequence 34, Appl	Sequence 34, Appl	1345	47	2.1	1305	3	US-09-242-859A-3	Sequence 3, Appli
1273	48	2.1	216	3	US-09-175-928-34	Sequence 34, Appl	Sequence 34, Appl	1346	47	2.1	1305	3	US-09-242-859A-7	Sequence 7, Appli
1274	48	2.1	237	4	US-09-621-976-10277	Sequence 10277, A	Sequence 10277, A	1347	47	2.1	1313	4	US-09-149-476-112	Sequence 112, App
1275	48	2.1	289	4	US-09-621-976-15142	Sequence 15142, A	Sequence 15142, A	1348	47	2.1	1338	2	US-08-484-993B-7	Sequence 7, Appli
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1277	48	2.1	391	4	US-09-621-976-18858	Sequence 18858, A	Sequence 18858, A	1350	47	2.1	1338	2	US-08-484-596A-7	Sequence 7, Appli
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1279	48	2.1	444	3	US-09-621-976-9484	Sequence 9484, Ap	Sequence 9484, Ap	1352	47	2.1	1338	3	US-08-458-731-7	Sequence 7, Appli
1280	48	2.1	879	1	US-08-688-988-44	Sequence 44, Appl	Sequence 44, Appl	1353	47	2.1	1338	3	US-08-149-223A-7	Sequence 7, Appli
1281	48	2.1	879	1	US-08-158-682A-1	Sequence 1, Appli	Sequence 1, Appli	1354	47	2.1	1395	4	US-09-924-703-5	Sequence 5, Appli
1282	48	2.1	890	4	US-09-621-976-2725	Sequence 2725, Ap	Sequence 2725, Ap	1355	47	2.1	1454	2	US-08-713-000-7	Sequence 7, Appli
1283	48	2.1	1118	4	US-09-614-912-181	Sequence 181, App	Sequence 181, App	1356	47	2.1	1454	2	US-08-975-316-7	Sequence 7, Appli
1284	48	2.1	1159	3	US-09-410-464-14	Sequence 14, Appl	Sequence 14, Appl	1357	47	2.1	1454	2	US-09-211-710-7	Sequence 7, Appli
1285	48	2.1	1192	4	US-09-439-554-23	Sequence 23, Appl	Sequence 23, Appl	1358	47	2.1	1454	4	US-09-615-192A-7	Sequence 7, Appli
1286	48	2.1	1364	1	US-08-265-087-3	Sequence 3, Appli	Sequence 3, Appli	1359	47	2.1	1454	4	US-09-169-789-7	Sequence 7, Appli
1287	48	2.1	1364	1	US-08-621-493-3	Sequence 3, Appli	Sequence 3, Appli	1360	47	2.1	1460	4	US-09-615-192A-95	Sequence 95, Appl
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1289	48	2.1	1364	3	US-09-260-173-3	Sequence 3, Appli	Sequence 3, Appli	1362	47	2.1	1474	2	US-08-975-316-71	Sequence 71, Appl
1290	48	2.1	1405	4	US-09-668-097A-15	Sequence 15, Appl	Sequence 15, Appl	1363	47	2.1	1474	4	US-09-615-192A-71	Sequence 71, Appl
1291	48	2.1	1493	6	5340934-5	Patent No. 5340934	Patent No. 5340934	1364	47	2.1	1474	4	US-09-615-192A-402	Sequence 402, App
1292	48	2.1	1596	3	US-09-146-950-17	Sequence 17, Appl	Sequence 17, Appl	1365	47	2.1	1474	4	US-09-325-932A-202	Sequence 202, App
1293	48	2.1	1605	4	US-09-149-476-187	Sequence 187, App	Sequence 187, App	1366	47	2.1	1474	4	US-09-169-789-71	Sequence 71, Appl
1294	48	2.1	1748	4	US-08-635-967-1	Sequence 1, Appli	Sequence 1, Appli	1367	47	2.1	1474	4	US-09-169-789-184	Sequence 184, App
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1306	48	2.1	2822	4	US-10-140-002-305	Sequence 305, App	Sequence 305, App	1379	47	2.1	2134	4	US-09-629-222A-23	Sequence 23, Appl
1307	48	2.1	2822	4	US-09-903-603A-48	Sequence 48, Appl	Sequence 48, Appl	1380	47	2.1	2152	4	US-09-629-222A-1	Sequence 1, Appli
1308	48	2.1	3772	4	US-10-140-002-391	Sequence 391, App	Sequence 391, App	1381	47	2.1	2152	4	US-09-629-222A-25	Sequence 25, Appl
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1317	47	2.1	159	4	US-09-621-976-8655	Sequence 8655, Ap	Sequence 8655, Ap	1390	47	2.1	2943	4	US-09-404-879A-385	Sequence 385, App
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1416 46 US-09-227-357-30 Sequence 30, Appl
1417 46 US-09-381-488-6 Sequence 6, Appli
1418 46 US-09-800-729-48 Sequence 48, Appl
1419 46 US-08-893-654B-5 Sequence 5, Appli
1420 46 US-09-452-239-3 Sequence 3, Appli
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1422 46 PCT-US95-07752-1 Sequence 1, Appli
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1425 46 US-08-846-784-1 Sequence 1, Appli
1426 46 US-09-904-615-21 Sequence 21, Appl
1427 46 US-09-020-956-107 Sequence 107, App
1428 46 US-09-030-607-107 Sequence 107, App
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1430 46 US-09-352-616A-107 Sequence 107, App
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1436 46 US-09-688-489-107 Sequence 107, App
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1449 46 US-09-234-827B-3 Sequence 3, Appli
1450 46 US-07-867-106-4 Sequence 4, Appli
1451 46 US-09-669-751-259 Sequence 259, App
1452 46 PCT-US93-00227-2 Sequence 2, Appli
1453 46 US-08-832-883-53 Sequence 53, Appl
1454 46 US-08-832-877-53 Sequence 53, Appl
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1456 46 US-09-991-258-11 Sequence 11, Appl
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1458 46 US-08-353-700-2 Sequence 2, Appli
1459 46 PCT-US95-16216-2 Sequence 2, Appli
1460 46 US-09-512-563C-25 Sequence 25, Appl
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1462 46 US-09-780-172-18 Sequence 18, Appl
1463 45 US-09-621-976-10766 Sequence 10766, A
1464 45 US-09-621-976-16692 Sequence 16692, A
1465 45 US-09-621-976-15320 Sequence 15320, A
1466 45 US-09-621-976-18588 Sequence 18588, A
1467 45 US-09-621-976-17925 Sequence 17925, A
1468 45 US-09-621-976-17670 Sequence 17670, A
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1473 45 US-09-152-060-26 Sequence 26, Appl
1474 45 US-09-621-976-1878 Sequence 1878, Ap
1475 45 US-09-227-357-102 Sequence 102, App
1476 45 US-09-248-335-51 Sequence 51, Appl
1477 45 US-09-800-729-14 Sequence 14, Appl
1478 45 US-09-699-266A-1 Sequence 1, Appli
1479 45 US-09-311-021-49 Sequence 49, Appl
1480 45 US-09-800-729-45 Sequence 45, Appl
1481 45 US-09-800-729-47 Sequence 47, Appl
1482 45 US-09-614-912-61 Sequence 61, Appl
1483 45 US-07-602-824A-1 Sequence 1, Appli
1484 45 US-07-983-451-1 Sequence 1, Appli
1485 45 US-08-261-577-6 Sequence 6, Appli
1486 45 US-09-585-173B-7 Sequence 7, Appli
1487 45 US-10-140-002-429 Sequence 429, App

1488 45 US-09-807-258-11 Sequence 11, Appl
1489 45 US-09-227-357-139 Sequence 139, App
1490 45 US-09-672-785-3 Sequence 3, Appli
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1492 45 US-08-076-093A-3 Sequence 3, Appli
1493 45 US-08-701-265-3 Sequence 3, Appli
1494 45 US-08-284-586-3 Sequence 3, Appli
1495 45 US-08-805-478-3 Sequence 3, Appli
1496 45 US-08-802-627A-3 Sequence 3, Appli
1497 45 US-08-801-238-3 Sequence 3, Appli
1498 45 US-08-801-228-3 Sequence 3, Appli
1499 45 US-09-104-296-3 Sequence 3, Appli
1500 45 PCT-US94-06380-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-621-976-97
; Sequence 97, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 97
; LENGTH: 672
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 227..670
; NAME/KEY: sig_peptide
; LOCATION: 227..307
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 7.09999990463257
; OTHER INFORMATION: seq VLLLLLLERGMFS/SP
; NAME/KEY: misc feature
; LOCATION: 586,602..603
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-97

Query Match 14.0%; Score 314; DB 4; Length 672;
Best Local Similarity 99.5%; Pred. No. 2.8e-122;
Matches 554; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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Db 507 CCTCGTGGACATGGGTCTCTCAGCAGCTGCCGATGGTTCAGAGTCTTCCAATACCTCCCG 566
QY 538 TCATCCTGGCCGAACTG 554
Db 567 TCATCCTGGCCGAACTG 583

RESULT 2
US-09-513-999C-13950
; Sequence 13950, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 13950
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
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; LOCATION: 7
; OTHER INFORMATION: r=a or g
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US-09-513-999C-13950

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RESULT 3
US-09-073-569-1
; Sequence 1, Application US/09073569
; Patent No. 6084088
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: NOVEL TUMOR ANTIGENS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,569
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1733 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 34...1344
; OTHER INFORMATION:
US-09-073-569-1

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Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1603 CTCCCAA 1662
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RESULT 4
US-09-621-976-8550
; Sequence 8550, Application US/09621976
; Patent No. 6639063

; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8550
; LENGTH: 146
; TYPE: DNA
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US-09-621-976-8550

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Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2183 TCCCAA 2242
Db 58 TCCCAA 117

RESULT 5
US-09-621-976-8551
; Sequence 8551, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8551
; LENGTH: 147
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8551

Query Match 2.7%; Score 60; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 9.7e-16;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2183 TCCCAA 2242
Db 58 TCCCAA 117

RESULT 6
US-10-140-002-99
; Sequence 99, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C59
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 99
; LENGTH: 1904
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-002-99

Query Match 2.7%; Score 60; DB 4; Length 1904;
Best Local Similarity 100.0%; Pred. No. 7.7e-16;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2183 TCCCAA 2242
Db 1787 TCCCAA 1846

RESULT 7
US-09-702-705-1801
; Sequence 1801, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1801
; LENGTH: 4086
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-702-705-1801

Query Match 2.7%; Score 60; DB 4; Length 4086;
Best Local Similarity 100.0%; Pred. No. 7.1e-16;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2183 TCCCAA 2242
Db 3989 TCCCAA 4048

RESULT 8
US-09-736-457-1801
; Sequence 1801, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Wang, Aijun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.478C15
 ; CURRENT APPLICATION NUMBER: US/09/736,457
 ; CURRENT FILING DATE: 2000-12-13

	Query Match	2.7%;	Score 60;	DB 4;	Length 4086;	
	Best Local Similarity	100.0%;	Pred. No. 7.1e-16;			
	Matches 60;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
CY	2183	TCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAA	2242
Dp	3989	TCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAA	4048

[illegible]

```

; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 10271
; LENGTH: 157
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-10271

```

[illegible]

	Query Match	2.6%;	Score 59;	DB 4;	Length 190;
	Best Local Similarity	100.0%;	Pred. No.	2.5e-15;	
	Matches 59; Conservative	0;	Mismatches	0;	Gaps 0;
OY	2184	CCCCAAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAAAA	2242
DG	107	CCCAAAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAAAA	165

[illegible]


```
RESULT 13
US-09-482-273-49
; Sequence 49, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: PZ030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; CURRENT FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-482-273-49

Query Match      2.6%; Score 59; DB 4; Length 639;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2184 CCCAAAAA 2242
Db 560 CCCAAAAA 618

RESULT 14
US-09-800-729-41
; Sequence 41, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 1651
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1522)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1528)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1540)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1544)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1556)
; OTHER INFORMATION: n equals a,t,g, or c
```

```
; NAME/KEY: SITE
; LOCATION: (1572)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-800-729-41

Query Match      2.6%; Score 59; DB 4; Length 1651;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2184 CCCAAAAA 2242
Db 1586 CCCAAAAA 1644

RESULT 15
US-09-739-455-1
; Sequence 1, Application US/09739455
; Patent No. 6413756
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000653
; CURRENT APPLICATION NUMBER: US/09/739,455
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1868
; TYPE: DNA
; ORGANISM: Human
US-09-739-455-1

Query Match      2.6%; Score 59; DB 4; Length 1868;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2184 CCCAAAAA 2242
Db 1802 CCCAAAAA 1860

Search completed: February 1, 2005, 21:27:47
Job time : 246 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2005, 11:19:08 ; Search time 4 Seconds
(without alignments)
4.497 Million cell updates/sec

Title: us-10-036-342-56
Perfect score: 2242
Sequence: 1 gaatgaataacctccgaagcc.....aaaaaaaaaaaaaaaaaaaaa 2242

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 3 seqs, 4012 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 56dba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2137.1	95.3	2152	1 AAZ65270	Human secreted pro
2	126.6	5.6	127	1 AAX10638	Human biallelic po
3	62.4	2.8	1733	1 AAV81394	Human tumour antig
4	23.8	1.1	2152	1 AAZ65270	Human secreted pro
5	21.4	1.0	1733	1 AAV81394	Human tumour antig
6	14.6	0.7	127	1 AAX10638	Human biallelic po

ALIGNMENTS

RESULT 1
AAZ65270
ID AAZ65270 standard; DNA; 2152 BP.
XX
AC AAZ65270;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human secreted protein gene 21.
XX

KW Human; secreted protein; cancer; tumour; developmental abnormality;
KW foetal deficiency; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW therapy; chromosome 18q22-23; ds.

XX Homo sapiens.
OS
XX
PN WO9958660-A1.
XX

PD 18-NOV-1999.
XX
PF 06-MAY-1999; 99WO-US009847.
XX
PR 12-MAY-1998; 98US-0085093P.
PR 12-MAY-1998; 98US-0085094P.
PR 12-MAY-1998; 98US-0085105P.
PR 12-MAY-1998; 98US-0085180P.
PR 18-MAY-1998; 98US-0085906P.
PR 18-MAY-1998; 98US-0085920P.
PR 18-MAY-1998; 98US-0085921P.
PR 18-MAY-1998; 98US-0085922P.
PR 18-MAY-1998; 98US-0085923P.
PR 18-MAY-1998; 98US-0085924P.
PR 18-MAY-1998; 98US-0085925P.
PR 18-MAY-1998; 98US-0085927P.
PR 18-MAY-1998; 98US-0085928P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR, Lafleur DW;
PI Endress GA, Ebner R;
XX
DR WPI; 2000-062296/05.
DR P-PSDB; AAY76144.
XX
PT New isolated human genes and the secreted polypeptides they encode,
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
PS Claim 1; Page 309; 475pp; English.
XX
CC AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
CC This sequence was found to be present on human chromosome 18q22-23.
CC AAY76124 to AAY76223 represent the secreted proteins encoded by the 97
CC human genes. The genes and their corresponding secreted polypeptides are
CC useful for preventing, treating or ameliorating medical conditions, e.g.
CC by protein or gene therapy. Also pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new genes. Specific uses are
CC described for each of the 97 genes, based on which tissues they are most
CC highly expressed in, and include developing products for the diagnosis or
CC treatment of cancer, tumours, developmental abnormalities and foetal
CC deficiencies, blood disorders, diseases of the immune system, autoimmune
CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
CC also useful for identifying their binding partners. The sequences shown
CC in AAY76224 to AAY76424 represent fragments of the secreted proteins
XX
SQ Sequence 2152 BP; 541 A; 526 C; 531 G; 553 T; 0 U; 1 Other;

Query Match 95.3%; Score 2137.1; DB 1; Length 2152;
Best Local Similarity 99.8%; Pred. No. 4e-11;
Matches 2148; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

Qy 19 CCGCTTTGTCTCCAGATGTAATAGCTCCACTATACAGCCTCGTCTCCTCCGGGGG 78
|||
Db 1 CCGCTTTGTCTCCAGATGTAATAGCTCCACTATACAGCCTCGTCTCCTCCGGGGG 60

Qy 79 ACAACGTGGTCAGGGCACAGAGAGATATTAAATGTACCCCTCTTGGGCTTTCATGGGA 138
|||
Db 61 ACAACGTGGTCAGGGCACAGAGAGATATTAAATGTACCCCTCTTGGGCTTTCATGGGA 120

Qy 139 CTCCCTCTGCCACATTTTTTGGAGGTTGGGAAAGTTGCTAGAGGCTTCAGAACTCCAGCC 198
|||
Db 121 CTCCCTCTGCCACATTTTTTGGAGGTTGGGAAAGTTGCTAGAGGCTTCAGAACTCCAGCC 180

Qy 199 TAATGGATCCCAAACCTCGGGAGAATGGCTCGTCCCTCGTGGCTG---TGCTGCTGCTGC 255
|||
Db 181 TAATGGATCCCAAACCTCGGGAGAATGGCTCGTCCCTCGTGGCTGTGCTGCTGCTGCTGC 240

QY	256	TGCTGGAGCGCGCATGTTCTCCTCACCCCTCCCGCCCGCGCTGTTAGAGAAAGTCT	315
Db	241	TGCTGGAGCGCGCATGTTCTCCTCACCCCTCCCGCCCGCGCTGTTAGAGAAAGTCT	300
QY	316	TCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGGAGTGGTGCCCA	375
Db	301	TCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGGAGTGGTGCCCA	360
QY	376	TCGAGAGCGACTCTGTCCAGCCTGTGCCTTCGCTTCAGACAAGAGCTCTTCAGAATGATGG	435
Db	361	TCGAGAGCGACTCTGTCCAGCCTGTGCCTTCGCTTCAGACAAGAGCTCTTCAGAATGATGG	420
QY	436	CCGTGGCTGCGGACACGCTGCAGCGCCTGGGGCCCGTGTGGCCCTCGGTGGACATGGGTC	495
Db	421	CCGTGGCTGCGGACACGCTGCAGCGCCTGGGGCCCGTGTGGCCCTCGGTGGACATGGGTC	480
QY	496	CTCAGAGCTGCCCCGATGGTCAAGTCTTCCAATACCTCCCGTCATCCTGGCCCCGAAGTGG	555
Db	481	CTCAGAGCTGCCCCGATGGTCAAGTCTTCCAATACCTCCCGTCATCCTGGCCCCGAAGTGG	540
QY	556	GGAGCGATCCACGAAAGGCACCGTGTGCTTACGGCCACTTGGACGTGCAGCCTGCTG	615
Db	541	GGAGCGATCCACGAAAGGCACCGTGTGCTTACGGCCACTTGGACGTGCAGCCTGCTG	600
QY	616	ACCGGGCGATGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACGGGAACTTT	675
Db	601	ACCGGGCGATGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACGGGAACTTT	660
QY	676	ATGGACGAGGACGACCGACAAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCG	735
Db	661	ATGGACGAGGACGACCGACAAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCG	720
QY	736	CCTTCAGAGCCCTGGAGCAAGATCTTCCTGTGAATATCAAAATTCATCATTTGAGGGGATGG	795
Db	721	CCTTCAGAGCCCTGGAGCAAGATCTTCCTGTGAATATCAAAATTCATCATTTGAGGGGATGG	780
QY	796	AAGAGGCTGGCTCTGTTGCCCTGGAGGAACTTGTGGAAAAAGAAAGGACCGGATTCCTCT	855
Db	781	AAGAGGCTGGCTCTGTTGCCCTGGAGGAACTTGTGGAAAAAGAAAGGACCGGATTCCTCT	840
QY	856	CTGGTGTGGAATACATTGTAATTTTCAGATAACCTGTGGATCAGCCAAAGGAGCCAGCAA	915
Db	841	CTGGTGTGGAATACATTGTAATTTTCAGATAACCTGTGGATCAGCCAAAGGAGCCAGCAA	900
QY	916	TCACCTTATGGAACCCGGGGGAAACAGCTACTTCATGGTGGAGGTAATGCAGAGACCAGG	975
Db	901	TCACCTTATGGAACCCGGGGGAAACAGCTACTTCATGGTGGAGGTAATGCAGAGACCAGG	960
QY	976	ATTTTCACCTCAGGAACCTTTGGTGGCATCCCTTCATGAACCAATGGCTGATCTGGTTGCTC	1035
Db	961	ATTTTCACCTCAGGAACCTTTGGTGGCATCCCTTCATGAACCAATGGCTGATCTGGTTGCTC	1020
QY	1036	TTCTCGGTAGCCTGGTAGACTCGTCTGGTCAATCCTGGTCCCTGGAATCTATGATGAAG	1095
Db	1021	TTCTCGGTAGCCTGGTAGACTCGTCTGGTCAATCCTGGTCCCTGGAATCTATGATGAAG	1080
QY	1096	TGGTTCCCTCTTACAGAAAGGAAATAAATACATACAAAGCCATCCATCTAGACCTAGAAG	1155
Db	1081	TGGTTCCCTCTTACAGAAAGGAAATAAATACATACAAAGCCATCCATCTAGACCTAGAAG	1140
QY	1156	AATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTCGATACCTAAGGAGGAGATTCTAA	1215
Db	1141	AATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTCGATACCTAAGGAGGAGATTCTAA	1200
QY	1216	TGCACCTCTGGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGGGCGGCTTGTATGAGC	1275
Db	1201	TGCACCTCTGGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGGGCGGCTTGTATGAGC	1260
QY	1276	CTGGAACATAAACAGTCATACCTGGCCGAGTTATAGGAAAAATTTTCAATCCGCTAGTCC	1335
Db	1261	CTGGAACATAAACAGTCATACCTGGCCGAGTTATAGGAAAAATTTTCAATCCGCTAGTCC	1320

QY	1336	CTCACATGAATGTGTCTCGGTTGGAAAAACACAGGTGACACGACATCTTTGAAGATGTGTTCT	1395
Db	1321	CTCACATGAATGTGTCTCGGTTGGAAAAACACAGGTGACACGACATCTTTGAAGATGTGTTCT	1380
QY	1396	CCAAAAGAAATAGTTCCAAACAAGATGGTGTTCATGACTCTAGACTACACCCGTGGA	1455
Db	1381	CCAAAAGAAATAGTTCCAAACAAGATGGTGTTCATGACTCTAGACTACACCCGTGGA	1440
QY	1456	TTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGATCAGAACAGTGTG	1515
Db	1441	TTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGATCAGAACAGTGTG	1500
QY	1516	GAACAGAACCCAGATATGATCCGGGATGGATCCACCATTCCAATTGCCAAAATGTTCCAGG	1575
Db	1501	GAACAGAACCCAGATATGATCCGGGATGGATCCACCATTCCAATTGCCAAAATGTTCCAGG	1560
QY	1576	AGATCGTCCACAAGAGCGGTGCTAATTCGCTGGGAGCTGTTGATGATGGAGAACATT	1635
Db	1561	AGATCGTCCACAAGAGCGGTGCTAATTCGCTGGGAGCTGTTGATGATGGAGAACATT	1620
QY	1636	CGCAGAAATGAGAAAAATCAACAGGTGGAACTACATAGAGGGAACCAAAATATTGCTGCCT	1695
Db	1621	CGCAGAAATGAGAAAAATCAACAGGTGGAACTACATAGAGGGAACCAAAATATTGCTGCCT	1680
QY	1696	TTTTCTTAGAGATGGCCAGCTCCATTAAATCACAAGAACCTTCTAGTCTGATCTGATCCA	1755
Db	1681	TTTTCTTAGAGATGGCCAGCTCCATTAAATCACAAGAACCTTCTAGTCTGATCTGATCCA	1740
QY	1756	CTGACAGATTACCTCCCCACATCCCTAGACAGGGATGGAATGTAAATATCCAGAGAAAT	1815
Db	1741	CTGACAGATTACCTCCCCACATCCCTAGACAGGGATGGAATGTAAATATCCAGAGAAAT	1800
QY	1816	TTGGGTCTAGTATAGTACATTTTCCCTTCCATTAAATGTCTTTGGGATATCTGGATCAG	1875
Db	1801	TTGGGTCTAGTATAGTACATTTTCCCTTCCATTAAATGTCTTTGGGATATCTGGATCAG	1860
QY	1876	TAATAAAATATTTCAAAGGCACAGATGTTGGAAATGGTTTAAGGTCCCCACTGCACACC	1935
Db	1861	TAATAAAATATTTCAAAGGCACAGATGTTGGAAATGGTTTAAGGTCCCCACTGCACACC	1920
QY	1936	TTCTTCAAGTCATAGCTGCTTGACAGCAACTTGAATTTCCCAAGTCTCTGTCATAAGCCCC	1995
Db	1921	TTCTTCAAGTCATAGCTGCTTGACAGCAACTTGAATTTCCCAAGTCTCTGTCATAAGCCCC	1980
QY	1996	AGGATTGGATTCTTCCAACTTTTAGCATATCTCCTCAACCTTGCAATTTGATGGCATAA	2055
Db	1981	AGGATTGGATTCTTCCAACTTTTAGCATATCTCCTCAACCTTGCAATTTGATGGCATAA	2040
QY	2056	TCACTCCGGTTTGTCTTAGGTCTCAAGTCTCGTGACACATAATCATTCATCCAAT	2115
Db	2041	TCACTCCGGTTTGTCTTAGGTCTCAAGTCTCGTGACACATAATCATTCATCCAAT	2100
QY	2116	GATCGCCTTTGCTTTACCACTCTTTCCCTTTTATCTTAAATAAAATGTTG	2167
Db	2101	GATCGCCTTTGCTTTACCACTCTTTCCCTTTTATCTTAAATAAAATGTTG	2152

RESULT 2
AAX10638/c
ID AAX10638 standard; DNA; 127 BP.
XX
AC AAX10638;
XX
DT 30-MAR-1999 (first entry)
XX
DE Human biallelic polymorphic DNA fragment WI-15225.
XX
KW Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW detection; phenotypic typing; characteristic; infection; hereditary;
KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;
KW treatment; marker; ss.
XX
OS Homo sapiens.

XX WO9820165-A2.
PN
XX
PD 14-MAY-1998.
XX
PF 05-NOV-1997; 97WO-US020313.
XX
PR 06-NOV-1996; 96US-0030455P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Lander ES, Wang D, Hudson T;
XX
DR WPI; 1998-286974/25.
XX
PT New isolated nucleic acid segments from the human genome - used for
PT determining polymorphic forms for use in e.g. forensics, paternity
PT testing or phenotypic typing for disease.
XX
PS Claim 1; Page 67; 310pp; English.
XX
CC AAX10269-X12937 are human DNA fragments which contain biallelic
CC polymorphic markers which have been isolated using the primers
CC represented in AAX09121-X10268. The base occupying the polymorphic site
CC is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
CC can be used in methods for determining polymorphic forms in an individual
CC for use in e.g. forensics, paternity testing or for phenotypic typing for
CC diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan.
CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
CC familial hypercholesterolemia, polycystic kidney disease, hereditary
CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC autoimmune diseases, inflammation, cancer, diseases of the nervous
CC system, infection by pathogenic microorganisms, and characteristics such
CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC endurance, fertility, and susceptibility or receptivity to particular
CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC segments can also be used to produce medicaments for the treatment or
CC prophylaxis of such diseases
XX
SQ Sequence 127 BP; 47 A; 16 C; 36 G; 27 T; 0 U; 1 Other;

Query Match 5.6%; Score 126.6; DB 1; Length 127;
Best Local Similarity 99.2%; Pred. No. 9.2;
Matches 126; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2017 TTTTAGCATATCTCCAACCTTGCAATTTGATTGGCATAATCACTCCGGTTGCTTTCTAG 2076
Db 127 TTTTAGCATATCTCCAACCTTGCAATTTGATTGGCATAATCACTCCGGTTGCTTTCTAG 68
QY 2077 GTCCTCAAGTGCTCGACACATAATCATTCATCCATCCCAATGATCGCCTTTTACCAC 2136
Db 67 GTCCTCAAGTGCTCGACACATAATCATTCATCCATCCCAATGATCGCCTTTTACCAC 8
QY 2137 CTTTCCT 2143
Db 7 CTTTCCT 1

RESULT 3
AAV81394
ID AAV81394 standard; DNA; 1733 BP.
XX
AC AAV81394;
XX
DT 16-MAR-1999 (first entry)
XX
DE Human tumour antigen zsig15 coding sequence.
XX
KW Secretion; differentiation marker; tumour; epithelial cell; colon; blood;
KW breast; prostate; growth; development; antagonist; receptor; bone marrow;
KW cancer; metastasis; ss.

XX Homo sapiens.
OS
XX
FH Key
FT CDS
FT Location/Qualifiers
FT 34..1347
FT /*tag= a
FT /product= "zsig15"
XX
PN WO9850552-A1.
XX
PD 12-NOV-1998.
XX
PF 06-MAY-1998; 98WO-US009584.
XX
PR 06-MAY-1997; 97US-0045703P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sheppard PO, Grossmann A;
XX
DR WPI; 1999-034723/03.
DR P-PSDB; AAW67722.
XX
PT New nucleic acid encoding secreted polypeptide zsig15 - used as a marker
PT for tumour cells, useful for diagnosis and treatment of cancers,
PT inflammation and hyperplasia.
XX
PS Claim 4; Page 81-84; 100pp; English.
XX
CC This sequence encodes a secreted polypeptide, designated zsig15, which is
CC a marker for differentiation in normal and tumour cells (particularly
CC epithelial cells and derived tumours of colon, breast and prostate). The
CC zsig15 protein is useful for the promotion of growth and development of
CC epithelial cells; to identify specific (ant)agonists, also where
CC conjugated to a toxin, to deliver these to cells expressing the cognate
CC receptor (e.g. to kill cells of blood, colon, breast and bone marrow
CC cancers), and to identify/isolate receptors involved in cancer
CC metastases. The sequence was isolated from a colon cancer library after
CC screening an EST (expressed sequence tag) database for sequences
CC containing putative secretion signal sequences
XX
SQ Sequence 1733 BP; 448 A; 504 C; 442 G; 339 T; 0 U; 0 Other;

Query Match 2.8%; Score 62.4; DB 1; Length 1733;
Best Local Similarity 96.9%; Pred. No. 1.3;
Matches 63; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2178 CTGNCCTCCAAAAA
Db 1599 CTTTCTCCAAAAA
QY 2238 AAAAA 2242
Db 1659 AAAAA 1663

RESULT 4
AAZ65270/c
ID AAZ65270 standard; DNA; 2152 BP.
XX
AC AAZ65270;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human secreted protein gene 21.
XX
KW Human; secreted protein; cancer; tumour; developmental abnormality;
KW foetal deficiency; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW therapy; chromosome 18q22-23; ds.

XX 30-MAR-1999 (first entry)
DT Human biallelic polymorphic DNA fragment WI-15225.
XX Polymorphism; biallelic; human; forensic; paternity testing; disease;
DE detection; phenotypic typing; characteristic; infection; hereditary;
XX autoimmune disease; cancer; inflammation; drug; therapy; medicament;
KW treatment; marker; ss.
XX Homo sapiens.
OS
XX WO9820165-A2.
PN
XX 14-MAY-1998.
PD
XX 05-NOV-1997; 97WO-US020313.
PF
XX 06-NOV-1996; 96US-0030455P.
PR
XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA
XX Lander ES, Wang D, Hudson T;
PI
XX WPI; 1998-286974/25.
DR
XX New isolated nucleic acid segments from the human genome - used for
PT determining polymorphic forms for use in e.g. forensics, paternity
PT testing or phenotypic typing for disease.
PT
XX
PS Claim 1; Page 67; 310pp; English.
XX
CC AAX10269-X12937 are human DNA fragments which contain biallelic
CC polymorphic markers which have been isolated using the primers
CC represented in AAX09121-X10268. The base occupying the polymorphic site
CC is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
CC can be used in methods for determining polymorphic forms in an individual
CC for use in e.g. forensics, paternity testing or for phenotypic typing for
CC diseases such as agammaglobulinemia, diabetes insipidus, Leach-Nyhan
CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
CC familial hypercholesterolemia, polycystic kidney disease, hereditary
CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC autoimmune diseases, inflammation, cancer, diseases of the nervous
CC system, infection by pathogenic microorganisms, and characteristics such
CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC endurance, fertility, and susceptibility or receptivity to particular
CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC segments can also be used to produce medicaments for the treatment or
CC prophylaxis of such diseases
XX
SQ Sequence 127 BP; 47 A; 16 C; 36 G; 27 T; 0 U; 1 Other;

Query Match 0.7%; Score 14.6; DB 1; Length 127;
Best Local Similarity 57.8%; Pred. No. 26;
Matches 26; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 136 GGACTCCCTCTGCCACATTTTGGAGGTTGGGAAAGTTGCTAGA 180
||| | | ||||| ||| | | ||| | |||||
Db 82 GGAGTGATTATGCCAATTCAAATTGCAAGTTGGAGATATGCTAAA 126

Search completed: February 16, 2005, 11:19:14
Job time : 5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2005, 11:23:54 ; Search time 553 Seconds
(without alignments)
3.980 Million cell updates/sec

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Perfect score: 2242
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 13 seqs, 490885 residues

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 56dbb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	614.8	27.4	672	1 AR412460	ACCESSION:AR412460
2	614.8	27.4	672	1 AX969294	ACCESSION:AX969294
3	614.8	27.4	672	1 BD108013	ACCESSION:BD108013
4	567.5	25.3	3755	1 AK131263	ACCESSION:AK131263
5	524.6	23.4	164394	1 AC116904	ACCESSION:AC116904
6	292.8	13.1	300	1 AX898087	ACCESSION:AX898087
7	292.8	13.1	300	1 BD033620	ACCESSION:BD033620
8	279	12.4	279	1 CQ715367	ACCESSION:CQ715367
9	225	10.0	178691	1 AC009704	ACCESSION:AC009704
10	203.4	9.1	64201	1 AC117833	ACCESSION:AC117833
11	203.4	9.1	64201	1 AC117833	ACCESSION:AC117833
12	169.4	7.6	73476	1 AC123772	ACCESSION:AC123772
13	154.4	6.9	2006	1 BC047599	ACCESSION:BC047599
14	153	6.8	73476	1 AC123772	ACCESSION:AC123772
15	152.8	6.8	1467	1 BC065925	ACCESSION:BC065925
16	46.6	2.1	178691	1 AC009704	ACCESSION:AC009704
17	34.4	1.5	164394	1 AC116904	ACCESSION:AC116904
18	32	1.4	2006	1 BC047599	ACCESSION:BC047599
19	25	1.1	300	1 AX898087	ACCESSION:AX898087
20	25	1.1	300	1 BD033620	ACCESSION:BD033620
21	23.8	1.1	672	1 AR412460	ACCESSION:AR412460
22	23.8	1.1	672	1 AX969294	ACCESSION:AX969294
23	23.8	1.1	672	1 BD108013	ACCESSION:BD108013
24	21.6	1.0	3755	1 AK131263	ACCESSION:AK131263
25	20.4	0.9	1467	1 BC065925	ACCESSION:BC065925
26	19.4	0.9	279	1 CQ715367	ACCESSION:CQ715367

ALIGNMENTS

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LOCUS	AR412460	Sequence 97 from patent US 6639063.	672 bp	DNA	linear	PAT 18-DEC-2003
DEFINITION	Sequence 97 from patent US 6639063.					
ACCESSION	AR412460					
VERSION	AR412460.1	GI:40167570				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 672)					
AUTHORS	Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.					
TITLE	EST's and encoded human proteins					
JOURNAL	Patent: US 6639063-A 97 28-OCT-2003;					
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Best Local Similarity	98.1%;	Pred. No. 5.7;				
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QY	1	GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCC	60			
Db	27	GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCC	86			
QY	61	TCGTCTTCTTCCGGGGGACAAACGTGGTCCAGGGCACAGAGAGATATTAAATGTCACCCCT	120			
Db	87	TCGTCTTCTTCCGGGGGACAAACGTGGTCCAGGGCACAGAGAGATATTAAATGTCACCCCT	146			
QY	121	CTTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTTGGGAAAAGTTGCTAGA	180			
Db	147	CTTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTTGGGAAAAGTTGCTAGA	206			
QY	181	GGCTTCAGAACTCCAGCCTAATGGATCCAAACTCGGGAGAAATGGTGCCTCCCTGCTGG	240			
Db	207	GGCTTCAGAACTCCAGCCTAATGGATCCAAACTCGGGAGAAATGGTGCCTCCCTGCTGG	266			
QY	241	CTG---TGCTGCTGCTGCTGCTGGAGCGGGGCATGTTCTCCTCACCCCTCCCGCCCCCGG	297			
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QY	298	CGCTGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGC	357			
Db	327	CGCTGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGC	386			
QY	358	TGAAGGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTCGCTTCAGACAAG	417			
Db	387	TGAAGGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTCGCTTCAGACAAG	446			
QY	418	AGCTCTTCAGAAATGATGGCCGTGGTGGGACACGCTGCAGCGCTGGGGGCCCCGTGTGG	477			
Db	447	AGCTCTTCAGAAATGATGGCCGTGGTGGGACACGCTGCAGCGCTGGGGGCCCCGTGTGG	506			
QY	478	CCTCGTGGACATGGGTCTCCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCG	537			
Db	507	CCTCGTGGACATGGGTCTCCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCG	566			
QY	538	TCATCCTGSCCGAACTGGGGAGCGATCCACGAAAGGACCGGTGTGCTTCTACGGCCACT	597			
Db	567	TCATCCTGSCCGAACTGKDNAGCGATCCACGAVHNNACCCGTGT-STTCTACGGCCACT	625			
QY	598	TGGACGTGACGCTGCTGACCCGGGGCGATGGGTGGCTCACGGACCCC	644			
Db	626	TGGACGTGACGCTGCTGACCCGGGGCGATGGGTGGCTCACGGACCCC	672			
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LOCUS	AX969294	Sequence 97 from Patent EP1104808.	672 bp	DNA	linear	PAT 15-JAN-2004
DEFINITION	Sequence 97 from Patent EP1104808.					
ACCESSION	AX969294					
VERSION	AX969294.1	GI:40975507				
KEYWORDS						

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y.
AUTHORS ESTs and encoded human proteins
TITLE Patent: EP 1104808-A 97 06-JUN-2001;
JOURNAL Genset (FR)
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QY 1 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCC 60
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QY 27 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCC 86
DB |
QY 61 TCGTCTTCCTCCGGGGGACAAACGTGGGTCCAGGACAGAGAGATTAATGTCAACCCT 120
DB |
QY 87 TCGTCTTCCTCCGGGGGACAAACGTGGGTCCAGGACAGAGAGATTAATGTCAACCCT 146
DB |
QY 121 CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTGGAGGTTGGGAAAGTTGCTAGA 180
DB |
QY 147 CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTGGAGGTTGGGAAAGTTGCTAGA 206
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QY 181 GGCTTCAGAACTCCAGCCTAATGGATCCCAAACTCCGAGAGATGGTCCCTGCTGG 240
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QY 207 GGCTTCAGAACTCCAGCCTAATGGATCCCAAACTCCGAGAGATGGTCCCTGCTGG 266
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QY 267 CTGTGCTGCTGCTGCTGGAGCGCGGCATGTTCTCCTCACCCCTCCCCGCCCGG 326
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QY 298 CGCTGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTCAGACGC 357
DB |
QY 327 CGCTGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTCAGACGC 386
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DB |
QY 387 TGAAGGAGTGGGTGGCCCATCGAGAGCGGACTCTGTCCAGCTGTGCTCGCTTCAGACAAG 446
QY 418 AGCTCTTCAGAAATGATGGCGGTGGCTGCGGACACGCTGAGCGGCTGGGGGCCCGTGTGG 477
DB |
QY 447 AGCTCTTCAGAAATGATGGCGGTGGCTGCGGACACGCTGAGCGGCTGGGGGCCCGTGTGG 506
QY 478 CCTCGGTGGACATGGGTCTCCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCG 537
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QY 507 CCTCGGTGGACATGGGTCTCCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCG 566
QY 538 TCATCTGGCCGAACCTGGGAGCGGATCCACGAAAGGCACCGTGTGCTTCTACGGGCCACT 597
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QY 567 TCATCTGGCCGAACCTGKNAGCGATCCACGAVHNNACCGTGT-STTCTACGGGCCACT 625
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RESULT 3
BD108013
LOCUS BD108013
DEFINITION EST and encoded human protein.
ACCESSION BD108013
VERSION BD108013.1 GI:23202831
KEYWORDS JP 2002010789-A/90.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 672)
Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
EST and encoded human protein
Patent: JP 2002010789-A 90 15-JAN-2002;
GENSET CORP
OS Homo sapiens (human)
PN JP 2002010789-A/90
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
GIORDANO
PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC
C12N15/00
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CC score 7.09999990463257
CC seq VLLLLLLERGMFS/SP
CC n=a, g, c or t Location/Qualifiers
FH Key
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FT sig_peptide 227..307
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Query Match 27.4%; Score 614.8; DB 1; Length 672;
Best Local Similarity 98.1%; Pred. No. 5.7;
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QY 1 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCC 60
DB |
QY 27 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCC 86
DB |
QY 61 TCGTCTTCCTTCGGGGGACAAACGTGGGTCCAGGACAGAGAGATATTTAATGTCAACCCT 120
DB |
QY 87 TCGTCTTCCTTCGGGGGACAAACGTGGGTCCAGGACAGAGAGATATTTAATGTCAACCCT 146
DB |
QY 121 CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTGGAGGTTGGGAAAGTTGCTAGA 180
DB |
QY 147 CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTGGAGGTTGGGAAAGTTGCTAGA 206
DB |
QY 181 GGCTTCAGAACTCCAGCCTAATGGATCCCAAACTCCGAGAGATGGTCCCTGCTGG 240
DB |
QY 207 GGCTTCAGAACTCCAGCCTAATGGATCCCAAACTCCGAGAGATGGTCCCTGCTGG 266
QY 241 CTG---TGCTGCTGCTGCTGGAGCGCGGCATGTTCTCCTCACCCCTCCCCGCCCGG 297
DB |
QY 267 CTGTGCTGCTGCTGCTGGAGCGCGGCATGTTCTCCTCACCCCTCCCCGCCCGG 326
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QY 298 CGCTGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTCAGACGC 357
DB |
QY 327 CGCTGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTCAGACGC 386
QY 358 TGAAGGAGTGGGTGGCCCATCGAGAGCGGACTCTGTCCAGCTGTGCTCGCTTCAGACAAG 417

Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L26198
Center clone name: 1112_M_8

FEATURES

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RESULT 6
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LOCUS      Sequence 13950 from Patent EP1033401.
DEFINITION      AX898087
ACCESSION      AX898087
VERSION      AX898087.1      GI:40053000
KEYWORDS      .
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE      Expressed sequence tags and encoded human proteins
JOURNAL      Patent: EP 1033401-A 13950 06-SEP-2000;
GENSET      (FR)
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ACCESSION      BD033620
VERSION      BD033620.1      GI:22575362
KEYWORDS      JP 2001269182-A/9866.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1      (bases 1 to 300)
AUTHORS      Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE      Sequence tag and encoded human protein
JOURNAL      Patent: JP 2001269182-A 9866 02-OCT-2001;
GENSET
OS      Homo sapiens (human)
PN      JP 2001269182-A/9866
PD      02-OCT-2001
PF      24-FEB-2000      JP 2000118773
PR      26-FEB-1999      US      60/122487
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PI      JEAN BAPTIST DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PI      JORDAN
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VERSION      CQ715367.1      GI:42276224
KEYWORDS      .
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE      Kits, such as nucleic acid arrays, comprising a majority of
      humanexons or transcripts, for detecting expression and other uses
      thereof
JOURNAL      Patent: WO 02068579-A 1301 06-SEP-2002;
      PE Corporation (NY) (US)
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      /mol_type="unassigned DNA"
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Thu Feb 17 18:38:12 2005

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JOURNAL
REFERENCE
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1 (bases 1 to 64201)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 18, clone CTD-2088C24
Unpublished
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
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Direct Submission
Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L26228
Center clone name: 2088_C_24

TITLE
JOURNAL
COMMENT

* NOTE: This record contains 80 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L27294
Center clone name: 911_E_16

* NOTE: This record contains 89 individual
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* However, it should not be assumed that this clone
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Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 497 TCAGCAGCTGCCCGATGGTTCAGAGTCTTCCATACCTCCCGTCATCCTGGCGAACTGGG 556
    |||||||
Db 11159 TCTGCAGCTGCCCGATGGTTCAGAGTCTTCCATACCTCCCGTCATCCTGGCGAACTGGG 11218

QY 557 GAGCGATCCCAAGGACCGTGTGCTTCTACGGCCACTTGGACGTGACGCTGCTGA 616
    |||||||
Db 11219 GAGCGATCCCAAGGACCGTGTGCTTCTACGGCCACTTGGACGTGACGCTGCTGA 11278

QY 617 CCGGGCGATGGTGGCTCAGGACCCCTATGTGCTGACGGAGGTAGACGG 667
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Db 11279 CCGGGCGATGGTGGCTCAGGACCCCTATGTGCTGACGGAGGTAGACGG 11329
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DEFINITION Homo sapiens cDNA clone IMAGE:5528129, partial cds.
ACCESSION  BC047599
VERSION     BC047599.2  GI:34192884
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2006)
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```
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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TITLE
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2238257
12477932
2 (bases 1 to 2006)
Strausberg,R.
Direct Submission
Submitted (03-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
```

```
REMARK
COMMENT
NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 25, 2003 this sequence version replaced gi:28838418.
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC/DCTP/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Series: IRAK Plate: 88 Row: d Column: 4.

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FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5528129"
/tissue_type="Skin, melanotic melanoma."
/clone_lib="NIH MGC_72"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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Query Match 6.9%; Score 154.4; DB 1; Length 2006;
Best Local Similarity 99.4%; Pred. No. 2.3e+02;
Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 352 AGACGCTGAAGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTTCA 411
    |||||||
Db 1071 AGACGCTGAAGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTTCA 1012

QY 412 GACAAGAGCTCTTCAGAAATGATGGCCGTGGCTGCGGACACGCTGCAGCGCTGGGGGCC 471
    |||||||
Db 1011 GACAAGAGCTCTTCAGAAATGATGGCCGTGGCTGCGGACACGCTGCAGCGCTGGGGGCC 952

QY 472 GTGTGGCCTCGGTGGACATGGGTCTTCAGCAGCTGC 507
    |||||||
Db 951 GTGTGGCCTCGGTGGACATGGGTCTTCAGCAGCTGC 916
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RESULT 14
AC123772/c
LOCUS      AC123772      73476 bp      DNA      linear      HTG 01-JUN-2002
DEFINITION Homo sapiens chromosome 18 clone RP11-911E16 map 18, LOW-PASS
SEQUENCE SAMPLING.
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AC123772
AC123772.1  GI:21307335
HTG; HTGS_PHASE0.
Homo sapiens (human)
Homo sapiens
```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 73476)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 18, clone RP11-911E16
Unpublished
2 (bases 1 to 73476)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N.,

TITLE
JOURNAL

COMMENT

Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L27294
Center clone name: 911_E_16

* NOTE: This record contains 89 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1
* 732 731: contig of 731 bp in length
* 832 831: gap of 100 bp
* 1554 1554: contig of 723 bp in length
* 1555 1654: gap of 100 bp
* 1655 2373: contig of 719 bp in length
* 2374 2473: gap of 100 bp
* 2474 3190: contig of 717 bp in length
* 3191 3290: gap of 100 bp
* 3291 4026: contig of 736 bp in length
* 4027 4126: gap of 100 bp
* 4127 4845: contig of 719 bp in length
* 4846 4945: gap of 100 bp
* 4946 5666: contig of 721 bp in length
* 5667 5766: gap of 100 bp
* 5767 6496: contig of 730 bp in length
* 6497 6596: gap of 100 bp
* 6597 7320: contig of 724 bp in length
* 7321 7420: gap of 100 bp
* 7421 8149: contig of 729 bp in length
* 8150 8249: gap of 100 bp
* 8250 8986: contig of 737 bp in length
* 8987 9086: gap of 100 bp
* 9087 9817: contig of 731 bp in length
* 9818 9917: gap of 100 bp
* 9918 10649: contig of 732 bp in length
* 10650 10749: gap of 100 bp
* 10750 11474: contig of 725 bp in length
* 11475 11574: gap of 100 bp
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* 12314 12413: gap of 100 bp
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* 13983 14082: gap of 100 bp
* 14083 14798: contig of 716 bp in length
* 14799 14898: gap of 100 bp

14899
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18915: contig of 709 bp in length
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19742: contig of 727 bp in length
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Query Match	6.8%;	Score 153;	DB 1;	Length 73476;
Best Local Similarity	100.0%;	Pred. No. 8.3;		
Matches 153;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY	1627	GAGAACATTCCGAGATGAGAAAATCAACAGGT	1659
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RESULT 15
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LOCUS Homo sapiens cDNA clone IMAGE:6157986, partial cds. PRI 03-FEB-2004
DEFINITION BC065925
ACCESSION BC065925
VERSION BC065925.1 GI:41943841
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1467)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1467)
Strausberg,R.
Direct Submission
Submitted (02-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 140 Row: m Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES	Location/Qualifiers
source	1. .1467 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6157986" /tissue_type="Skin, melanotic melanoma." /clone_lib="NIH MGC_72" /lab_host="DH10B" /note="Vector: pCMV-SPORT6"

Query Match	6.8%;	Score 152.8;	DB 1;	Length 1467;
Best Local Similarity	98.7%;	Pred. No. 3.1e+02;		
Matches 154;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	352	AGACGCTGAGGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTTCA	411
Db	544	AGACGCTGAGGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTTCA	485

QY	412	GACAAGAGCTTTCAGAATGATGGCCGTGGTGCGGACACGCTGCAGCGCTGGGGCCC	471
Db	484	GACAAGAGCTTTCAGAATGATGGCCGTGGTGCGGACACGCTGCAGCGCTGGGGCCC	425

QY	472	GTGTGGCCTCGGTGGACATGGGTCCCTCAGCAGCTGC	507
Db	424	GTGTGGCCTCGGTGGACATGGGTCCCTCAGCAAGTGC	389

RESULT 16
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LOCUS Homo sapiens chromosome 18, clone RP11-231E4, complete sequence.
DEFINITION AC009704
ACCESSION AC009704

VERSION	AC009704.8	GI:15799618	
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 178691)		
TITLE	Birren,B., Linton,L., Nusbaum,C. and Lander,E.		
JOURNAL	Homo sapiens chromosome 18, clone RP11-231E4		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 178691)		
	Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A., Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Depayre,E., Devon,K., Dewar,K., Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L., Karatas,A., Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J., Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B., Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P., Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A., Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (28-AUG-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
REFERENCE	3 (bases 1 to 178691)		
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C., MacDonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., MCPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (28-SEP-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
COMMENT	On Sep 28, 2001 this sequence version replaced gi:15706132. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html		
	----- Genome Center Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu ----- Project Information Center project name: L2362 Center clone name: 231_E_4 ----- Location/Qualifiers 1. 178691 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"		
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Best Local Similarity 83.9%; Pred. No. 5.3;		
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Db	99161 ACTCCGTCTCA	99161 ACTCCGTCTCA
QY	2237 AA	2237 AA
Db	99101 AA	99101 AA
RESULT 17		
AC116904	LOCUS	AC116904
DEFINITION	Homo sapiens chromosome 18, clone RP11-1112M8, complete sequence.	PRI 03-SEP-2002
ACCESSION	AC116904	
VERSION	AC116904.7	GI:22655819
KEYWORDS	HTG.	
SOURCE	Homo sapiens (human)	

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 164394)
TITLE	Birren, B., Nusbaum, C. and Lander, E.
JOURNAL	Homo sapiens chromosome 18, clone RP11-1112M8
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 164394)
REFERENCE	Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczký, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Trigg, J., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
TITLE	Direct Submission
JOURNAL	Submitted (02-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE	3 (bases 1 to 164394)
AUTHORS	Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
TITLE	Direct Submission
JOURNAL	Submitted (28-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE	4 (bases 1 to 164394)
AUTHORS	Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
TITLE	Direct Submission
JOURNAL	Submitted (28-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE	4 (bases 1 to 164394)
AUTHORS	Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL
COMMENT

Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (03-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 3, 2002 this sequence version replaced gi:22532750.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
Center project name: L26198
Center clone name: 1112_M_8

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Db 65325 TGGTGAACCCCGTCTCTACTAAATAACAAACAAACAAACAAACAAAT 65384
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QY 2226 A 2226

Db 65385 A 65385

RESULT 18
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LOCUS BC047599 2006 bp mRNA linear PRI 25-AUG-2003
DEFINITION Homo sapiens cDNA clone IMAGE:5528129, partial cds.
ACCESSION BC047599
VERSION BC047599.2 GI:34192884
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


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Qy 219 AGAATGGCTGCGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 278
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Db 239 AGGAGCCAGCCATTCTCTGAGTTGGATCCATTAGGCTGGAGTTCTGAAGCCTCTAG 180
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RESULT 21
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DEFINITION Sequence 97 from patent US 6639063.
ACCESSION AR412460
VERSION AR412460.1 GI:40167570
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 672)
AUTHORS Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
TITLE EST's and encoded human proteins
JOURNAL Patent: US 6639063-A 97 28-OCT-2003;
FEATURES
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RESULT 22
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LOCUS AX969294 672 bp DNA linear PAT 15-JAN-2004
DEFINITION Sequence 97 from Patent EP1104808.
ACCESSION AX969294
VERSION AX969294.1 GI:40975507
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y.
TITLE ESTs and encoded human proteins
JOURNAL Patent: EP 1104808-A 97 06-JUN-2001;
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Best Local Similarity 55.4%; Pred. No. 1.3e+03;
Matches 46; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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RESULT 23
BD108013/c
LOCUS BD108013 672 bp DNA linear PAT 18-SEP-2002
DEFINITION EST and encoded human protein.
ACCESSION BD108013
VERSION BD108013.1 GI:23202831
KEYWORDS JP 2002010789-A/90.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 672)
AUTHORS Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 90 15-JAN-2002;
GENSET CORP
COMMENT
    OS Homo sapiens (human)
    PN JP 2002010789-A/90
    PD 15-JAN-2002
    PF 07-AUG-2000 JP 2000280989
    PR 05-AUG-1999 US 60/147499
    PI JEAN BAPTIST DUMAS MILNE EDWARDS,SEVELIN JOBERT,JEAN EVE PI
        GIORDANO
    PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,PC
        C12N1/21,
    PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00,PC
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    CC score 7.09999990463257
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Matches 46; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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Thu Feb 17 18:38:12 2005

Db 387 CAGCACTTGCTGAGGACCATGTCCACCGAGGGCCACACGGGGCCCCCAGGGCGTGCAGCGT 446
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RESULT 26
CQ715367/c
LOCUS 279 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 1301 from Patent WO02068579.
ACCESSION CQ715367
VERSION CQ715367.1 GI:42276224
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 1301 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
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Best Local Similarity 57.4%; Pred. No. 3.1e+03;
Matches 35; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Db 276 CTGAGGACCCATGTCCACCGAGGCCACACGGGGCCCCCAGGGCGTGCAGCGTGTCCGCAGC 217
QY 522 C 522
Db 216 C 216

Search completed: February 16, 2005, 11:33:14
Job time : 560 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2005, 19:10:01 ; Search time 822 Seconds
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Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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26	1531.6	68.3	1587	4	AAS43075
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131	73	3.3	216	10	ACD94023	Acd94023 Human col
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517	3.0	68	199	13	ACN56273	Acn56273 Cotton an
549	3.0	68	200	13	ACN52303	Acn52303 Cotton an
636	3.0	68	201	6	ABL86758	Abi86758 Human ova
850	3.0	68	202	6	AAD42252	Aad42252 Soybean F
850	3.0	68	203	13	ADR04268	Adr04268 Soybean F
1690	3.0	68	204	3	AAZ90632	Aaz90632 Human adi
4130	3.0	68	205	10	ADL08408	Adl08408 Human can
309	3.0	67.8	206	5	ABV44994	Abv44994 Human pro
420	3.0	67.8	207	13	ACN61822	Acn61822 Cotton gy
429	3.0	67.8	208	5	ABV56874	Abv56874 Human pro
554	3.0	67.8	209	13	ACN51258	Acn51258 Cotton an
556	3.0	67.8	210	5	ABV40163	Abv40163 Human pro
556	3.0	67.8	211	5	ABV40063	Abv40063 Human pro
556	3.0	67.8	212	5	ABV42105	Abv42105 Human pro
556	3.0	67.8	213	5	ABV43601	Abv43601 Human pro
574	3.0	67.8	214	13	ACN56366	Acn56366 Cotton an
588	3.0	67.8	215	13	ACN46068	Acn46068 Cotton pr
690	3.0	67.8	216	13	ADR63575	Adr63575 Cotton CD
810	3.0	67.8	217	4	AAS27002	Aas27002 cDNA enco
810	3.0	67.8	218	10	ADB93180	Adb93180 Human cDN
1274	3.0	67.8	219	5	ADM19285	Adm19285 Novel hum
2126	3.0	67.8	220	13	ACN39160	Acn39160 Tumour-as
2126	3.0	67.8	221	13	ADP23018	Adp23018 PRO polyp
553	3.0	67.6	222	13	ACN62578	Acn62578 Cotton de
575	3.0	67.6	223	3	AAC59682	Aac59682 Human sec
575	3.0	67.6	224	8	ABZ73430	Abz73430 Secreted
575	3.0	67.6	225	8	ADA97993	Ada97993 Human sec
575	3.0	67.6	226	8	ADA43897	Ada43897 Human sec
575	3.0	67.6	227	10	ADC20156	Adc20156 Human sec
575	3.0	67.6	228	10	ADF10596	Adf10596 Human sec
575	3.0	67.6	229	10	ABZ67037	Abz67037 Human sec
578	3.0	67.6	230	13	ACN53254	Acn53254 Cotton an
583	3.0	67.6	231	13	ACN51300	Acn51300 Cotton an
896	3.0	67.6	232	4	AAH33168	Aah33168 Human col
1194	3.0	67.6	233	13	ACN40941	Acn40941 Tumour-as
1639	3.0	67.6	234	3	AAC98202	Aac98202 Human col
3899	3.0	67.6	235	2	AAV63192	Aav63192 cDNA from
3899	3.0	67.6	236	6	ABQ92042	Abq92042 Human pol
5625	3.0	67.6	237	12	ADQ24888	Adq24888 Human sof
453	3.0	67.4	238	5	ABV56723	Abv56723 Human pro
545	3.0	67.4	239	4	AAH70126	Aah70126 Human cer

c 240	67.4	3.0	637	11	ACN87636	Acn87636 Breast ca	313	66.6	3.0	2846	8	ACD25135	AcD25135 Human sec
241	67.4	3.0	4397	5	ABV30288	Abv30288 Human pro	314	66.6	3.0	2846	8	ACF00184	Acf00184 Human sec
c 242	67.2	3.0	376	5	ABV56400	Abv56400 Human pro	315	66.6	3.0	2846	8	ACA60381	Aca60381 Novel hum
243	67.2	3.0	384	4	AAI88639	Aai88639 Human pol	316	66.6	3.0	2846	8	ACA72241	Aca72241 Novel hum
244	67.2	3.0	386	4	AAI89019	Aai89019 Human pol	317	66.6	3.0	2846	8	ACD04765	Acd04765 Novel hum
245	67.2	3.0	477	9	ACH37468	Ach37468 Human end	318	66.6	3.0	2846	8	ACD18226	Acd18226 Human sec
246	67.2	3.0	498	9	ACH21767	Ach21767 Human adu	319	66.6	3.0	2846	8	ACD08233	Acd08233 Human sec
c 247	67.2	3.0	557	13	ACN47785	Acn47785 Cotton pr	320	66.6	3.0	2846	8	ACA88667	Aca88667 Novel hum
248	67.2	3.0	680	3	AAC79893	Aac79893 Human sec	321	66.6	3.0	2846	8	ACA70109	Aca70109 Human sec
249	67.2	3.0	749	3	AAC77999	Aac77999 Human can	322	66.6	3.0	2846	8	ACD12331	Acd12331 Novel hum
c 250	67.2	3.0	749	6	ABQ54165	Abq54165 Human ova	323	66.6	3.0	2846	8	ACC74246	Acc74246 Human sec
251	67.2	3.0	1043	4	AAH72615	Aah72615 Human cer	324	66.6	3.0	2846	8	ACD15874	Acd15874 Human sec
252	67.2	3.0	1058	6	ABQ54594	Abq54594 Human ova	325	66.6	3.0	2846	8	ACD25442	Acd25442 Novel hum
253	67.2	3.0	1091	4	AAC89723	Aac89723 Maize 2mG	326	66.6	3.0	2846	8	ACD17919	Acd17919 Human sec
254	67.2	3.0	1091	8	ABX95035	Abx95035 cDNA enco	327	66.6	3.0	2846	8	ACC88206	Acc88206 Human sec
c 255	67.2	3.0	2007	12	ADQ23886	Adq23886 Human sof	328	66.6	3.0	2846	8	ACD21560	Acd21560 Human sec
c 256	67	3.0	346	5	ADL37542	Adl37542 Human ova	329	66.6	3.0	2846	8	ACD18627	Acd18627 Human sec
c 257	67	3.0	346	5	ADI72399	Adi72399 Human ova	330	66.6	3.0	2846	8	ACA58828	Aca58828 cDNA enco
c 258	67	3.0	404	5	ABV56394	Abv56394 Human pro	331	66.6	3.0	2846	8	ABX98237	Abx98237 Human cDN
c 259	67	3.0	461	5	ADL43889	Adl43889 Human ova	332	66.6	3.0	2846	8	ACD13988	Acd13988 Human PRO
c 260	67	3.0	508	13	ACN50622	Acn50622 Cotton ma	333	66.6	3.0	2846	8	ACD09768	Acd09768 Human sec
c 261	67	3.0	528	13	ACN47028	Acn47028 Cotton pr	334	66.6	3.0	2846	8	ACC88513	Acc88513 Human sec
c 262	67	3.0	768	4	AAL08093	Aal08093 Human bre	335	66.6	3.0	2846	8	ACD21253	Acd21253 Human sec
263	67	3.0	976	4	AAS01021	Aas01021 Sugarcane	336	66.6	3.0	2846	8	ABX75625	Abx75625 Human cDN
264	67	3.0	1925	2	AAV34271	Aav34271 Human sec	337	66.6	3.0	2846	8	ACA64004	Aca64004 cDNA enco
265	67	3.0	1925	8	ACD08142	Acd08142 cDNA enco	338	66.6	3.0	2846	8	ABX97828	Abx97828 Human PRO
c 266	66.8	3.0	330	5	ADL43756	Adl43756 Human ova	339	66.6	3.0	2846	8	ACA97304	Aca97304 Novel hum
267	66.8	3.0	411	4	AAI93716	Aai93716 Human pol	340	66.6	3.0	2846	8	ACA57767	Aca57767 Human PRO
c 268	66.8	3.0	445	5	ADI76334	Adi76334 Human ova	341	66.6	3.0	2846	8	ACD14295	Acd14295 Human PRO
c 269	66.8	3.0	445	5	ADI70001	Adi70001 Human ova	342	66.6	3.0	2846	8	ACC91078	Acc91078 Human sec
c 270	66.8	3.0	553	13	ACN53206	Acn53206 Cotton an	343	66.6	3.0	2846	8	ACC88820	Acc88820 Human sec
c 271	66.8	3.0	610	5	ADL37504	Adl37504 Human ova	344	66.6	3.0	2846	8	ACD07017	Acd07017 Human PRO
c 272	66.8	3.0	610	5	ADI72360	Adi72360 Human ova	345	66.6	3.0	2846	8	ACA67468	Aca67468 Human PRO
273	66.8	3.0	705	6	ABQ54208	Abq54208 Human ova	346	66.6	3.0	2846	8	ACC81523	Acc81523 Human sec
274	66.8	3.0	1365	4	AAS02661	Aas02661 Human sec	347	66.6	3.0	2846	8	ACA91268	Aca91268 cDNA enco
275	66.8	3.0	1365	8	ABZ73522	Abz73522 Secreted	348	66.6	3.0	2846	8	ACC89127	Acc89127 Human sec
276	66.8	3.0	1365	10	ABZ67129	Abz67129 Human sec	349	66.6	3.0	2846	8	ACC86483	Acc86483 Human sec
277	66.8	3.0	2187	10	ADE79073	Ade79073 Human pro	350	66.6	3.0	2846	8	ACC89741	Acc89741 Human sec
278	66.8	3.0	2329	5	AAD07661	Aad07661 Human sec	351	66.6	3.0	2846	8	ACC92920	Acc92920 Human sec
279	66.8	3.0	2343	6	ABQ54904	Abq54904 Human ova	352	66.6	3.0	2846	8	ABX80775	Abx80775 Human sec
280	66.8	3.0	2755	6	ABQ54342	Abq54342 Human ova	353	66.6	3.0	2846	8	ACA72548	Aca72548 Human PRO
281	66.8	3.0	3144	3	AAF18172	Aaf18172 Lung canc	354	66.6	3.0	2846	8	ACA89066	Aca89066 Human sec
c 282	66.8	3.0	6155	6	ABK28362	Abk28362 DNA trans	355	66.6	3.0	2846	8	ACA69802	Aca69802 Human sec
c 283	66.6	3.0	291	5	ADI73348	Adi73348 Human ova	356	66.6	3.0	2846	8	ACA96945	Aca96945 Novel hum
c 284	66.6	3.0	291	5	ADL38479	Adl38479 Human ova	357	66.6	3.0	2846	8	ACA90941	Aca90941 Novel hum
285	66.6	3.0	310	6	ABK09625	Abk09625 Human ova	358	66.6	3.0	2846	8	ACA70723	Aca70723 Human sec
c 286	66.6	3.0	390	5	ADL43918	Adl43918 Human ova	359	66.6	3.0	2846	8	ACA95233	Aca95233 Novel hum
c 287	66.6	3.0	445	5	ADL43518	Adl43518 Human ova	360	66.6	3.0	2846	8	ACD44284	Acd44284 cDNA enco
c 288	66.6	3.0	458	13	ACN50953	Acn50953 Cotton an	361	66.6	3.0	2846	8	ACC86176	Acc86176 Human sec
289	66.6	3.0	498	13	ACN56190	Acn56190 Cotton an	362	66.6	3.0	2846	8	ACD45167	Acd45167 Human sec
290	66.6	3.0	591	13	ACN58226	Acn58226 Cotton gy	363	66.6	3.0	2846	8	ACC90048	Acc90048 Human sec
c 291	66.6	3.0	688	4	AAL15556	Aal15556 Human bre	364	66.6	3.0	2846	8	ACD12656	Acd12656 Human sec
c 292	66.6	3.0	912	11	ACN85543	Acn85543 Breast ca	365	66.6	3.0	2846	8	ACF19886	Acf19886 Human sec
293	66.6	3.0	936	2	AAZ06226	Aaz06226 Human sec	366	66.6	3.0	2846	8	ABX76830	Abx76830 Human PRO
294	66.6	3.0	2022	6	AAD33261	Aad33261 Human sec	367	66.6	3.0	2846	8	ACA73162	Aca73162 Novel hum
295	66.6	3.0	2311	7	ADR41309	Adr41309 Human CD-	368	66.6	3.0	2846	8	ACA68705	Aca68705 Novel hum
296	66.6	3.0	2843	9	ADA00368	Ada00368 Human sec	369	66.6	3.0	2846	8	ACA74549	Aca74549 cDNA enco
297	66.6	3.0	2846	3	AAZ65034	Aaz65034 Membrane-	370	66.6	3.0	2846	8	ACA70416	Aca70416 Human sec
298	66.6	3.0	2846	4	AAS46009	Aas46009 Human DNA	371	66.6	3.0	2846	8	ACD14602	Acd14602 Human PRO
299	66.6	3.0	2846	4	AAF92076	Aaf92076 Human PRO	372	66.6	3.0	2846	8	ACA93715	Aca93715 Human cDN
300	66.6	3.0	2846	5	AAF44180	Aaf44180 Human PRO	373	66.6	3.0	2846	8	ACA68274	Aca68274 Novel hum
301	66.6	3.0	2846	6	ABS74396	Abs74396 Human cDN	374	66.6	3.0	2846	8	ABX98739	Abx98739 Novel hum
302	66.6	3.0	2846	8	ACA89459	Aca89459 cDNA enco	375	66.6	3.0	2846	8	ACC81216	Acc81216 Human sec
303	66.6	3.0	2846	8	ACA73469	Aca73469 Human sec	376	66.6	3.0	2846	8	ACA95540	Aca95540 Novel hum
304	66.6	3.0	2846	8	ACA05784	Aca05784 Human sec	377	66.6	3.0	2846	8	ACD04458	Acd04458 Novel hum
305	66.6	3.0	2846	8	ACA66618	Aca66618 cDNA enco	378	66.6	3.0	2846	8	ACC87899	Acc87899 Human sec
306	66.6	3.0	2846	8	ACA64316	Aca64316 Novel hum	379	66.6	3.0	2846	8	ACF12561	Acf12561 Human sec
307	66.6	3.0	2846	8	ACA91182	Aca91182 Novel hum	380	66.6	3.0	2846	8	ACH6262	Ach6262 Novel hum
308	66.6	3.0	2846	8	ACD81559	Acd81559 Human cDN	381	66.6	3.0	2846	8	ABX79455	Abx79455 Human sec
309	66.6	3.0	2846	8	ACF20193	Acf20193 Human sec	382	66.6	3.0	2846	8	ACA96276	Aca96276 Human PRO
310	66.6	3.0	2846	8	ACF19579	Acf19579 Human sec	383	66.6	3.0	2846	8	ACA65050	Aca65050 Human PRO
311	66.6	3.0	2846	8	ACD21867	Acd21867 Human sec	384	66.6	3.0	2846	8	ACA73776	Aca73776 Human sec
312	66.6	3.0	2846	8	ACF13032	Acf13032 Human sec	385	66.6	3.0	2846	8	ACA74188	Aca74188 Novel hum

386	66.6	3.0	2846	8	ACA96583	Aca96583 Human PRO	459	66.6	3.0	2846	9	ACD41572	Ac41572 Human sec
387	66.6	3.0	2846	8	ACD10689	Ac410689 cDNA enco	460	66.6	3.0	2846	9	ADA37741	Ada37741 Human CDN
388	66.6	3.0	2846	8	ACC91385	Acc91385 Human sec	461	66.6	3.0	2846	9	ACF31985	Acf31985 Human sec
389	66.6	3.0	2846	8	ACA93476	Aca93476 Novel hum	462	66.6	3.0	2846	9	ACF23263	Acf23263 Human sec
390	66.6	3.0	2846	8	ACD02720	Ac402720 cDNA enco	463	66.6	3.0	2846	9	ACF39953	Acf39953 Human sec
391	66.6	3.0	2846	8	ACC87285	Acc87285 Human sec	464	66.6	3.0	2846	9	ACD45475	Ac45475 Human sec
392	66.6	3.0	2846	8	ACC85869	Acc85869 Human sec	465	66.6	3.0	2846	9	ACF53132	Acf53132 Human sec
393	66.6	3.0	2846	8	ABX81158	Abx81158 Human sec	466	66.6	3.0	2846	9	ACF27312	Acf27312 Human sec
394	66.6	3.0	2846	8	ACA65357	Aca65357 Human PRO	467	66.6	3.0	2846	9	ACF45150	Acf45150 Human sec
395	66.6	3.0	2846	8	ACA94174	Aca94174 Human sec	468	66.6	3.0	2846	9	ACF29768	Acf29768 Human sec
396	66.6	3.0	2846	8	ACA97918	Aca97918 Human PRO	469	66.6	3.0	2846	9	ACD89844	Acd89844 Human sec
397	66.6	3.0	2846	8	ACA91420	Aca91420 Novel hum	470	66.6	3.0	2846	9	ACD84625	Acd84625 Human PRO
398	66.6	3.0	2846	8	ACA90634	Aca90634 Novel hum	471	66.6	3.0	2846	9	ACD98785	Acd98785 cDNA enco
399	66.6	3.0	2846	8	ACD16181	Acd16181 Human sec	472	66.6	3.0	2846	9	ACF77077	Acf77077 Human sec
400	66.6	3.0	2846	8	ACD17342	Acd17342 Human sec	473	66.6	3.0	2846	9	ACF76770	Acf76770 Human sec
401	66.6	3.0	2846	8	ACC91999	Acc91999 Human sec	474	66.6	3.0	2846	9	ACF49755	Acf49755 Human sec
402	66.6	3.0	2846	8	ACD02316	Ac402316 Novel hum	475	66.6	3.0	2846	9	ACF50062	Acf50062 Human sec
403	66.6	3.0	2846	8	ACA74856	Aca74856 cDNA enco	476	66.6	3.0	2846	9	ADA21427	Ada21427 Human CDN
404	66.6	3.0	2846	8	ACA91727	Aca91727 Human PRO	477	66.6	3.0	2846	9	ACD09461	Acd09461 Human sec
405	66.6	3.0	2846	8	ACA89307	Aca89307 Novel hum	478	66.6	3.0	2846	9	ACD08540	Acd08540 Human sec
406	66.6	3.0	2846	8	ACA71371	Aca71371 Human sec	479	66.6	3.0	2846	9	ACH03594	Ach03594 Human sec
407	66.6	3.0	2846	8	ACC90771	Acc90771 Human sec	480	66.6	3.0	2846	9	ACF12254	Acf12254 Human sec
408	66.6	3.0	2846	8	ACA65781	Aca65781 cDNA enco	481	66.6	3.0	2846	9	ACC94762	Acc94762 Human sec
409	66.6	3.0	2846	8	ACA68944	Aca68944 Novel hum	482	66.6	3.0	2846	9	ACD22481	Acd22481 Human sec
410	66.6	3.0	2846	8	ACA92974	Aca92974 Novel hum	483	66.6	3.0	2846	9	ACF15181	Acf15181 Human sec
411	66.6	3.0	2846	8	ACA94926	Aca94926 cDNA enco	484	66.6	3.0	2846	9	ACC97276	Acc97276 Human sec
412	66.6	3.0	2846	8	ACD16488	Acd16488 Human sec	485	66.6	3.0	2846	9	ACC92306	Acc92306 Human sec
413	66.6	3.0	2846	8	ACD15567	Acd15567 Human sec	486	66.6	3.0	2846	9	ACF13953	Acf13953 Human sec
414	66.6	3.0	2846	8	ACA98466	Aca98466 Human PRO	487	66.6	3.0	2846	9	ACF14260	Acf14260 Human sec
415	66.6	3.0	2846	8	ABX17058	Abx17058 Human PRO	488	66.6	3.0	2846	9	ADA10214	Ada10214 Human CDN
416	66.6	3.0	2846	8	ABX16670	Abx16670 Human CDN	489	66.6	3.0	2846	9	ACF09491	Acf09491 Human sec
417	66.6	3.0	2846	9	ACA67913	Aca67913 Novel hum	490	66.6	3.0	2846	9	ACD45782	Acd45782 Human sec
418	66.6	3.0	2846	9	ACA63391	Aca63391 cDNA enco	491	66.6	3.0	2846	9	ACD47931	Acd47931 Human sec
419	66.6	3.0	2846	9	ACA97611	Aca97611 Human PRO	492	66.6	3.0	2846	9	ACD67662	Acd67662 cDNA enco
420	66.6	3.0	2846	9	ACA99060	Aca99060 Novel hum	493	66.6	3.0	2846	9	ACF25470	Acf25470 Human sec
421	66.6	3.0	2846	9	ACC91692	Acc91692 Human sec	494	66.6	3.0	2846	9	ACF29154	Acf29154 Human sec
422	66.6	3.0	2846	9	ACD11103	Acd11103 Novel hum	495	66.6	3.0	2846	9	ACD84932	Acd84932 Human sec
423	66.6	3.0	2846	9	ACD14953	Acd14953 Human sec	496	66.6	3.0	2846	9	ACD84011	Acd84011 Human PRO
424	66.6	3.0	2846	9	ACA88362	Aca88362 Human sec	497	66.6	3.0	2846	9	ACD88002	Acd88002 Human sec
425	66.6	3.0	2846	9	ACD81869	Acd81869 cDNA enco	498	66.6	3.0	2846	9	ACF30689	Acf30689 Human sec
426	66.6	3.0	2846	9	ACD11717	Acd11717 Human sec	499	66.6	3.0	2846	9	ACF32292	Acf32292 Human sec
427	66.6	3.0	2846	9	ACC95846	Acc95846 Human sec	500	66.6	3.0	2846	9	ACH11952	Ach11952 cDNA enco
428	66.6	3.0	2846	9	ACF16409	Acf16409 Human sec	501	66.6	3.0	2846	9	ACH12259	Ach12259 cDNA enco
429	66.6	3.0	2846	9	ACF02527	Acf02527 Human sec	502	66.6	3.0	2846	9	ADA19899	Ada19899 Novel hum
430	66.6	3.0	2846	9	ACF02834	Acf02834 Human sec	503	66.6	3.0	2846	9	ACD40651	Acd40651 Human sec
431	66.6	3.0	2846	9	ACF21421	Acf21421 Human sec	504	66.6	3.0	2846	9	ADB17282	Adb17282 Human CDN
432	66.6	3.0	2846	9	ACF10105	Acf10105 Human sec	505	66.6	3.0	2846	9	ADA17758	Ada17758 cDNA enco
433	66.6	3.0	2846	9	ACF77998	Acf77998 Human sec	506	66.6	3.0	2846	9	ACF18123	Acf18123 Human sec
434	66.6	3.0	2846	9	ACD46703	Acd46703 Human sec	507	66.6	3.0	2846	9	ACF08570	Acf08570 Human sec
435	66.6	3.0	2846	9	ACD49466	Acd49466 Human sec	508	66.6	3.0	2846	9	ACF31371	Acf31371 Human sec
436	66.6	3.0	2846	9	ACF28233	Acf28233 Human sec	509	66.6	3.0	2846	9	ACF52211	Acf52211 Human sec
437	66.6	3.0	2846	9	ACD88923	Acd88923 Human sec	510	66.6	3.0	2846	9	ACD50080	Acd50080 Human sec
438	66.6	3.0	2846	9	ACD84318	Acd84318 Human PRO	511	66.6	3.0	2846	9	ACF38783	Acf38783 Human sec
439	66.6	3.0	2846	9	ACD99092	Acd99092 cDNA enco	512	66.6	3.0	2846	9	ACF26698	Acf26698 Human sec
440	66.6	3.0	2846	9	ADA77921	Ada77921 Human sec	513	66.6	3.0	2846	9	ACF46378	Acf46378 Human sec
441	66.6	3.0	2846	9	ACF48834	Acf48834 Human sec	514	66.6	3.0	2846	9	ACF24798	Acf24798 Human sec
442	66.6	3.0	2846	9	ACD09154	Acd09154 Human sec	515	66.6	3.0	2846	9	ACF27926	Acf27926 Human sec
443	66.6	3.0	2846	9	ACF11947	Acf11947 Human sec	516	66.6	3.0	2846	9	ACD89230	Acd89230 Human sec
444	66.6	3.0	2846	9	ACF41181	Acf41181 Human sec	517	66.6	3.0	2846	9	ACF63802	Acf63802 Human sec
445	66.6	3.0	2846	9	ACF15795	Acf15795 Human sec	518	66.6	3.0	2846	9	ACF60442	Acf60442 Human sec
446	66.6	3.0	2846	9	ACF16102	Acf16102 Human sec	519	66.6	3.0	2846	9	ACH12566	Ach12566 cDNA enco
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449	66.6	3.0	2846	9	ACF18737	Acf18737 Human sec	522	66.6	3.0	2846	9	ACD10382	Acd10382 Human sec
450	66.6	3.0	2846	9	ACF09184	Acf09184 Human sec	523	66.6	3.0	2846	9	ACD12024	Acd12024 Human sec
451	66.6	3.0	2846	9	ACF78305	Acf78305 Human sec	524	66.6	3.0	2846	9	ACF42409	Acf42409 Human sec
452	66.6	3.0	2846	9	ACF51904	Acf51904 Human sec	525	66.6	3.0	2846	9	ADA27866	Ada27866 Human CDN
453	66.6	3.0	2846	9	ACF26391	Acf26391 Human sec	526	66.6	3.0	2846	9	ACF18430	Acf18430 Human sec
454	66.6	3.0	2846	9	ACF24184	Acf24184 Human sec	527	66.6	3.0	2846	9	ACF02220	Acf02220 Human sec
455	66.6	3.0	2846	9	ACF63495	Acf63495 Human sec	528	66.6	3.0	2846	9	ACF21728	Acf21728 Human sec
456	66.6	3.0	2846	9	ACF50369	Acf50369 Human sec	529	66.6	3.0	2846	9	ACF10412	Acf10412 Human sec
457	66.6	3.0	2846	9	ACH07840	Ach07840 Human sec	530	66.6	3.0	2846	9	ACF33864	Acf33864 Human sec
458	66.6	3.0	2846	9	ACF13646	Acf13646 Human sec	531	66.6	3.0	2846	9	ACF44826	Acf44826 Human sec

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629 66.6 3.0 2846 9 ACD43037 Acd43037 cDNA enco
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679	66.6	3.0	2846	9	ACF10719	Acf10719 Human sec	752	66.6	3.0	2846	10	ACF54974	Acf54974 Human sec
680	66.6	3.0	2846	9	ACC93534	Acc93534 Human sec	753	66.6	3.0	2846	10	ADB90913	Adb90913 Novel hum
681	66.6	3.0	2846	9	ACC96153	Acc96153 Human sec	754	66.6	3.0	2846	10	ADC57710	Adc57710 Human PRO
682	66.6	3.0	2846	9	ACD24828	Acd24828 Human sec	755	66.6	3.0	2846	10	ADC55074	Adc55074 Human PRO
683	66.6	3.0	2846	9	ACF01913	Acf01913 Human sec	756	66.6	3.0	2846	10	ADC11941	Adc11941 Human CDN
684	66.6	3.0	2846	9	ACF22035	Acf22035 Human sec	757	66.6	3.0	2846	10	ADC06993	Adc06993 Human PRO
685	66.6	3.0	2846	9	ACF22649	Acf22649 Human sec	758	66.6	3.0	2846	10	ADC56363	Adc56363 Human PRO
686	66.6	3.0	2846	9	ACF08877	Acf08877 Human sec	759	66.6	3.0	2846	10	ADC17172	Adc17172 cDNA sequ
687	66.6	3.0	2846	9	ACE33213	Acf33213 Human sec	760	66.6	3.0	2846	10	ADC07418	Adc07418 Human CDN
688	66.6	3.0	2846	9	ACF54667	Acf54667 Human sec	761	66.6	3.0	2846	10	ADC11408	Adc11408 Human CDN
689	66.6	3.0	2846	9	ACF48527	Acf48527 Human sec	762	66.6	3.0	2846	10	ADC14870	Adc14870 Novel hum
690	66.6	3.0	2846	9	ACD47317	Acd47317 Human sec	763	66.6	3.0	2846	10	ADC52365	Adc52365 Novel hum
691	66.6	3.0	2846	9	ACD49159	Acd49159 Human sec	764	66.6	3.0	2846	10	ADC14530	Adc14530 Novel hum
692	66.6	3.0	2846	9	ACF37862	Acf37862 Human sec	765	66.6	3.0	2846	10	ADD08062	Add08062 Novel hum
693	66.6	3.0	2846	9	ACF30075	Acf30075 Human sec	766	66.6	3.0	2846	10	ADC81887	Adc81887 Human PRO
694	66.6	3.0	2846	9	ACD87388	Acd87388 Human sec	767	66.6	3.0	2846	10	ADD07529	Add07529 Novel hum
695	66.6	3.0	2846	9	ACF61977	Acf61977 Human sec	768	66.6	3.0	2846	10	ADC82420	Adc82420 Human PRO
696	66.6	3.0	2846	9	ACH10910	Ach10910 Human sec	769	66.6	3.0	2846	10	ADD05642	Add05642 Human sec
697	66.6	3.0	2846	9	ACDI10075	Acd10075 Human sec	770	66.6	3.0	2846	10	ADD08600	Add08600 Novel hum
698	66.6	3.0	2846	9	ACH65430	Ach65430 Human CDN	771	66.6	3.0	2846	10	ADD06849	Add06849 Novel hum
699	66.6	3.0	2846	9	ACC99097	Acc99097 Human sec	772	66.6	3.0	2846	10	ADC83096	Adc83096 Human PRO
700	66.6	3.0	2846	9	ACF00491	Acf00491 Human sec	773	66.6	3.0	2846	10	ADD55203	Add55203 Human PRO
701	66.6	3.0	2846	9	ACD40958	Acd40958 Human sec	774	66.6	3.0	2846	10	ADD36041	Add36041 Novel hum
702	66.6	3.0	2846	9	ACF14567	Acf14567 Human sec	775	66.6	3.0	2846	10	ADD56161	Add56161 Human PRO
703	66.6	3.0	2846	9	ACF22342	Acf22342 Human sec	776	66.6	3.0	2846	10	ADD54599	Add54599 Human PRO
704	66.6	3.0	2846	9	ACF78919	Acf78919 Human sec	777	66.6	3.0	2846	10	ADE26753	Ade26753 Novel hum
705	66.6	3.0	2846	9	ACF11640	Acf11640 Human sec	778	66.6	3.0	2846	10	ADE26220	Ade26220 Novel hum
706	66.6	3.0	2846	9	ADA22353	Ada22353 Human CDN	779	66.6	3.0	2846	10	ADF67157	Adf67157 Human PRO
707	66.6	3.0	2846	9	ACF51597	Acf51597 Human sec	780	66.6	3.0	2846	10	ADG01042	Adg01042 Novel hum
708	66.6	3.0	2846	9	ACF33520	Acf33520 Human sec	781	66.6	3.0	2846	10	ADG08595	Adg08595 Novel hum
709	66.6	3.0	2846	9	ACD49773	Acd49773 Human sec	782	66.6	3.0	2846	10	ADG02637	Adg02637 Novel hum
710	66.6	3.0	2846	9	ACF37555	Acf37555 Human sec	783	66.6	3.0	2846	10	ADG01344	Adg01344 Novel hum
711	66.6	3.0	2846	9	ACF28540	Acf28540 Human sec	784	66.6	3.0	2846	10	ADF95519	Adf95519 Novel hum
712	66.6	3.0	2846	9	ACD88616	Acd88616 Human sec	785	66.6	3.0	2846	10	ADF95216	Adf95216 Novel hum
713	66.6	3.0	2846	9	ACF75235	Acf75235 Human sec	786	66.6	3.0	2846	10	ADG12334	Adg12334 Novel hum
714	66.6	3.0	2846	9	ACF61056	Acf61056 Human sec	787	66.6	3.0	2846	10	ADH24069	Adh24069 Novel hum
715	66.6	3.0	2846	9	ACF44212	Acf44212 Human sec	788	66.6	3.0	2846	10	ADH34095	Adh34095 Novel hum
716	66.6	3.0	2846	9	ACH08454	Ach08454 Human sec	789	66.6	3.0	2846	10	ADH23899	Adh23899 Novel hum
717	66.6	3.0	2846	9	ACD39420	Acd39420 Human PRO	790	66.6	3.0	2846	10	ADH08994	Adh08994 Human PRO
718	66.6	3.0	2846	9	ACC93841	Acc93841 Human sec	791	66.6	3.0	2846	10	ADG85303	Adg85303 Novel hum
719	66.6	3.0	2846	9	ACD20946	Acd20946 Human sec	792	66.6	3.0	2846	10	ADH24579	Adh24579 Novel hum
720	66.6	3.0	2846	9	ACD20639	Acd20639 Human sec	793	66.6	3.0	2846	10	ADH37435	Adh37435 Human sec
721	66.6	3.0	2846	9	ACF06728	Acf06728 Human sec	794	66.6	3.0	2846	10	ADH02024	Adh02024 Human PRO
722	66.6	3.0	2846	9	ACD22788	Acd22788 Human sec	795	66.6	3.0	2846	10	ADH37605	Adh37605 Human sec
723	66.6	3.0	2846	9	ACF41488	Acf41488 Human sec	796	66.6	3.0	2846	10	ADG85643	Adg85643 Novel hum
724	66.6	3.0	2846	9	ADA06519	Ada06519 Human sec	797	66.6	3.0	2846	10	ADH24239	Adh24239 Novel hum
725	66.6	3.0	2846	9	ADA39212	Ada39212 Human CDN	798	66.6	3.0	2846	10	ADH38533	Adh38533 Novel hum
726	66.6	3.0	2846	9	ACF07035	Acf07035 Human sec	799	66.6	3.0	2846	10	ADG83654	Adg83654 Human PRO
727	66.6	3.0	2846	9	ACF77691	Acf77691 Human sec	800	66.6	3.0	2846	10	ADH29462	Adh29462 Novel hum
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729	66.6	3.0	2846	9	ACF46992	Acf46992 Human sec	802	66.6	3.0	2846	10	ADH37775	Adh37775 Human sec
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731	66.6	3.0	2846	9	ACF45764	Acf45764 Human sec	804	66.6	3.0	2846	10	ADH57372	Adh57372 Novel hum
732	66.6	3.0	2846	9	ACF45457	Acf45457 Human sec	805	66.6	3.0	2846	10	ADH53514	Adh53514 Novel hum
733	66.6	3.0	2846	9	ACF38476	Acf38476 Human sec	806	66.6	3.0	2846	10	ADH53684	Adh53684 Novel hum
734	66.6	3.0	2846	9	ACD89537	Acd89537 Human sec	807	66.6	3.0	2846	10	ADH52020	Adh52020 Novel hum
735	66.6	3.0	2846	9	ACD85239	Acd85239 Human sec	808	66.6	3.0	2846	10	ADH49875	Adh49875 Novel hum
736	66.6	3.0	2846	9	ACD85853	Acd85853 Human sec	809	66.6	3.0	2846	10	ADI25385	Adi25385 Novel hum
737	66.6	3.0	2846	9	ACF75849	Acf75849 Human sec	810	66.6	3.0	2846	10	ADH90178	Adh90178 Novel hum
738	66.6	3.0	2846	9	ACF60749	Acf60749 Human sec	811	66.6	3.0	2846	10	ADI25555	Adi25555 Novel hum
739	66.6	3.0	2846	9	ACH05636	Ach05636 cDNA enco	812	66.6	3.0	2846	10	ADH97729	Adh97729 Novel hum
740	66.6	3.0	2846	9	ADA82604	Ada82604 Human sec	813	66.6	3.0	2846	10	ADI35411	Adi35411 Human PRO
741	66.6	3.0	2846	9	ADB85610	Adb85610 Novel hum	814	66.6	3.0	2846	10	ADI03577	Adi03577 Novel hum
742	66.6	3.0	2846	9	ADB96238	Adb96238 Human PRO	815	66.6	3.0	2846	10	ADI11934	Adi11934 Human PRO
743	66.6	3.0	2846	9	ACF55895	Acf55895 Human sec	816	66.6	3.0	2846	10	ADH90008	Adh90008 Novel hum
744	66.6	3.0	2846	9	ACF55281	Acf55281 Human sec	817	66.6	3.0	2846	10	ADH99903	Adh99903 Novel hum
745	66.6	3.0	2846	10	ADB85912	Adb85912 Human sec	818	66.6	3.0	2846	10	ADH98409	Adh98409 Novel hum
746	66.6	3.0	2846	10	ACF56202	Acf56202 Human sec	819	66.6	3.0	2846	10	ADI11084	Adi11084 Human PRO
747	66.6	3.0	2846	10	ACF56509	Acf56509 Human sec	820	66.6	3.0	2846	10	ADI11594	Adi11594 Human PRO
748	66.6	3.0	2846	10	ADB68289	Adb68289 Human PRO	821	66.6	3.0	2846	10	ADH98239	Adh98239 Novel hum
749	66.6	3.0	2846	10	ADB68096	Adb68096 Human PRO	822	66.6	3.0	2846	10	ADH98579	Adh98579 Novel hum
750	66.6	3.0	2846	10			823	66.6	3.0	2846	10		

824	66.6	3.0	2846	10	ADH98069	Adh98069	Novel	hum	897	66.6	3.0	2846	12	ADH33721	Adh33721	Human	PRO
825	66.6	3.0	2846	10	ABX78612	Abx78612	Human	PRO	898	66.6	3.0	2846	12	ADG82818	Adg82818	Human	PRO
826	66.6	3.0	2846	10	ACA75584	Aca75584	Novel	hum	899	66.6	3.0	2846	12	ADH02364	Adh02364	Human	PRO
827	66.6	3.0	2846	10	ACA71064	Aca71064	Human	sec	900	66.6	3.0	2846	12	ADH07971	Adh07971	Novel	hum
828	66.6	3.0	2846	10	ACC87592	Acc87592	Human	sec	901	66.6	3.0	2846	12	ADG69368	Adg69368	Novel	hum
829	66.6	3.0	2846	10	ACC86978	Acc86978	Human	sec	902	66.6	3.0	2846	12	ADH39189	Adh39189	Novel	hum
830	66.6	3.0	2846	10	ACD04151	Acc04151	Human	sec	903	66.6	3.0	2846	12	ADH26099	Adh26099	Novel	hum
831	66.6	3.0	2846	10	ABX77859	Abx77859	Human	PRO	904	66.6	3.0	2846	12	ADG83929	Adg83929	Human	PRO
832	66.6	3.0	2846	10	ABX80271	Abx80271	Human	sec	905	66.6	3.0	2846	12	ADH19476	Adh19476	Human	CDN
833	66.6	3.0	2846	10	ACA69177	Aca69177	Human	sec	906	66.6	3.0	2846	12	ADG85473	Adg85473	Novel	hum
834	66.6	3.0	2846	10	ACA69482	Aca69482	CDNA	enco	907	66.6	3.0	2846	12	ADH06267	Adh06267	Novel	hum
835	66.6	3.0	2846	10	ACA90327	Aca90327	Novel	hum	908	66.6	3.0	2846	12	ADH30097	Adh30097	Novel	hum
836	66.6	3.0	2846	10	ACC89434	Acc89434	Human	sec	909	66.6	3.0	2846	12	ADH24409	Adh24409	Novel	hum
837	66.6	3.0	2846	10	ABX90248	Abx90248	Human	sec	910	66.6	3.0	2846	12	ADH33068	Adh33068	Human	PRO
838	66.6	3.0	2846	10	ACA98225	Aca98225	Novel	hum	911	66.6	3.0	2846	12	ADG69538	Adg69538	Novel	hum
839	66.6	3.0	2846	10	ACA93867	Aca93867	Human	sec	912	66.6	3.0	2846	12	ADH07801	Adh07801	Novel	hum
840	66.6	3.0	2846	10	ACD15260	Acc15260	Human	sec	913	66.6	3.0	2846	12	ADG85813	Adg85813	Novel	hum
841	66.6	3.0	2846	10	ACD08847	Acc08847	Human	sec	914	66.6	3.0	2846	12	ADH39359	Adh39359	Novel	hum
842	66.6	3.0	2846	10	ACC96767	Acc96767	Human	sec	915	66.6	3.0	2846	12	ADH33551	Adh33551	Human	PRO
843	66.6	3.0	2846	10	ACF15488	Acc15488	Human	sec	916	66.6	3.0	2846	12	ADH33891	Adh33891	Human	PRO
844	66.6	3.0	2846	10	ABX64094	Abx64094	CDNA	enco	917	66.6	3.0	2846	12	ADH01101	Adh01101	Human	PRO
845	66.6	3.0	2846	10	ACA72855	Aca72855	Human	PRO	918	66.6	3.0	2846	12	ADG69708	Adg69708	Novel	hum
846	66.6	3.0	2846	10	ACD03027	Acc03027	Novel	hum	919	66.6	3.0	2846	12	ADH20969	Adh20969	Human	CDN
847	66.6	3.0	2846	10	ACD01842	Acc01842	Novel	hum	920	66.6	3.0	2846	12	ADH02194	Adh02194	Human	PRO
848	66.6	3.0	2846	10	ACA92034	Aca92034	Novel	hum	921	66.6	3.0	2846	12	ADG69198	Adg69198	Novel	hum
849	66.6	3.0	2846	10	ADI05057	Adi05057	Novel	hum	922	66.6	3.0	2846	12	ADG85983	Adg85983	Novel	hum
850	66.6	3.0	2846	10	ADI03407	Adi03407	Novel	hum	923	66.6	3.0	2846	12	ADH24919	Adh24919	Novel	hum
851	66.6	3.0	2846	10	ADI04802	Adi04802	Novel	hum	924	66.6	3.0	2846	12	ADH39536	Adh39536	Novel	hum
852	66.6	3.0	2846	10	ADH78256	Adh78256	Human	PRO	925	66.6	3.0	2846	12	ADH20009	Adh20009	Human	CDN
853	66.6	3.0	2846	10	ADH90348	Adh90348	Novel	hum	926	66.6	3.0	2846	12	ADH02534	Adh02534	Human	PRO
854	66.6	3.0	2846	10	ADH90367	Adh90367	Novel	hum	927	66.6	3.0	2846	12	ADG69028	Adg69028	Novel	hum
855	66.6	3.0	2846	10	ADH77916	Adh77916	Human	PRO	928	66.6	3.0	2846	12	ADH07631	Adh07631	Novel	hum
856	66.6	3.0	2846	10	ADH97899	Adh97899	Novel	hum	929	66.6	3.0	2846	12	ADG86153	Adg86153	Novel	hum
857	66.6	3.0	2846	10	ADI01284	Adi01284	Novel	hum	930	66.6	3.0	2846	12	ADH24749	Adh24749	Novel	hum
858	66.6	3.0	2846	10	ADI01979	Adi01979	Novel	hum	931	66.6	3.0	2846	12	ADH25797	Adh25797	Novel	hum
859	66.6	3.0	2846	10	ADI03237	Adi03237	Novel	hum	932	66.6	3.0	2846	12	ADH38363	Adh38363	Novel	hum
860	66.6	3.0	2846	10	ADI11424	Adi11424	Human	PRO	933	66.6	3.0	2846	12	ADH57202	Adh57202	Novel	hum
861	66.6	3.0	2846	10	ADI02326	Adi02326	Novel	hum	934	66.6	3.0	2846	12	ADH52190	Adh52190	Novel	hum
862	66.6	3.0	2846	10	ADI11764	Adi11764	Human	PRO	935	66.6	3.0	2846	12	ADH49556	Adh49556	Novel	hum
863	66.6	3.0	2846	10	ADI05401	Adi05401	Novel	hum	936	66.6	3.0	2846	12	ADH90518	Adh90518	Novel	hum
864	66.6	3.0	2846	10	ADH79473	Adh79473	Novel	hum	937	66.6	3.0	2846	12	ADI11254	Adi11254	Human	PRO
865	66.6	3.0	2846	10	ADI05231	Adi05231	Novel	hum	938	66.6	3.0	2846	12	ADH98919	Adh98919	Novel	hum
866	66.6	3.0	2846	10	ADI19430	Adi19430	Novel	hum	939	66.6	3.0	2846	12	ADI02149	Adi02149	Novel	hum
867	66.6	3.0	2846	10	ADH79643	Adh79643	Novel	hum	940	66.6	3.0	2846	12	ADH90688	Adh90688	Novel	hum
868	66.6	3.0	2846	10	ADI01469	Adi01469	Novel	hum	941	66.6	3.0	2846	12	ADJ54807	Adj54807	Human	PRO
869	66.6	3.0	2846	10	ADI01639	Adi01639	Novel	hum	942	66.6	3.0	2846	12	ADJ98563	Adj98563	Novel	hum
870	66.6	3.0	2846	10	ADI01809	Adi01809	Novel	hum	943	66.6	3.0	2846	12	ADJ98733	Adj98733	Novel	hum
871	66.6	3.0	2846	10	ADH79813	Adh79813	Novel	hum	944	66.6	3.0	2846	12	ADH78892	Adh78892	Novel	hum
872	66.6	3.0	2846	10	ADI04631	Adi04631	Novel	hum	945	66.6	3.0	2846	12	ADJ99126	Adj99126	Novel	hum
873	66.6	3.0	2846	10	ADI02767	Adi02767	Novel	hum	946	66.6	3.0	2846	12	ADJ99296	Adj99296	Novel	hum
874	66.6	3.0	2846	10	ADH78086	Adh78086	Human	PRO	947	66.6	3.0	2846	12	ADJ98914	Adj98914	Novel	hum
875	66.6	3.0	2846	10	ADI25725	Adi25725	Novel	hum	948	66.6	3.0	2846	12	ADH79062	Adh79062	Novel	hum
876	66.6	3.0	2846	10	ADI25895	Adi25895	Novel	hum	949	66.6	3.0	2846	12	ADK00922	Adk00922	Human	PRO
877	66.6	3.0	2846	10	ADK65407	Adk65407	Novel	hum	950	66.6	3.0	2846	12	ADK14443	Adk14443	Novel	hum
878	66.6	3.0	2846	10	ADH98749	Adh98749	Novel	hum	951	66.6	3.0	2846	12	ADJ64578	Adj64578	Human	PRO
879	66.6	3.0	2846	10	ADH79990	Adh79990	Novel	hum	952	66.6	3.0	2846	12	ADM31474	Adm31474	Novel	hum
880	66.6	3.0	2846	11	ADL32775	Adl32775	Novel	hum	953	66.6	3.0	2846	12	ADM36521	Adm36521	Novel	hum
881	66.6	3.0	2846	11	ADM30309	Adm30309	Novel	hum	954	66.6	3.0	2846	12	ADM40326	Adm40326	Novel	hum
882	66.6	3.0	2846	11	ADL93721	Adl93721	Novel	hum	955	66.6	3.0	2846	12	ADM80892	Adm80892	Human	PRO
883	66.6	3.0	2846	12	ADC52175	Adc52175	Novel	hum	956	66.6	3.0	2846	12	ADN37934	Adn37934	Novel	hum
884	66.6	3.0	2846	12	ADE74306	Ade74306	Human	sec	957	66.6	3.0	2848	8	ACA67289	Aca67289	CDNA	enco
885	66.6	3.0	2846	12	ADE74918	Ade74918	Human	sec	c 958	66.4	3.0	228	5	ADL43698	Adl43698	Human	ova
886	66.6	3.0	2846	12	ADF35356	Adf35356	CDNA	enco	c 959	66.4	3.0	255	5	Aah82206	Aah82206	Rat	diffe
887	66.6	3.0	2846	12	ADG11606	Adg11606	CDNA	enco	c 960	66.4	3.0	266	5	ABV07596	Abv07596	Human	pro
888	66.6	3.0	2846	12	ADG04402	Adg04402	Novel	hum	c 961	66.4	3.0	300	5	ABV04310	Abv04310	Human	pro
889	66.6	3.0	2846	12	ADG00562	Adg00562	Novel	hum	c 962	66.4	3.0	489	13	ACN49736	Acn49736	Cotton	pr
890	66.6	3.0	2846	12	ADH06607	Adh06607	Novel	hum	c 963	66.4	3.0	522	5	ABV39211	Abv39211	Human	pro
891	66.6	3.0	2846	12	ADH06437	Adh06437	Novel	hum	964	66.4	3.0	550	13	ACN47393	Acn47393	Cotton	pr
892	66.6	3.0	2846	12	ADG68858	Adg68858	Novel	hum	965	66.4	3.0	823	4	AAL02457	Aal02457	Human	rep
893	66.6	3.0	2846	12	ADH27748	Adh27748	Novel	hum	966	66.4	3.0	823	4	ABA07664	Abao7664	Human	ova
894	66.6	3.0	2846	12	ADH27748	Adh27748	Novel	hum	967	66.4	3.0	1781	8	ABX15518	Abx15518	CDNA	enco
895	66.6	3.0	2846	12	ADH25089	Adh25089	Novel	hum	968	66.4	3.0	1781	10	AA47901	Aad47901	Human	tra
896	66.6	3.0	2846	12	ADH25089	Adh25089	Novel	hum	969	66.4	3.0	1874	10	ADI62940	Adi62940	Human	apo

970 66.4 3.0 1927 4 AAF44987 Aaf44987 Human Gen
971 66.4 3.0 4816 10 ADE15662 Adel5662 Human str
c 972 66.2 3.0 379 4 AAL20476 Aal20476 Human bre
973 66.2 3.0 388 4 AAI89390 Aai89390 Human pol
974 66.2 3.0 433 13 ACN51900 Acn51900 Cotton an
975 66.2 3.0 470 5 ABV55159 Abv55159 Human pro
c 976 66.2 3.0 476 5 ADL37109 Adl37109 Human ova
c 977 66.2 3.0 476 5 ADI71958 Adi71958 Human ova
c 978 66.2 3.0 486 13 ACN46735 Acn46735 Cotton pr
c 979 66.2 3.0 499 13 ACN46935 Acn46935 Cotton pr
c 980 66.2 3.0 526 13 ACN59983 Acn59983 Cotton gy
c 981 66.2 3.0 532 13 ACN61789 Acn61789 Cotton gy
c 982 66.2 3.0 560 13 ACN51599 Acn51599 Cotton an
c 983 66.2 3.0 693 4 AAL14804 Aal14804 Human bre
c 984 66.2 3.0 723 5 ADI71984 Adi71984 Human ova
c 985 66.2 3.0 723 5 ADL37134 Adl37134 Human ova
c 986 66.2 3.0 810 5 ADL38237 Adl38237 Human ova
c 987 66.2 3.0 810 5 ADI73104 Adi73104 Human ova
c 988 66.2 3.0 874 11 ACN84830 Acn84830 Breast ca
c 989 66.2 3.0 878 8 ACC62513 Acc62513 Human sec
990 66.2 3.0 1153 13 ADP55850 Adp55850 Human PRO
991 66.2 3.0 1315 4 AAF81788 Aaf81788 Human sec
992 66.2 3.0 1315 8 ADA40552 Ada40552 Human sec
993 66.2 3.0 1315 8 ACC50854 Acc50854 Human sec
994 66.2 3.0 1315 10 ADC73986 Adc73986 Human sec
995 66.2 3.0 1315 10 ADP37810 Add37810 Human sec
996 66.2 3.0 1315 10 ADA56701 Ada56701 Gene enco
c 997 66.2 3.0 1317 8 ADA40234 Ada40234 Human sec
c 998 66.2 3.0 1317 8 ACC50674 Acc50674 Human sec
999 66.2 3.0 1317 10 ADC73758 Adc73758 Human sec
1000 66.2 3.0 1317 10 ADD37713 Add37713 Human sec
1001 66.2 3.0 1317 10 ADA56395 Ada56395 Gene enco
1002 66.2 3.0 1321 3 AAC98225 Aac98225 Human col
1003 66.2 3.0 1337 12 ADI42582 Adi42582 Plant tra
1004 66.2 3.0 1337 12 ADO02883 Ado02883 Soybean o
1005 66.2 3.0 1378 2 AAV59706 Aav59706 Human sec
1006 66.2 3.0 1378 6 ABS73695 Abs73695 Human cdn
1007 66.2 3.0 1378 9 ACD82838 Acd82838 cDNA sequ
1008 66.2 3.0 1378 10 ADI22923 Adi22923 cDNA enco
1009 66.2 3.0 1378 12 ADH73925 Adh73925 Human sec
1010 66.2 3.0 1856 8 ACC69466 Acc69466 Human mal
1011 66.2 3.0 1867 10 ACA92442 Aca92442 DNA enco
1012 66.2 3.0 2323 2 AAV59524 Aav59524 Human sec
1013 66.2 3.0 2323 6 ABS73511 Abs73511 Human cdn
1014 66.2 3.0 2323 9 ACD82654 Acd82654 cDNA sequ
1015 66.2 3.0 2323 10 ADI22739 Adi22739 cDNA enco
1016 66.2 3.0 2323 12 ADH73741 Adh73741 Human sec
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c1018 66 2.9 384 5 ADI69792 Adi69792 Human ova
c1019 66 2.9 384 5 ADI76128 Adi76128 Human ova
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c1021 66 2.9 464 5 ABV03810 Abv03810 Human pro
c1022 66 2.9 483 13 ACN61841 Acn61841 Cotton gy
1023 66 2.9 516 13 ACN59785 Acn59785 Cotton gy
1024 66 2.9 940 12 ADO62500 Ado62500 Transcrip
1025 66 2.9 1181 2 AAV59803 Aav59803 Human sec
1026 66 2.9 1181 6 ABS73797 Abs73797 Human cdn
1027 66 2.9 1181 9 ACD82940 Acd82940 cDNA sequ
1028 66 2.9 1181 10 ADI23025 Adi23025 cDNA enco
1029 66 2.9 1181 12 ADH74027 Adh74027 Human sec
1030 66 2.9 1212 2 AAV59686 Aav59686 Human sec
1031 66 2.9 1212 6 ABQ54333 Abq54333 Human ova
1032 66 2.9 1212 6 ABS73673 Abs73673 Human cdn
1033 66 2.9 1212 9 ACD82816 Acd82816 cDNA sequ
1034 66 2.9 1212 10 ADI22901 Adi22901 cDNA enco
1035 66 2.9 1212 12 ADH73903 Adh73903 Human sec
1036 66 2.9 1447 5 ABX71274 Abx71274 Human bra
1037 66 2.9 1453 2 AAQ50573 Aaq50573 Asparagin
1038 66 2.9 1585 12 ADQ25305 Adq25305 Human sof
1039 66 2.9 1640 3 AAQ50575 Aaq50575 Asparagin
1040 66 2.9 1793 3 AAC77949 Aac77949 Human can
1041 66 2.9 1910 2 AAQ50579 Aaq50579 Asparagin
1042 66 2.9 2291 9 AAL62477 Aal62477 Human oxi

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1044 66 2.9 2988 12 ADQ23141 Adq23141 Human sof
1045 66 2.9 3116 3 AAZ52568 Aaz52568 Human sec
1046 66 2.9 4824 12 ADQ22371 Adq22371 Human sof
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c1048 65.8 2.9 216 5 ADI72258 Adi72258 Human ova
1049 65.8 2.9 391 4 AAI83087 Aai83087 Human pol
1050 65.8 2.9 398 4 AAI85290 Aai85290 Human pol
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1063 65.8 2.9 1883 3 AAA37066 Aaa37066 Human PRO
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1073 65.8 2.9 1883 9 ADA61724 Ada61724 Homo sapi
1074 65.8 2.9 1883 9 ADB19509 Adb19509 Novel hum
1075 65.8 2.9 1883 9 ADB28050 Adb28050 cDNA enco
1076 65.8 2.9 1883 9 ADA86529 Ada86529 Novel hum
1077 65.8 2.9 1883 9 ADB16093 Adb16093 Human PRO
1078 65.8 2.9 1883 9 ADA47879 Ada47879 Human PRO
1079 65.8 2.9 1883 9 ACD68339 Acd68339 Novel hum
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1081 65.8 2.9 1883 9 ADB30681 Adb30681 cDNA enco
1082 65.8 2.9 1883 9 ADA85977 Ada85977 Novel hum
1083 65.8 2.9 1883 9 ADA97189 Ada97189 Human PRO
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1085 65.8 2.9 1883 9 ADA87632 Ada87632 Novel hum
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1087 65.8 2.9 1883 9 ADA91926 Ada91926 Novel hum
1088 65.8 2.9 1883 9 ADB14989 Adb14989 Human PRO
1089 65.8 2.9 1883 9 ADB18950 Adb18950 Novel hum
1090 65.8 2.9 1883 9 ADA94165 Ada94165 Human PRO
1091 65.8 2.9 1883 9 ADB20061 Adb20061 Novel hum
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1093 65.8 2.9 1883 9 ACD98674 Acd98674 Novel hum
1094 65.8 2.9 1883 9 ADA74627 Ada74627 Human PRO
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1096 65.8 2.9 1883 9 ADA82384 Ada82384 Human PRO
1097 65.8 2.9 1883 9 ADA75347 Ada75347 Human PRO
1098 65.8 2.9 1883 9 ADA85425 Ada85425 Novel hum
1099 65.8 2.9 1883 9 ADA84873 Ada84873 Novel hum
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1105 65.8 2.9 1883 9 ADA93596 Ada93596 Human PRO
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1107 65.8 2.9 1883 9 ADB31233 Adb31233 cDNA enco
1108 65.8 2.9 1883 9 ADA61161 Ada61161 Homo sapi
1109 65.8 2.9 1883 9 ADB24308 Adb24308 Human PRO
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1111 65.8 2.9 1883 9 ADA81209 Ada81209 Human PRO
1112 65.8 2.9 1883 9 ADA96085 Ada96085 Human PRO
1113 65.8 2.9 1883 9 ADB26394 Adb26394 cDNA enco
1114 65.8 2.9 1883 9 ADB21879 Adb21879 Novel hum
1115 65.8 2.9 1883 9 ADA77658 Ada77658 Human PRO

1116	65.8	2.9	1883	9	ADB18398	Adb18398 cDNA enco	1189	65.8	2.9	1883	10	ADE50435	Ade50435 Human cDN
1117	65.8	2.9	1883	9	ADA87081	Ada87081 Novel hum	1190	65.8	2.9	1883	10	ADD92635	Add92635 Human PRO
1118	65.8	2.9	1883	9	ACH04441	Ach04441 Human cDN	1191	65.8	2.9	1883	10	ADD91531	Add91531 Human PRO
1119	65.8	2.9	1883	9	ADA88184	Ada88184 Novel hum	1192	65.8	2.9	1883	10	ADE04145	Ade04145 Human PRO
1120	65.8	2.9	1883	9	ADA46572	Ada46572 Novel hum	1193	65.8	2.9	1883	10	ADE20047	Ade20047 Human cDN
1121	65.8	2.9	1883	9	ADB28602	Adb28602 cDNA enco	1194	65.8	2.9	1883	10	ADE32442	Ade32442 Novel hum
1122	65.8	2.9	1883	9	ADB29154	Adb29154 cDNA enco	1195	65.8	2.9	1883	10	ADE22374	Ade22374 cDNA enco
1123	65.8	2.9	1883	9	ADA77106	Ada77106 Human PRO	1196	65.8	2.9	1883	10	ADD79598	Add79598 cDNA enco
1124	65.8	2.9	1883	9	ACD67985	Acd67985 Novel hum	1197	65.8	2.9	1883	10	ADE42134	Ade42134 Human PRO
1125	65.8	2.9	1883	9	ADA88736	Ada88736 Novel hum	1198	65.8	2.9	1883	10	ADE17951	Ade17951 Human PRO
1126	65.8	2.9	1883	9	ADA97741	Ada97741 Human PRO	1199	65.8	2.9	1883	10	ADD92083	Add92083 Human PRO
1127	65.8	2.9	1883	9	ADB27498	Adb27498 cDNA enco	1200	65.8	2.9	1883	10	ADE33546	Ade33546 Novel hum
1128	65.8	2.9	1883	9	ADB22431	Adb22431 Novel hum	1201	65.8	2.9	1883	10	ADE34098	Ade34098 Novel hum
1129	65.8	2.9	1883	9	ADA67122	Ada67122 Human PRO	1202	65.8	2.9	1883	10	ADD80150	Add80150 cDNA enco
1130	65.8	2.9	1883	9	ADB22983	Adb22983 Human PRO	1203	65.8	2.9	1883	10	ADE49958	Ade49958 Human cDN
1131	65.8	2.9	1883	9	ADB23756	Adb23756 Human PRO	1204	65.8	2.9	1883	10	ADD93187	Add93187 Human PRO
1132	65.8	2.9	1883	9	ADA92478	Ada92478 Novel hum	1205	65.8	2.9	1883	10	ADE19607	Ade19607 Human PRO
1133	65.8	2.9	1883	9	ADB15541	Adb15541 Human PRO	1206	65.8	2.9	1883	10	ADE21516	Ade21516 Human cDN
1134	65.8	2.9	1883	9	ADB38793	Adb38793 Novel hum	1207	65.8	2.9	1883	10	ADE19055	Ade19055 Human PRO
1135	65.8	2.9	1883	9	ADB38241	Adb38241 Novel hum	1208	65.8	2.9	1883	10	ADE43251	Ade43251 Human PRO
1136	65.8	2.9	1883	9	ADB66713	Adb66713 Novel hum	1209	65.8	2.9	1883	10	ADD96040	Add96040 Human PRO
1137	65.8	2.9	1883	10	ADB89793	Adb89793 Human PRO	1210	65.8	2.9	1883	10	ADE22926	Ade22926 cDNA enco
1138	65.8	2.9	1883	10	ADB90525	Adb90525 Human PRO	1211	65.8	2.9	1883	10	ADD79044	Add79044 cDNA enco
1139	65.8	2.9	1883	10	ADB39626	Adb39626 Novel hum	1212	65.8	2.9	1883	10	ADE32994	Ade32994 Novel hum
1140	65.8	2.9	1883	10	ADB47249	Adb47249 Novel hum	1213	65.8	2.9	1883	10	ADE42686	Ade42686 Human PRO
1141	65.8	2.9	1883	10	ADB86856	Adb86856 Human PRO	1214	65.8	2.9	1883	10	ADD80702	Add80702 cDNA enco
1142	65.8	2.9	1883	10	ADB77461	Adb77461 Novel hum	1215	65.8	2.9	1883	10	ADD89730	Add89730 Human PRO
1143	65.8	2.9	1883	10	ADB34618	Adb34618 Human PRO	1216	65.8	2.9	1883	10	ADE41014	Ade41014 Human PRO
1144	65.8	2.9	1883	10	ADB35722	Adb35722 Human PRO	1217	65.8	2.9	1883	10	ADE04813	Ade04813 Human PRO
1145	65.8	2.9	1883	10	ADB34066	Adb34066 Human PRO	1218	65.8	2.9	1883	10	ADE92942	Ade92942 Human PRO
1146	65.8	2.9	1883	10	ADB35170	Adb35170 Human PRO	1219	65.8	2.9	1883	10	ADF29941	Adf29941 Human cDN
1147	65.8	2.9	1883	10	ADB36274	Adb36274 Human PRO	1220	65.8	2.9	1883	10	ADF55834	Adf55834 Human cDN
1148	65.8	2.9	1883	10	ADB46669	Adb46669 Novel hum	1221	65.8	2.9	1883	10	ADG21651	Adg21651 Novel hum
1149	65.8	2.9	1883	10	ADC18014	Adc18014 Human PRO	1222	65.8	2.9	1883	10	ADG23292	Adg23292 Novel hum
1150	65.8	2.9	1883	10	ADC50542	Adc50542 Novel hum	1223	65.8	2.9	1883	10	ADF97627	Adf97627 Human PRO
1151	65.8	2.9	1883	10	ADC72089	Adc72089 Novel hum	1224	65.8	2.9	1883	10	ADG80691	Adg80691 Human PRO
1152	65.8	2.9	1883	10	ADC60068	Adc60068 Novel hum	1225	65.8	2.9	1883	10	ADG80139	Adg80139 Human PRO
1153	65.8	2.9	1883	10	ADC53075	Adc53075 Novel hum	1226	65.8	2.9	1883	10	ADH55431	Adh55431 Novel hum
1154	65.8	2.9	1883	10	ADC57429	Adc57429 Novel hum	1227	65.8	2.9	1883	10	ADH55983	Adh55983 Novel hum
1155	65.8	2.9	1883	10	ADC60620	Adc60620 Novel hum	1228	65.8	2.9	1883	10	ADH99338	Adh99338 Human cDN
1156	65.8	2.9	1883	10	ADC51095	Adc51095 Novel hum	1229	65.8	2.9	1883	10	ADI64202	Adi64202 Novel hum
1157	65.8	2.9	1883	10	ADC65622	Adc65622 Human PRO	1230	65.8	2.9	1883	10	ADI65151	Adi65151 Novel hum
1158	65.8	2.9	1883	10	ADC54720	Adc54720 Novel hum	1231	65.8	2.9	1883	10	ADI63650	Adi63650 Novel hum
1159	65.8	2.9	1883	10	ADC53681	Adc53681 Novel hum	1232	65.8	2.9	1883	10	ADH82064	Adh82064 Novel hum
1160	65.8	2.9	1883	10	ADC59204	Adc59204 Novel hum	1233	65.8	2.9	1883	10	ADH81512	Adh81512 Novel hum
1161	65.8	2.9	1883	10	ADC56082	Adc56082 Novel hum	1234	65.8	2.9	1883	10	ACD24103	Acd24103 Novel hum
1162	65.8	2.9	1883	10	ADC58652	Adc58652 Novel hum	1235	65.8	2.9	1883	10	ACA67244	Aca67244 cDNA enco
1163	65.8	2.9	1883	10	ADD03326	Add03326 Novel hum	1236	65.8	2.9	1883	11	ADM82681	Adm82681 Novel hum
1164	65.8	2.9	1883	10	ADC90318	Adc90318 Novel hum	1237	65.8	2.9	1883	11	ADN16080	Adn16080 Novel hum
1165	65.8	2.9	1883	10	ADC69737	Adc69737 cDNA enco	1238	65.8	2.9	1883	11	ADN16709	Adn16709 Novel hum
1166	65.8	2.9	1883	10	ADC48626	Adc48626 Human PRO	1239	65.8	2.9	1883	11	ADN15528	Adn15528 Novel hum
1167	65.8	2.9	1883	10	ADD10155	Add10155 Human PRO	1240	65.8	2.9	1883	11	ADN14976	Adn14976 Novel hum
1168	65.8	2.9	1883	10	ADD04730	Add04730 Novel hum	1241	65.8	2.9	1883	12	ADC81238	Adc81238 Novel hum
1169	65.8	2.9	1883	10	ADC80686	Adc80686 Novel hum	1242	65.8	2.9	1883	12	ADD76686	Add76686 Human PRO
1170	65.8	2.9	1883	10	ADD11193	Add11193 Human PRO	1243	65.8	2.9	1883	12	ADD88050	Add88050 Human PRO
1171	65.8	2.9	1883	10	ADC48074	Adc48074 Human PRO	1244	65.8	2.9	1883	12	ADD86454	Add86454 Human PRO
1172	65.8	2.9	1883	10	ADC80134	Adc80134 Novel hum	1245	65.8	2.9	1883	12	ADE75902	Ade75902 Human PRO
1173	65.8	2.9	1883	10	ADD09603	Add09603 Human PRO	1246	65.8	2.9	1883	12	ADE23478	Ade23478 cDNA enco
1174	65.8	2.9	1883	10	ADD41316	Add41316 Novel hum	1247	65.8	2.9	1883	12	ADE24030	Ade24030 cDNA enco
1175	65.8	2.9	1883	10	ADD52455	Add52455 cDNA enco	1248	65.8	2.9	1883	12	ADE24673	Ade24673 cDNA enco
1176	65.8	2.9	1883	10	ADD70660	Add70660 Human cDN	1249	65.8	2.9	1883	12	ADD87498	Add87498 Human PRO
1177	65.8	2.9	1883	10	ADD39737	Add39737 Human cDN	1250	65.8	2.9	1883	12	ADE89364	Ade89364 Human PRO
1178	65.8	2.9	1883	10	ADD53195	Add53195 cDNA enco	1251	65.8	2.9	1883	12	ADE18503	Ade18503 Human PRO
1179	65.8	2.9	1883	10	ADD53747	Add53747 Novel hum	1252	65.8	2.9	1883	12	ADE88812	Ade88812 Human PRO
1180	65.8	2.9	1883	10	ADD70183	Add70183 Human cDN	1253	65.8	2.9	1883	12	ADE96518	Ade96518 Human cDN
1181	65.8	2.9	1883	10	ADD38304	Add38304 Human cDN	1254	65.8	2.9	1883	12	ADE94832	Ade94832 cDNA enco
1182	65.8	2.9	1883	10	ADD39260	Add39260 Human cDN	1255	65.8	2.9	1883	12	ADE91243	Ade91243 Human PRO
1183	65.8	2.9	1883	10	ADD51903	Add51903 cDNA enco	1256	65.8	2.9	1883	12	ADF25829	Adf25829 Human cDN
1184	65.8	2.9	1883	10	ADD02702	Add02702 Human PRO	1257	65.8	2.9	1883	12	ADE95384	Ade95384 cDNA enco
1185	65.8	2.9	1883	10	ADD02136	Add02136 Human PRO	1258	65.8	2.9	1883	12	ADE93494	Ade93494 Human PRO
1186	65.8	2.9	1883	10	ADD54318	Add54318 Novel hum	1259	65.8	2.9	1883	12	ADF24728	Adf24728 Human cDN
1187	65.8	2.9	1883	10	ADD38783	Add38783 Human cDN	1260	65.8	2.9	1883	12	ADF29464	Adf29464 Human cDN
1188	65.8	2.9	1883	10	ADD40214	Add40214 Human cDN	1261	65.8	2.9	1883	12	ADF35075	Adf35075 cDNA enco

1262	65.8	2.9	1883	12	ADE96995	Ade96995 Human cDN	c1335	65.6	2.9	319	5	ADL38504	Adl38504 Human ova
1263	65.8	2.9	1883	12	ADE92390	Ade92390 Novel hum	c1336	65.6	2.9	319	5	ADI73373	Adi73373 Human ova
1264	65.8	2.9	1883	12	ADE90691	Ade90691 Human PRO	c1337	65.6	2.9	361	11	ACN87469	Acn87469 Breast ca
1265	65.8	2.9	1883	12	ADE91838	Ade91838 Novel hum	c1338	65.6	2.9	372	5	ABV37528	Abv37528 Human pro
1266	65.8	2.9	1883	12	ADG02417	Adg02417 Human PRO	c1339	65.6	2.9	394	5	ADL44065	Adl44065 Human ova
1267	65.8	2.9	1883	12	ADG22203	Adg22203 Novel hum	1340	65.6	2.9	429	5	ABV58465	Abv58465 Human pro
1268	65.8	2.9	1883	12	ADG20273	Adg20273 cDNA enco	1341	65.6	2.9	442	5	ABV54422	Abv54422 Human pro
1269	65.8	2.9	1883	12	ADF98179	Adf98179 Human PRO	c1342	65.6	2.9	458	4	AAI88397	Aai88397 Human pol
1270	65.8	2.9	1883	12	ADG24396	Adg24396 Novel hum	1343	65.6	2.9	464	4	AAH33241	Aah33241 Human col
1271	65.8	2.9	1883	12	ADF98750	Adf98750 Human PRO	c1344	65.6	2.9	545	13	ACN51318	Acn51318 Cotton an
1272	65.8	2.9	1883	12	ADG03581	Adg03581 Human PRO	1345	65.6	2.9	604	3	AAC59787	Aac59787 Human sec
1273	65.8	2.9	1883	12	ADF99302	Adf99302 Human PRO	1346	65.6	2.9	639	13	ADR59449	Adr59449 Cotton cD
1274	65.8	2.9	1883	12	ADG16887	Adg16887 cDNA enco	1347	65.6	2.9	1180	2	AAV84347	Aav84347 Human Apo
1275	65.8	2.9	1883	12	ADG05346	Adg05346 Human PRO	1348	65.6	2.9	1180	6	ABS53571	Abs53571 cDNA enco
1276	65.8	2.9	1883	12	ADG19613	Adg19613 cDNA enco	1349	65.6	2.9	1180	6	ABS53570	Abs53570 cDNA enco
1277	65.8	2.9	1883	12	ADG13450	Adg13450 cDNA enco	1350	65.6	2.9	1180	10	AAD64037	Aad64037 Human Apo
1278	65.8	2.9	1883	12	ADG08507	Adg08507 Novel hum	1351	65.6	2.9	1180	10	AAD64038	Aad64038 Human Apo
1279	65.8	2.9	1883	12	ADG15677	Adg15677 cDNA enco	1352	65.6	2.9	1285	3	AAC59828	Aac59828 Human sec
1280	65.8	2.9	1883	12	ADF97075	Adf97075 Human PRO	1353	65.6	2.9	1342	3	AAA26424	Aaa26424 Human sec
1281	65.8	2.9	1883	12	ADG06260	Adg06260 Human PRO	1354	65.6	2.9	1342	12	ADL71485	Adl71485 Novel hum
1282	65.8	2.9	1883	12	ADG23844	Adg23844 Novel hum	1355	65.6	2.9	1401	3	AAC78016	Aac78016 Human can
1283	65.8	2.9	1883	12	ADG04133	Adg04133 Human PRO	1356	65.6	2.9	2652	9	ACA98920	Aca98920 cDNA enco
1284	65.8	2.9	1883	12	ADG25034	Adg25034 Novel hum	1357	65.6	2.9	5059	12	ADQ23993	Adq23993 Human sof
1285	65.8	2.9	1883	12	ADG07331	Adg07331 Novel hum	c1358	65.6	2.9	5216	6	ABL32347	Ab132347 Human imm
1286	65.8	2.9	1883	12	ADG07883	Adg07883 Novel hum	c1359	65.6	2.9	5216	6	ABL34459	Ab134459 Human met
1287	65.8	2.9	1883	12	ADG55378	Adg55378 Novel hum	c1360	65.6	2.9	5216	7	ADS99720	Ads99720 Complemen
1288	65.8	2.9	1883	12	ADG61042	Adg61042 Novel hum	c1361	65.4	2.9	330	4	AAH69540	Aah69540 Human cer
1289	65.8	2.9	1883	12	ADG62146	Adg62146 Novel hum	c1362	65.4	2.9	373	8	ABX35671	Abx35671 Bovine ES
1290	65.8	2.9	1883	12	ADH03033	Adh03033 Human cDN	c1363	65.4	2.9	373	13	ACN50919	Acn50919 Cotton an
1291	65.8	2.9	1883	12	ADG82347	Adg82347 Human PRO	1364	65.4	2.9	408	4	AAI83697	Aai83697 Human pol
1292	65.8	2.9	1883	12	ADG57586	Adg57586 Novel hum	c1365	65.4	2.9	413	4	AAI19684	Aai19684 Human bre
1293	65.8	2.9	1883	12	ADG57034	Adg57034 Novel hum	1366	65.4	2.9	430	9	ACH41045	-Ach41045 Human foe
1294	65.8	2.9	1883	12	ADG55930	Adg55930 Novel hum	1367	65.4	2.9	433	4	AAI82080	Aai82080 Human pol
1295	65.8	2.9	1883	12	ADG58690	Adg58690 Novel hum	1368	65.4	2.9	457	4	AAI85461	Aai85461 Human pol
1296	65.8	2.9	1883	12	ADG71056	Adg71056 Novel hum	c1369	65.4	2.9	525	13	ACN45429	Acn45429 Cotton pr
1297	65.8	2.9	1883	12	ADH03987	Adh03987 Human cDN	c1370	65.4	2.9	536	13	ACN55415	Acn55415 Cotton an
1298	65.8	2.9	1883	12	ADH03510	Adh03510 Human cDN	c1371	65.4	2.9	563	13	ACN47476	Acn47476 Cotton pr
1299	65.8	2.9	1883	12	ADG58138	Adg58138 Novel hum	1372	65.4	2.9	578	3	AAC79470	Aac79470 cDNA sequ
1300	65.8	2.9	1883	12	ADG53722	Adg53722 Novel hum	1373	65.4	2.9	578	4	AAI67224	Aai67224 B511S CDN
1301	65.8	2.9	1883	12	ADG71608	Adg71608 Novel hum	1374	65.4	2.9	578	6	ABK29014	Abk29014 Human bre
1302	65.8	2.9	1883	12	ADG81795	Adg81795 Human PRO	c1375	65.4	2.9	600	11	ACN87284	Acn87284 Breast ca
1303	65.8	2.9	1883	12	ADH30757	Adh30757 Human PRO	c1376	65.4	2.9	752	4	AAI233455	Aal23455 Human bre
1304	65.8	2.9	1883	12	ADH12124	Adh12124 Novel hum	1377	65.4	2.9	1312	6	AAD24774	Aad24774 Glycine m
1305	65.8	2.9	1883	12	ADG52546	Adg52546 Novel hum	1378	65.4	2.9	1626	4	AA501160	Aas01160 Fertilisa
1306	65.8	2.9	1883	12	ADG54274	Adg54274 Novel hum	1379	65.4	2.9	1626	10	ADC29845	Adc29845 Fertiliza
1307	65.8	2.9	1883	12	ADG81243	Adg81243 Human PRO	1380	65.4	2.9	1663	3	AAC59302	Aac59302 Human sec
1308	65.8	2.9	1883	12	ADG56482	Adg56482 Novel hum	1381	65.4	2.9	1663	8	ABZ73679	Abz73679 Secreted
1309	65.8	2.9	1883	12	ADH12748	Adh12748 Novel hum	1382	65.4	2.9	1663	8	ADA98154	Ada98154 Human sec
1310	65.8	2.9	1883	12	ADG61594	Adg61594 Novel hum	1383	65.4	2.9	1663	10	ABT16860	Abt16860 Human sec
1311	65.8	2.9	1883	12	ADH28681	Adh28681 Human PRO	1384	65.4	2.9	1663	10	ABZ67274	Abz67274 Human sec
1312	65.8	2.9	1883	12	ADG54826	Adg54826 Novel hum	1385	65.4	2.9	1691	4	AAS03892	Aas03892 Human sec
1313	65.8	2.9	1883	12	ADG59866	Adg59866 Novel hum	1386	65.4	2.9	2069	12	ADQ67271	Adq67271 Novel hum
1314	65.8	2.9	1883	12	ADH04464	Adh04464 Human cDN	1387	65.4	2.9	2435	12	ADQ22529	Adq22529 Human sof
1315	65.8	2.9	1883	12	ADI81290	Adi81290 cDNA enco	1388	65.4	2.9	2608	3	AAC74241	Aac74241 Human sof
1316	65.8	2.9	1883	12	ADH61465	Adh61465 Human cDN	1389	65.4	2.9	2785	12	ADQ22627	Adq22627 Human sof
1317	65.8	2.9	1883	12	ADG10033	Adg10033 Novel hum	1390	65.4	2.9	3021	3	AAC77541	Aac77541 Human ORF
1318	65.8	2.9	1883	12	ADI15504	Adi15504 Novel hum	1391	65.4	2.9	3034	4	AAS03899	Aas03899 Human sec
1319	65.8	2.9	1883	12	ADG09381	Adg09381 Novel hum	1392	65.4	2.9	3034	8	ABZ73661	Abz73661 Secreted
1320	65.8	2.9	1883	12	ADI14836	Adi14836 Novel hum	1393	65.4	2.9	3034	8	ADA98146	Ada98146 Human sec
1321	65.8	2.9	1883	12	ADI18431	Adi18431 Novel hum	1394	65.4	2.9	3034	10	ABT16854	Abt16854 Human sec
1322	65.8	2.9	1883	12	ADJ63712	Adj63712 Novel hum	1395	65.4	2.9	3034	10	ABZ67255	Abz67255 Human sec
1323	65.8	2.9	1883	12	ADJ77607	Adj77607 Human PRO	1396	65.4	2.9	4777	9	AAI62016	Aal62016 Human cel
1324	65.8	2.9	1883	12	ADJ65729	Adj65729 cDNA enco	1397	65.4	2.9	7295	5	AAS85462	Aas85462 DNA encod
1325	65.8	2.9	1883	12	ADM27865	Adm27865 cDNA enco	1398	65.2	2.9	181	4	AAI34678	Aal34678 Human mus
1326	65.8	2.9	1883	12	ADM42589	Adm42589 cDNA enco	1399	65.2	2.9	181	8	ABX57666	Abx57666 cDNA enco
1327	65.8	2.9	1883	12	ADL94664	Adl94664 Human cDN	1400	65.2	2.9	181	12	ADJ27393	Adj27393 Human mus
1328	65.8	2.9	1883	12	ADM28451	Adm28451 cDNA enco	1401	65.2	2.9	273	12	ADL10902	Adl10902 Cat flea
1329	65.8	2.9	1883	13	ADI95933	Adi95933 cDNA enco	1402	65.2	2.9	287	11	ADL98155	Adl98155 Human tum
1330	65.8	2.9	1883	13	ADI96485	Adi96485 Novel hum	c1403	65.2	2.9	318	5	ADI73647	Adi73647 Human ova
1331	65.8	2.9	1883	13	ADT94370	Adt94370 Human PRO	c1404	65.2	2.9	318	5	ADL38776	Adl38776 Human ova
1332	65.8	2.9	2440	12	ADM98706	Adm98706 HMG-CoA r	c1405	65.2	2.9	327	5	ABV06120	Abv06120 Human pro
1333	65.8	2.9	3145	13	ADR46629	Adr46629 Cancer-as	c1406	65.2	2.9	337	5	ABV60906	Abv60906 Human pro
c1334	65.8	2.9	17534	6	ABK40026	Abk40026 Human che	c1407	65.2	2.9	368	4	AAI14593	Aal14593 Human bre

1408	65.2	2.9	410	9	ACH48825	Ach48825 Human leu
C1409	65.2	2.9	552	13	ACN45312	Acn45312 Cotton pr
C1410	65.2	2.9	566	5	ADL43620	Adl43620 Human ova
C1411	65.2	2.9	643	4	AAH70618	Aah70618 Human cer
C1412	65.2	2.9	693	10	ABT22222	Abt22222 Breast ca
1413	65.2	2.9	773	2	AAX37388	Aax37388 Human sec
1414	65.2	2.9	931	12	ADM33388	Adm33388 Human PRO
C1415	65.2	2.9	969	11	ACN84632	Acn84632 Breast ca
1416	65.2	2.9	1493	3	AZA243802	Aaz43802 Human adu
C1417	65.2	2.9	1513	5	AAD20261	Aad20261 Rat integ
1418	65.2	2.9	1733	3	AAA37036	Aaa37036 Human PRO
1419	65.2	2.9	1733	4	AAF54238	Aaf54238 DNA encod
1420	65.2	2.9	1734	4	AAC87038	Aac87038 Nucleotid
1421	65.2	2.9	1734	4	AAS46025	Aas46025 Human DNA
1422	65.2	2.9	1734	4	AAF92083	Aaf92083 Human PRO
1423	65.2	2.9	1734	6	ABK33613	Abk33613 cDNA enco
1424	65.2	2.9	1734	6	ABS74403	Abs74403 Human cDN
1425	65.2	2.9	1734	6	ABL95635	Ab195635 Human ang
1426	65.2	2.9	1734	8	ACA89475	Aca89475 cDNA enco
1427	65.2	2.9	1734	8	ACA73485	Aca73485 Human sec
1428	65.2	2.9	1734	8	ACA05800	Aca05800 Human sec
1429	65.2	2.9	1734	8	ACA66634	Aca66634 cDNA enco
1430	65.2	2.9	1734	8	ACA91189	Aca91189 Novel hum
1431	65.2	2.9	1734	8	ACD81566	Acd81566 Human cDN
1432	65.2	2.9	1734	8	ACF20209	Acf20209 Human sec
1433	65.2	2.9	1734	8	ACF19595	Acf19595 Human sec
1434	65.2	2.9	1734	8	ACD21883	Acd21883 Human sec
1435	65.2	2.9	1734	8	ACF13048	Acf13048 Human sec
1436	65.2	2.9	1734	8	ACD25151	Acd25151 Human sec
1437	65.2	2.9	1734	8	ACF00200	Acf00200 Human sec
1438	65.2	2.9	1734	8	ACA60388	Aca60388 Novel hum
1439	65.2	2.9	1734	8	ACA72257	Aca72257 Novel hum
1440	65.2	2.9	1734	8	ACD04781	Acd04781 Novel hum
1441	65.2	2.9	1734	8	ACD18242	Acd18242 Human sec
1442	65.2	2.9	1734	8	ACD08249	Acd08249 Human sec
1443	65.2	2.9	1734	8	ACA88683	Aca88683 Novel hum
1444	65.2	2.9	1734	8	ACA04997	Aca04997 Novel hum
1445	65.2	2.9	1734	8	ACA70125	Aca70125 Human sec
1446	65.2	2.9	1734	8	ACD12347	Acd12347 Novel hum
1447	65.2	2.9	1734	8	ACC74262	Acc74262 Human sec
1448	65.2	2.9	1734	8	ACD15890	Acd15890 Human sec
1449	65.2	2.9	1734	8	ACD25458	Acd25458 Novel hum
1450	65.2	2.9	1734	8	ACD17935	Acd17935 Human sec
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1452	65.2	2.9	1734	8	ACD21576	Acd21576 Human sec
1453	65.2	2.9	1734	8	ACD18643	Acd18643 Human sec
1454	65.2	2.9	1734	8	ACA58835	Aca58835 cDNA enco
1455	65.2	2.9	1734	8	ABX98253	Abx98253 Human cDN
1456	65.2	2.9	1734	8	ACD14004	Acd14004 Human PRO
1457	65.2	2.9	1734	8	ACD09784	Acd09784 Human sec
1458	65.2	2.9	1734	8	ACC88529	Acc88529 Human sec
1459	65.2	2.9	1734	8	ACD21269	Acd21269 Human sec
1460	65.2	2.9	1734	8	ABX75641	Abx75641 Human cDN
1461	65.2	2.9	1734	8	ACA64011	Aca64011 cDNA enco
1462	65.2	2.9	1734	8	ABX97844	Abx97844 Human PRO
1463	65.2	2.9	1734	8	ACA97320	Aca97320 Novel hum
1464	65.2	2.9	1734	8	ACA57783	Aca57783 Human PRO
1465	65.2	2.9	1734	8	ACD14311	Acd14311 Human PRO
1466	65.2	2.9	1734	8	ACC91094	Acc91094 Human sec
1467	65.2	2.9	1734	8	ACC88836	Acc88836 Human sec
1468	65.2	2.9	1734	8	ACD07033	Acd07033 Human PRO
1469	65.2	2.9	1734	8	ACA67484	Aca67484 Human PRO
1470	65.2	2.9	1734	8	ACC81539	Acc81539 Human sec
1471	65.2	2.9	1734	8	ACA91275	Aca91275 cDNA enco
1472	65.2	2.9	1734	8	ACC89143	Acc89143 Human sec
1473	65.2	2.9	1734	8	ACC86499	Acc86499 Human sec
1474	65.2	2.9	1734	8	ACC89757	Acc89757 Human sec
1475	65.2	2.9	1734	8	ACC92936	Acc92936 Human sec
1476	65.2	2.9	1734	8	ACA72564	Aca72564 Human PRO
1477	65.2	2.9	1734	8	ACA89082	Aca89082 Human sec
1478	65.2	2.9	1734	8	ACA69818	Aca69818 Human sec
1479	65.2	2.9	1734	8	ACA96961	Aca96961 Novel hum
1480	65.2	2.9	1734	8	ACA90957	Aca90957 Novel hum
1481	65.2	2.9	1734	8	ACA70739	Aca70739 Human sec
1482	65.2	2.9	1734	8	ACA95249	Aca95249 Novel hum
1483	65.2	2.9	1734	8	ACC86192	Acc86192 Human sec
1484	65.2	2.9	1734	8	ACD45174	Acd45174 Human sec
1485	65.2	2.9	1734	8	ACC90064	Acc90064 Human sec
1486	65.2	2.9	1734	8	ACD12672	Acd12672 Human sec
1487	65.2	2.9	1734	8	ACF19902	Acf19902 Human sec
1488	65.2	2.9	1734	8	ABX76846	Abx76846 Human PRO
1489	65.2	2.9	1734	8	ACA60527	Aca60527 Novel hum
1490	65.2	2.9	1734	8	ACA73178	Aca73178 Novel hum
1491	65.2	2.9	1734	8	ACA68721	Aca68721 Novel hum
1492	65.2	2.9	1734	8	ACA74565	Aca74565 cDNA enco
1493	65.2	2.9	1734	8	ACA04517	Aca04517 Novel hum
1494	65.2	2.9	1734	8	ACA70432	Aca70432 Human sec
1495	65.2	2.9	1734	8	ACD14618	Acd14618 Human PRO
1496	65.2	2.9	1734	8	ACA93722	Aca93722 Human cDN
1497	65.2	2.9	1734	8	ACA68290	Aca68290 Novel hum
1498	65.2	2.9	1734	8	ABX98755	Abx98755 Novel hum
1499	65.2	2.9	1734	8	ACA67296	Aca67296 cDNA enco
1500	65.2	2.9	1734	8	ACC81232	Acc81232 Human sec

ALIGNMENTS

RESULT 1

AAA96348

ID AAA96348 standard; cDNA; 2242 BP.

XX

AC AAA96348;

XX

DT 08-FEB-2001 (first entry)

XX

DE cDNA encoding a novel polypeptide designated PRO4380.

XX

KW Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122; PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356; PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030; PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes; insulinemia; kidney disorder; Bergers disease; nephropathy; Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis; Crohns disease; sb.

XX

OS Homo sapiens.

OS

FH Key

FT CDS

FT

FT Location/Qualifiers

FT 201..1724

FT /*tag= a

FT /transl_except= (pos: 888..890, aa: Ile)

FT sig_peptide

FT 201..278

FT /*tag= b

XX

PN WO200056889-A2.

XX

PN

PD

XX

XX 28-SEP-2000.

PF

XX

XX 01-MAR-2000; 2000WO-US005601.

XX

XX 23-MAR-1999; 99US-0125774P.

XX

XX 23-MAR-1999; 99US-0125778P.

XX

XX 24-MAR-1999; 99US-0125826P.

XX

XX 31-MAR-1999; 99US-0127035P.

XX

XX 05-APR-1999; 99US-0127706P.

XX

XX 21-APR-1999; 99US-0130359P.

XX

XX 27-APR-1999; 99US-0131270P.

XX

XX 27-APR-1999; 99US-0131272P.

XX

XX 27-APR-1999; 99US-0131291P.

XX

XX 04-MAY-1999; 99US-0132371P.

XX

XX 04-MAY-1999; 99US-0132379P.

XX

XX 04-MAY-1999; 99US-0132383P.

XX

XX 25-MAY-1999; 99US-0135750P.

XX

XX 08-JUN-1999; 99US-0138166P.

XX

XX 20-JUL-1999; 99US-0144791P.

Db 1561 CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGCTAATTCGCTGGAGCTGTTG 1620
Qy 1621 ATGATGGAGAACATTCCAGAAATGAGAAAATCAACAGGTGGAACACTACATAGAGGGAACCA 1680
Db 1621 ATGATGGAGAACATTCCAGAAATGAGAAAATCAACAGGTGGAACACTACATAGAGGGAACCA 1680
Qy 1681 AATTATTGCTGCCTTTTCTTAGAGATGGCCCGCTCCATTAATCAACAAGAACCTTCTA 1740
Db 1681 AATTATTGCTGCCTTTTCTTAGAGATGGCCCGCTCCATTAATCAACAAGAACCTTCTA 1740
Qy 1741 GTCTGATCTGATCCACTGACAGATTACCTCCCCACATCCCTAGACAGGATGGAATGT 1800
Db 1741 GTCTGATCTGATCCACTGACAGATTACCTCCCCACATCCCTAGACAGGATGGAATGT 1800
Qy 1801 AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTG 1860
Db 1801 AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTG 1860
Qy 1861 GGATATCTGGATCAGTAATAAATATTTCAAAGSCACAGATGTTGGAATGGTTTAAGGT 1920
Db 1861 GGATATCTGGATCAGTAATAAATATTTCAAAGSCACAGATGTTGGAATGGTTTAAGGT 1920
Qy 1921 CCCCCACTGCACACCTTCTCAAGTCATAGCTGTTGCAGCAACTTGATTTCCCAAGTC 1980
Db 1921 CCCCCACTGCACACCTTCTCAAGTCATAGCTGTTGCAGCAACTTGATTTCCCAAGTC 1980
Qy 1981 CTGTGCAATAGCCCCAGGATGGATTCTTCCAACTTTTAGCATATCTCCAACCTTGCA 2040
Db 1981 CTGTGCAATAGCCCCAGGATGGATTCTTCCAACTTTTAGCATATCTCCAACCTTGCA 2040
Qy 2041 ATTTGATTGGCATAATCACTCCGGTTTGCTTTTACCACTTTTATCTTATTAATAAA 2100
Db 2041 ATTTGATTGGCATAATCACTCCGGTTTGCTTTTACCACTTTTATCTTATTAATAAA 2100
Qy 2101 ATCATTTCCATCCAAATGATCGCCTTTGCTTTTACCACTTTTATCTTATTAATAAA 2160
Db 2101 ATCATTTCCATCCAAATGATCGCCTTTGCTTTTACCACTTTTATCTTATTAATAAA 2160
Qy 2161 AATGTTGGTCTCCACCCTGCTCCCAAAAAA 2242
Db 2161 AATGTTGGTCTCCACCCTGCTCCCAAAAAA 2242
Qy 2221 AAAAAA 2242
Db 2221 AAAAAA 2242

RESULT 2

ACD28837

ID ACD28837 standard; cDNA; 2242 BP.

XX ACD28837;

AC ACD28837;

DT 27-AUG-2003 (first entry)

XX 27-AUG-2003 (first entry)

DE Human secreted / transmembrane polypeptide PRO4380 cDNA.

XX Human; ss; gene; gene therapy; diabetes; obesity; hypoinsulinaemia.

KW Human; ss; gene; gene therapy; diabetes; obesity; hypoinsulinaemia.

XX Homo sapiens.

OS Homo sapiens.

XX US2003027249-A1.

PN US2003027249-A1.

XX 06-FEB-2003.

PD 06-FEB-2003.

XX 16-AUG-2001; 2001US-00931836.

PF 16-AUG-2001; 2001US-00931836.

XX 15-MAY-1998; 98US-0085579P.

PR 15-MAY-1998; 98US-0085579P.

PR 15-DEC-1998; 98US-0112514P.

PR 22-DEC-1998; 98US-0113300P.

PR 23-DEC-1998; 98US-0113430P.

PR 23-DEC-1998; 98US-0113605P.

PR 23-DEC-1998; 98US-0113621P.
PR 23-DEC-1998; 98US-0114140P.
PR 12-JAN-1999; 99US-0115552P.
PR 22-JAN-1999; 99US-0116843P.
PR 23-MAR-1999; 99US-0125774P.
PR 23-MAR-1999; 99US-0125778P.
PR 24-MAR-1999; 99US-0125826P.
PR 31-MAR-1999; 99US-0127035P.
PR 05-APR-1999; 99US-0127706P.
PR 13-APR-1999; 99US-0129122P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.
PR 27-APR-1999; 99US-0131291P.
PR 04-MAY-1999; 99US-0132371P.
PR 04-MAY-1999; 99US-0132379P.
PR 04-MAY-1999; 99US-0132383P.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-MAY-1999; 99US-0135750P.
PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 25-AUG-1999; 99US-00380142.
PR 29-OCT-1999; 99US-0162506P.
PR 22-DEC-1999; 99WO-US028551.
PR 22-DEC-1999; 99WO-US030720.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001US-00869599.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
XX
PA (GETH) GENENTECH INC.
XX
PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-492030/46.
DR P-PSDB; ABO19431.
XX
PT New isolated, secreted and transmembrane PRO polypeptides and encoding
PT nucleic acids, useful for the diagnosis and treatment of disorders such
PT as diabetes, obesity and/or hypoinsulinemia.
XX
PS Claim 1; Fig 25; 196pp; English.
XX
CC The invention relates to a new isolated nucleic acid which encodes a PRO
CC polypeptide. The methods and compositions of the present invention are
CC useful for the diagnosis and treatment of disorders associated with the
CC PRO polypeptides, such as diabetes, obesity and hypoinsulinaemia. The
CC present sequence represents cDNA encoding a human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 2242 BP; 606 A; 540 C; 536 G; 559 T; 0 U; 1 Other;

Query Match

100.0%; Score 2241; DB 8; Length 2242;

Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC	60						
Db	1	GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC	60						
QY	61	TCGTCTTCCTTCGGGGGACAACTGGGTTCAGGGCACAGAGAGATATTTAATGTACCCCT	120						
Db	61	TCGTCTTCCTTCGGGGGACAACTGGGTTCAGGGCACAGAGAGATATTTAATGTACCCCT	120						
QY	121	CTTGGGCTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTTGGAAAGTTGCTAGA	180						
Db	121	CTTGGGCTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTTGGAAAGTTGCTAGA	180						
QY	181	GGCTTCAGAACTCCAGCCCTAATGGATCCCAAACCTCGGAGAAATGGCTCCCTGCTGG	240						
Db	181	GGCTTCAGAACTCCAGCCCTAATGGATCCCAAACCTCGGAGAAATGGCTCCCTGCTGG	240						
QY	241	CTGTGCTGTGCTGCTGGAGCGCGGCATGTTCTCCTCACCCCTCCCGCCCCCGGCGC	300						
Db	241	CTGTGCTGTGCTGCTGGAGCGCGGCATGTTCTCCTCACCCCTCCCGCCCCCGGCGC	300						
QY	301	TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA	360						
Db	301	TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA	360						
QY	361	AGGAGTGGTGGCCATCGAGAGCGACTGTGTCCAGCCTGTGCCCTCGCTTCAGACAAGAGC	420						
Db	361	AGGAGTGGTGGCCATCGAGAGCGACTGTGTCCAGCCTGTGCCCTCGCTTCAGACAAGAGC	420						
QY	421	TCTTCAGAAATGATGGCCGTGGTGCGGACACGCTGCAGCGCCTGGGGGCCCGTGTGGCCT	480						
Db	421	TCTTCAGAAATGATGGCCGTGGTGCGGACACGCTGCAGCGCCTGGGGGCCCGTGTGGCCT	480						
QY	481	CGGTGGACATGGTCTCAGCAGCTGCCGATGGTCAGAGTCTTCCAATACCTCCCCTGA	540						
Db	481	CGGTGGACATGGTCTCAGCAGCTGCCGATGGTCAGAGTCTTCCAATACCTCCCCTGA	540						
QY	541	TCCTGGCCGAACCTGGGGAGCGATCCCACGAAAGGCACCGTGTCTTACCGCCACTTGG	600						
Db	541	TCCTGGCCGAACCTGGGGAGCGATCCCACGAAAGGCACCGTGTCTTACCGCCACTTGG	600						
QY	601	ACGTGCAGCCTGTGACCGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGG	660						
Db	601	ACGTGCAGCCTGTGACCGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGG	660						
QY	661	TAGACGGGAACTTTATGGACGAGGAGCGGACCAACAAAGGCCCTGTCTTGGCTTGA	720						
Db	661	TAGACGGGAACTTTATGGACGAGGAGCGGACCAACAAAGGCCCTGTCTTGGCTTGA	720						
QY	721	TCAATGCTGTAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCTGTGTAATATCAAAATCA	780						
Db	721	TCAATGCTGTAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCTGTGTAATATCAAAATCA	780						
QY	781	TCATTGAGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACTTGTGGAAGAAAGAA	840						
Db	781	TCATTGAGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACTTGTGGAAGAAAGAA	840						
QY	841	AGGACCGATTCTTCTGTGGTGTGGACTACATTGTAATTTTCAGATAACCTGTGGATCAGCC	900						
Db	841	AGGACCGATTCTTCTGTGGTGTGGACTACATTGTAATTTTCAGATAACCTGTGGATCAGCC	900						
QY	901	AAAGGAAGCCAGCAATCACTTATGGAAACCGGGGAAACAGCTACTTCAATGGTGGAGTGA	960						
Db	901	AAAGGAAGCCAGCAATCACTTATGGAAACCGGGGAAACAGCTACTTCAATGGTGGAGTGA	960						
QY	961	AATGCAGAGACCAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGG	1020						
Db	961	AATGCAGAGACCAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGG	1020						
QY	1021	CTGATCTGGTGTCTTCTCGGTAGCCTGGTAGACTCGTCTGGTCATATCCTGGTCCCTG	1080						
Db	1021	CTGATCTGGTGTCTTCTCGGTAGCCTGGTAGACTCGTCTGGTCATATCCTGGTCCCTG	1080						

Db	1021	CTGATCTGGTGTCTTCTCGGTAGCCTGGTAGACTCGTCTGGTCATATCCTGGTCCCTG	1080
QY	1081	GAATCTATGATGAAGTGGTTCCTCTTACAGAAAGGAAATAAATACATACAAAGCCATCC	1140
Db	1081	GAATCTATGATGAAGTGGTTCCTCTTACAGAAAGGAAATAAATACATACAAAGCCATCC	1140
QY	1141	ATCTAGACCTTAGAAGAAATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTTCGATACTA	1200
Db	1141	ATCTAGACCTTAGAAGAAATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTTCGATACTA	1200
QY	1201	AGGAGGAGATTCTAATGCA CCTCTGGAGGTACCCATCTCTTTCTATTCTATGGGATCGAGG	1260
Db	1201	AGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCTTTCTATTCTATGGGATCGAGG	1260
QY	1261	GCGCGTTTGTATGAGCCTGGAACCTAAACAGTCAATACCTGGCCGAGTTATAGGAAAAATTTT	1320
Db	1261	GCGCGTTTGTATGAGCCTGGAACCTAAACAGTCAATACCTGGCCGAGTTATAGGAAAAATTTT	1320
QY	1321	CAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAACAGGTGACACGACATC	1380
Db	1321	CAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAACAGGTGACACGACATC	1380
QY	1381	TTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAAACAAGATGGTGTGTTCCATGACTCTAG	1440
Db	1381	TTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAAACAAGATGGTGTGTTCCATGACTCTAG	1440
QY	1441	GACTACACCCCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGA	1500
Db	1441	GACTACACCCCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGA	1500
QY	1501	TCAGAACAGTGTGTTGGAACAGAACAGATATGATCCGGGATGGATCCACCAATTCCAATTG	1560
Db	1501	TCAGAACAGTGTGTTGGAACAGAACAGATATGATCCGGGATGGATCCACCAATTCCAATTG	1560
QY	1561	CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGTAAATTCGCTGGGAGCTGTTG	1620
Db	1561	CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGTAAATTCGCTGGGAGCTGTTG	1620
QY	1621	ATGATGGAGAACATTTCGAGAAATGAGAAAAATCAAAGGTGGAACTACATAGAGGGAACCA	1680
Db	1621	ATGATGGAGAACATTTCGAGAAATGAGAAAAATCAAAGGTGGAACTACATAGAGGGAACCA	1680
QY	1681	AATTATTGCTGCTCCTTTTCTTAGAGATGGCCCAAGTCCCATTAATCAACAAGAACCTTCTA	1740
Db	1681	AATTATTGCTGCTCCTTTTCTTAGAGATGGCCCAAGTCCCATTAATCAACAAGAACCTTCTA	1740
QY	1741	GTCTGATCTGATCCACTGCAGATTCACCTCCCCCAGTCCCTAGACAGGGATGGAATGT	1800
Db	1741	GTCTGATCTGATCCACTGCAGATTCACCTCCCCCAGTCCCTAGACAGGGATGGAATGT	1800
QY	1801	AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAAAATGCTTG	1860
Db	1801	AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAAAATGCTTG	1860
QY	1861	GGATATCTGGATCAGTAATAAAAAATTTTCAAAGGCGACAGATGTTGGAATGTTTAAAGT	1920
Db	1861	GGATATCTGGATCAGTAATAAAAAATTTTCAAAGGCGACAGATGTTGGAATGTTTAAAGT	1920
QY	1921	CCCCACTGCACACCTTCCCTCAAGTCATAGCTGCTTGCAGCAACTTGATTTCCCCCAAGTC	1980
Db	1921	CCCCACTGCACACCTTCCCTCAAGTCATAGCTGCTTGCAGCAACTTGATTTCCCCCAAGTC	1980
QY	1981	CTGTGCAATAGCCCCAGGATTGGAATTCCTTCCAAACCTTTTAGCATATCTCCAACCTTGCA	2040
Db	1981	CTGTGCAATAGCCCCAGGATTGGAATTCCTTCCAAACCTTTTAGCATATCTCCAACCTTGCA	2040
QY	2041	AATTGATTGGCATAAATCACTCCGGTTGCTTTCTAGGTCCTCAAGTCTCGTGACACATA	2100
Db	2041	AATTGATTGGCATAAATCACTCCGGTTGCTTTCTAGGTCCTCAAGTCTCGTGACACATA	2100
QY	2101	ATCATTCATCCCAATGATCGCCTTTGCTTTTACCACCTCTTTCTTTTATCTTATTAATAAA	2160
Db	2101	ATCATTCATCCCAATGATCGCCTTTGCTTTTACCACCTCTTTCTTTTATCTTATTAATAAA	2160

Qy	2161	AATGTTGGTCTCCACCACTGNCTCCC	AAAAAAAAAAAAAAAAAAAAA	2220
Db	2161	AATGTTGGTCTCCACCACTGNCTCCC	AAAAAAAAAAAAAAAAAAAAA	2220
Qy	2221	AAAAAAAAAAAAAAAAAAAAA	2242	
Db	2221	AAAAAAAAAAAAAAAAAAAAA	2242	

RESULT 3	
ACA06111	
ID	ACA06111 standard; cDNA; 2242 BP.
XX	
AC	ACA06111;
XX	
DT	02-JUN-2003 (first entry)
XX	
DE	cDNA encoding human PRO polypeptide #13.
XX	
KW	Human; PRO polypeptide; secreted and transmembrane protein; cancer;
KW	non-insulin dependent diabetes mellitus; septic shock; stroke;
KW	rheumatoid arthritis; graft-versus-host disease; cardiac ischaemia;
KW	psoriasis; inflammatory bowel disease; asthma; antidiabetic; cytostatic;
KW	immunosuppressive; antirheumatic; antiarthritic; cerebroprotective;
KW	vasotropic; antipsoriatic; antiinflammatory; antiasthmatic; gene therapy;
KW	gene; ss.

PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 16-AUG-2001; 2001US-00931836.
XX
XX (GETH) GENENTECH INC.
XX
PI Denoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-341326/32.
DR P-PSDB; ABU69092.
DR
XX
PT New PRO polypeptides and nucleic acid molecules, useful for diagnosing or
PT treating diabetes mellitus, cancers, septic shock, inflammatory bowel
PT disease or asthma, or in gene therapy, chromosome identification or
PT tissue typing.

	Query Match	100.0%;	Score 2241;	DB 8;	Length 2242;		
	Best Local Similarity	100.0%;	Pred. No. 0;				
	Matches 2242;	Conservative	0;	Mismatches	0; Indels	0; Gaps	0;
QY	1	GAATGAATACCTCCGAAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACACGCC	60				
DB	1	GAATGAATACCTCCGAAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACACGCC	60				
QY	61	TCGTCTTCTCCGGGGGACAAACGTGGTCAAGGACAGAGAGATATTTAATGTCAACCT	120				
DB	61	TCGTCTTCTCCGGGGGACAAACGTGGTCAAGGACAGAGAGATATTTAATGTCAACCT	120				
QY	121	CTTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTTCGAGGTTGGGAAAGTTGCTAGA	180				
DB	121	CTTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTTCGAGGTTGGGAAAGTTGCTAGA	180				
QY	181	GGCTTCAGAACTCCAGCCTAATGGATCCCAAACCTCGGGAGAAATGGCTGCGTCCCTGCTGG	240				
DB	181	GGCTTCAGAACTCCAGCCTAATGGATCCCAAACCTCGGGAGAAATGGCTGCGTCCCTGCTGG	240				
QY	241	CTGTGCTGTGCTGCTGTGGAGCGGGCAATGTTCTCCTCACCTCCCCGGCCCCCGGCGC	300				
DB	241	CTGTGCTGTGCTGCTGTGGAGCGGGCAATGTTCTCCTCACCTCCCCGGCCCCCGGCGC	300				
QY	301	TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA	360				
DB	301	TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA	360				

QY 361 AGGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCCTGTGCTCGCTTCAGACAAAGAGC 420
Db |||||
QY 421 TCCTCAGAATGATGGCCGTGGCTGCGGACACGCTGCAGCGCTGGGGCCCGTGTGGCT 480
Db |||||
QY 481 CGGTGGACATGGGTCTCTCAGCAGCTGCCCCGATGGTTCAGAGTCTTCCAAATACCTCCCCGTCA 540
Db |||||
QY 541 TCCTGGCCGAACTGGGGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGG 600
Db |||||
QY 601 ACGTGACGCTGCTGACCGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGG 660
Db |||||
QY 661 TAGACGGGAAACTTTATGGACGAGGACCGGACCGCAACAAGGCCCTGTCTTGGCTTGA 720
Db |||||
QY 721 TCAATGCTGTAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATTC 780
Db |||||
QY 781 TCATTGAGGGATGGAAGAGGCTGCTCTGTTGCCCTGGAGGAACTTGTGGAAGAAAGAAA 840
Db |||||
QY 841 AGGACCGATTCTTCTCTGGTGTGGACTACATTGTAATTTTCAGATAAACCTGTGGATCAGCC 900
Db |||||
QY 901 AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGAAACAGTACTTCATGGTGGAGTGA 960
Db |||||
QY 961 AATGCAGAGACCAAGATTTTCACTCAGGAACCTTTGGTGGCATCTTCATGAACCAATGG 1020
Db |||||
QY 1021 CTGATCTGGTGTCTTCTCGGTAGCCTGGTAGACTCGTCTGGTCATATCCTGGTCCCTG 1080
Db |||||
QY 1081 GAATCTATGATGAAGTGGTTCCTTTACAGAAGAGGAAATAAATACATACAAAGCCATCC 1140
Db |||||
QY 1141 ATCTAGACCTAGAAGAAATACCGGAATAGCAGCCGGTTGAGAAATTTCTGTTTCGATACTA 1200
Db |||||
QY 1201 AGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCTTCTATTTCATGGATCGAGG 1260
Db |||||
QY 1261 GCGCGTTTGTAGAGCCTGGAACCTAAACAGTACATACCTGGCCGAGTTATAGGAAATTTT 1320
Db |||||
QY 1321 CAATCCGCTAGTCCCTCACATGAATGTCTGCGGTGGAAGAAACAGGTGACACGACATC 1380
Db |||||
QY 1381 TTGAAGATGTGTTCTCCAAAGAAATAGTCCAAAGATGGTGTGTTCCATGACTCTAG 1440
Db |||||

QY 1441 GACTACACCCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGA 1500
Db |||||
QY 1501 TCAGAACAGTGTTTGGAAACAGAACAGATATGATCCGGGATGGATCCACCATTCCAATTG 1560
Db |||||
QY 1561 CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGTCTAATTCGCTGGGAGCTGTG 1620
Db |||||
QY 1621 ATGATGGAGAACATTTCGAGAATGAGAAAAATCAAAGTGGAACTACATAGAGGGAACCA 1680
Db |||||
QY 1681 AATTATTGCTGCCCTTTTCTTAGAGATGGCCAGCTCCATTAAATCACAAGAACCTTCTA 1740
Db |||||
QY 1741 GTCTGATCTGATCCACTGACAGATTACCTCCCCCATCCCTAGACAGGGATGGAATGT 1800
Db |||||
QY 1801 AAATATCCAGAGAAATTTGGTCTAGTATAGTACATTTCCCTTCCATTTAAATGTCTTG 1860
Db |||||
QY 1861 GGATATCTGGATCAGTAATAAAATATTTCAAAGGCACAGATGTTGGAAATGTTAAGGT 1920
Db |||||
QY 1921 CCCCCACTGCACACCTTCTCAAGTCATAGCTGCTTGCGAGCAACTTGATTTCCCCCAAGTC 1980
Db |||||
QY 1981 CTGTGCAATAGCCCCAGGATGGATTCTTCCAAACCTTTTAGCATATCTCCAACCTTGCA 2040
Db |||||
QY 2041 ATTTGATGGCATAATCACTCCCGTGTGCTTTCTAGTCTCTCAAGTCTCGTGACACATA 2100
Db |||||
QY 2101 ATCATTTCCATCCAATGATCGCTTGTCTTTACCACTCTTTCCTTTTATCTTATTAATAA 2160
Db |||||
QY 2161 AATGTTGGTCTCCACCACCTGCTCCCAAAAAA 2220
Db |||||
QY 2221 AAAAAA 2242
Db |||||

RESULT 4
ACA67734

ID ACA67734 standard; cDNA; 2242 BP.

XX ACA67734;

XX 24-JUN-2003 (first entry)

XX cDNA encoding human secreted polypeptide PRO4380.

DE Human; gene; ss; inflammatory disease; organ failure; atherosclerosis;
XX cardiac injury; infertility; birth defect; premature aging; AIDS; cancer;
KW differentiation disorder; cell adhesion disorder; skin disorder;
KW neural receptor disorder; diabetic complication; tissue typing.

XX Homo sapiens.

Db 901 AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGAACAGCTACTTTCATGGTGAGGTGA 960
QY 961 AATGCAGAGACCAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTTCATGAACCAATGG 1020
Db 961 AATGCAGAGACCAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTTCATGAACCAATGG 1020
QY 1021 CTGATCTGGTTGCTCTTCTCGGTAGCCTGGTAGACTCGTCTGGTCATATCCTGGTCCCTG 1080
Db 1021 CTGATCTGGTTGCTCTTCTCGGTAGCCTGGTAGACTCGTCTGGTCATATCCTGGTCCCTG 1080
QY 1081 GAATCTATGATGAAGTGGTTCCTCTTACAGAAGAGGAATAAATACATACAAAGCCATCC 1140
Db 1081 GAATCTATGATGAAGTGGTTCCTCTTACAGAAGAGGAATAAATACATACAAAGCCATCC 1140
QY 1141 ATCTAGACCTAGAAAGAAATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTCGATACTA 1200
Db 1141 ATCTAGACCTAGAAAGAAATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTCGATACTA 1200
QY 1201 AGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCTTTCTATTCTATGGGATCGAGG 1260
Db 1201 AGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCTTTCTATTCTATGGGATCGAGG 1260
QY 1261 GCGCGTTTGATGAGCCTGGAACCTAAACAGTCAATACCTGGCCGAGTTATAGGAAATTTT 1320
Db 1261 GCGCGTTTGATGAGCCTGGAACCTAAACAGTCAATACCTGGCCGAGTTATAGGAAATTTT 1320
QY 1321 CAATCCGCTCTAGTCCCTCACATGAATGTCTCGGTGGAACACAGGTGACACGACATC 1380
Db 1321 CAATCCGCTCTAGTCCCTCACATGAATGTCTCGGTGGAACACAGGTGACACGACATC 1380
QY 1381 TTGAAGATGTGTCTCCAAAGAAATAGTTTCAACAAGATGGTTGTTTCCATGACTCTAG 1440
Db 1381 TTGAAGATGTGTCTCCAAAGAAATAGTTTCAACAAGATGGTTGTTTCCATGACTCTAG 1440
QY 1441 GACTACACCCGTGGATTGCAAAATATTGTATGACACCCAGTATCTCGCAGCAAAAAGAGCGA 1500
Db 1441 GACTACACCCGTGGATTGCAAAATATTGTATGACACCCAGTATCTCGCAGCAAAAAGAGCGA 1500
QY 1501 TCAGAACAGTGTGTTGGAACAGAACCCAGATATGATCCGGGATGGATCCACCATTTCCAATTG 1560
Db 1501 TCAGAACAGTGTGTTGGAACAGAACCCAGATATGATCCGGGATGGATCCACCATTTCCAATTG 1560
QY 1561 CCAAAATGTTCCAGGAGATCGTCCACAAGCGTGGTGCTAATTCGGTGGGAGCTGTTG 1620
Db 1561 CCAAAATGTTCCAGGAGATCGTCCACAAGCGTGGTGCTAATTCGGTGGGAGCTGTTG 1620
QY 1621 ATGATGGAGAACATTCGCAGAAATGAGAAATCAACAGGTGGAACCTACATAGAGGGAACCA 1680
Db 1621 ATGATGGAGAACATTCGCAGAAATGAGAAATCAACAGGTGGAACCTACATAGAGGGAACCA 1680
QY 1681 AATTATTGCTGCTCTTTTCTTAGAGATGGCCAGCTCCATTAATCAAGAACCTTCTA 1740
Db 1681 AATTATTGCTGCTCTTTTCTTAGAGATGGCCAGCTCCATTAATCAAGAACCTTCTA 1740
QY 1741 GTCTGATCTGATCCACTGACAGATTCACCTCCCCACATCCCTAGACAGGGATGGAATGT 1800
Db 1741 GTCTGATCTGATCCACTGACAGATTCACCTCCCCACATCCCTAGACAGGGATGGAATGT 1800
QY 1801 AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTCCCTTCCATTTAAATGTCTTG 1860
Db 1801 AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTCCCTTCCATTTAAATGTCTTG 1860
QY 1861 GGATATCTGGATCAGTAATAAATAATTTCAAAGGCACAGATGTTGGAATGTTTAAGGT 1920
Db 1861 GGATATCTGGATCAGTAATAAATAATTTCAAAGGCACAGATGTTGGAATGTTTAAGGT 1920
QY 1921 CCCCCACTGCACACCTTCTCAAGTCATAGCTGTTGCAGCAACTTGATTTCCCCAAGTC 1980
Db 1921 CCCCCACTGCACACCTTCTCAAGTCATAGCTGTTGCAGCAACTTGATTTCCCCAAGTC 1980
QY 1981 CTGTGCAATAGCCCCAGGATGGATTCTTCCAACTTTTAGCATATCTCCAACCTTGCA 2040

Db 1981 CTGTGCAATAGCCCCAGGATTTGGATTCTTCCAACCTTTTAGCATATCTCCAACCTTGCA 2040
QY 2041 ATTTGATTGGCATAATCACTCCGGTTTGGTTTCTTAGGTCTCTCAAGTGTCTGTGACACATA 2100
Db 2041 ATTTGATTGGCATAATCACTCCGGTTTGGTTTCTTAGGTCTCTCAAGTGTCTGTGACACATA 2100
QY 2101 ATCATTTCCATCCATGATCGCCTTTGCTTTTACCACTCTTCTTTTATCTTATTAATAAA 2160
Db 2101 ATCATTTCCATCCATGATCGCCTTTGCTTTTACCACTCTTCTTTTATCTTATTAATAAA 2160
QY 2161 AATGTTGGTCTCCACCACTGNCTCCCAAAAAAATAAAAAAATAAAAAA 2220
Db 2161 AATGTTGGTCTCCACCACTGNCTCCCAAAAAAATAAAAAAATAAAAAA 2220
QY 2221 AAAAAAATAAAAAAATAAAAAA 2242
Db 2221 AAAAAAATAAAAAAATAAAAAA 2242
RESULT 5
ADA76581
ID ADA76581 standard; cDNA; 2242 BP.
XX
AC ADA76581;
XX
DT 20-NOV-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO4380 cDNA.
XX
KW human; secreted and transmembrane protein; PRO; gene; ss; tumour;
KW gene therapy; tissue typing; chromosome identification; cytostatic.
OS Homo sapiens.
XX
PN US2003036114-A1.
PD 20-FEB-2003.
XX
PF 26-DEC-2001; 2001US-00035719.
XX
PR 15-MAY-1998; 98US-0085579P.
PR 15-DEC-1998; 98US-0112514P.
PR 22-DEC-1998; 98US-0113300P.
PR 23-DEC-1998; 98US-0113430P.
PR 23-DEC-1998; 98US-0113605P.
PR 23-DEC-1998; 98US-0113621P.
PR 23-DEC-1998; 98US-0114140P.
PR 12-JAN-1999; 99US-0115552P.
PR 22-JAN-1999; 99US-0116843P.
PR 23-MAR-1999; 99US-0125774P.
PR 23-MAR-1999; 99US-0125778P.
PR 24-MAR-1999; 99US-0125826P.
PR 31-MAR-1999; 99US-0127035P.
PR 05-APR-1999; 99US-0127706P.
PR 13-APR-1999; 99US-0129122P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.
PR 27-APR-1999; 99US-0131291P.
PR 04-MAY-1999; 99US-0132371P.
PR 04-MAY-1999; 99US-0132379P.
PR 04-MAY-1999; 99US-0132383P.
PR 14-MAY-1999; 99WO-US010733.
PR 25-MAY-1999; 99US-0135750P.
PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-014791P.
PR 03-AUG-1999; 99US-0146970P.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99WO-US028551.
PR 22-DEC-1999; 99WO-US030720.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 22-MAY-2000; 2000WO-US014042.

Db 1321 CAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAACACAGGTGACACGACATC 1380

QY 1381 TTGAAGATGTGTTCTCCAAAAGAAATAGTTCACAAAGATGGTGTGTTTCCATGACTCTAG 1440

Db 1381 TTGAAGATGTGTTCTCCAAAAGAAATAGTTCACAAAGATGGTGTGTTTCCATGACTCTAG 1440

QY 1441 GACTACACCCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGA 1500

Db 1441 GACTACACCCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGA 1500

QY 1501 TCAGAACAGTGTGTTGGAACAGAACCCAGATATGATCCGGGATGGATCCACCAATTCOAATTG 1560

Db 1501 TCAGAACAGTGTGTTGGAACAGAACCCAGATATGATCCGGGATGGATCCACCAATTCOAATTG 1560

QY 1561 CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGCTAATTCGGCTGGGAGCTGTG 1620

Db 1561 CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGCTAATTCGGCTGGGAGCTGTG 1620

QY 1621 ATGATGGAGAACATTCGCAGAAATGAGAAAATCAACAGGTGGAACACTACATAGAGGGAACCA 1680

Db 1621 ATGATGGAGAACATTCGCAGAAATGAGAAAATCAACAGGTGGAACACTACATAGAGGGAACCA 1680

QY 1681 AATTATTTGCTGCCTTTTCTTAGAGATGGCCAGCTCCATTAAATCACAAGAACCTTCTA 1740

Db 1681 AATTATTTGCTGCCTTTTCTTAGAGATGGCCAGCTCCATTAAATCACAAGAACCTTCTA 1740

QY 1741 GTCTGATCTGATCCACTGACAGATTCACCTCCCCACATCCCTAGACAGGGATGGAATGT 1800

Db 1741 GTCTGATCTGATCCACTGACAGATTCACCTCCCCACATCCCTAGACAGGGATGGAATGT 1800

QY 1801 AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTAAAAATGTTAAGT 1860

Db 1801 AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTAAAAATGTTAAGT 1860

QY 1861 GGATATCTGGATCAGTAATAAATAATTTCAAAGGCACAGATGTTGGAATGTTAAGT 1920

Db 1861 GGATATCTGGATCAGTAATAAATAATTTCAAAGGCACAGATGTTGGAATGTTAAGT 1920

QY 1921 CCCCCACTGCACACCTTCCTCAAGTCATAGCTGCTTGCAAGCAACTTGATTTCCCCAAGTC 1980

Db 1921 CCCCCACTGCACACCTTCCTCAAGTCATAGCTGCTTGCAAGCAACTTGATTTCCCCAAGTC 1980

QY 1981 CTGTGCAATAGCCCCCAGGATTGGATTCTCTTCCAACTTTTAGCATATCTCCAACCTTGCA 2040

Db 1981 CTGTGCAATAGCCCCCAGGATTGGATTCTCTTCCAACTTTTAGCATATCTCCAACCTTGCA 2040

QY 2041 ATTTGATTGGCATAATCACTCCGGTTTGCTTTCTAGGTCTCTCAAGTCTCGTGACACATA 2100

Db 2041 ATTTGATTGGCATAATCACTCCGGTTTGCTTTCTAGGTCTCTCAAGTCTCGTGACACATA 2100

QY 2101 ATCATTCATCCCAATGATCGCCTTTGCTTTTACCACCTCTTCCCTTTATCTTATTAATAAA 2160

Db 2101 ATCATTCATCCCAATGATCGCCTTTGCTTTTACCACCTCTTCCCTTTATCTTATTAATAAA 2160

QY 2161 AATGTTGGTCTCCACCACCTGNCCTCCCAAAAAA 2242

Db 2161 AATGTTGGTCTCCACCACCTGNCCTCCCAAAAAA 2242

QY 2221 AAAAAAAAAAAAAAAAAAAAAA 2242

Db 2221 AAAAAAAAAAAAAAAAAAAAAA 2242

KW Human; ss; gene; PRO; secreted protein; transmembrane protein; septic shock; gene therapy.

KW Homo sapiens.

XX US2003044842-A1.

OS 06-MAR-2003.

XX 26-DEC-2001; 2001US-00036160.

PN 15-MAY-1998; 98US-0085579P.

XX 15-DEC-1998; 98US-0112514P.

PR 22-DEC-1998; 98US-0113300P.

PR 23-DEC-1998; 98US-0113430P.

PR 23-DEC-1998; 98US-0113605P.

PR 23-DEC-1998; 98US-0113621P.

PR 23-DEC-1998; 98US-0114140P.

PR 12-JAN-1999; 99US-0115552P.

PR 22-JAN-1999; 99US-0116843P.

PR 23-MAR-1999; 99US-0125774P.

PR 23-MAR-1999; 99US-0125778P.

PR 24-MAR-1999; 99US-0125826P.

PR 31-MAR-1999; 99US-0127035P.

PR 05-APR-1999; 99US-0127706P.

PR 13-APR-1999; 99US-0129122P.

PR 21-APR-1999; 99US-0130359P.

PR 27-APR-1999; 99US-0131270P.

PR 27-APR-1999; 99US-0131272P.

PR 27-APR-1999; 99US-0131291P.

PR 04-MAY-1999; 99US-0132371P.

PR 04-MAY-1999; 99US-0132379P.

PR 04-MAY-1999; 99US-0132383P.

PR 14-MAY-1999; 99US-0132917P.

PR 25-MAY-1999; 99US-0135750P.

PR 08-JUN-1999; 99US-0138166P.

PR 20-JUL-1999; 99US-0144791P.

PR 03-AUG-1999; 99US-0146970P.

PR 29-OCT-1999; 99US-0162506P.

PR 02-DEC-1999; 99US-0162506P.

PR 22-DEC-1999; 99US-0162506P.

PR 01-MAR-2000; 2000US-0005601.

PR 02-MAR-2000; 2000US-0005841.

PR 22-MAY-2000; 2000US-0014042.

PR 02-JUN-2000; 2000US-0015264.

PR 23-AUG-2000; 2000US-0023522.

PR 24-AUG-2000; 2000US-0023328.

PR 01-DEC-2000; 2000US-0032678.

PR 20-DEC-2000; 2000US-0034956.

PR 28-FEB-2001; 2001US-0006520.

PR 01-JUN-2001; 2001US-0017800.

PR 20-JUN-2001; 2001US-0019692.

PR 29-JUN-2001; 2001US-0021066.

PR 09-JUL-2001; 2001US-0021735.

PR 16-AUG-2001; 2001US-00931836.

XX (GETH) GENENTECH INC.

PA Desnoyers L, Baton DL, Goddard A, Godowski PJ, Gurney AL, Pan J; Stewart TA, Watanabe CK, Wood WI, Zhang Z; WPI; 2003-492260/46. P-PSDB; ABO25139.

XX Novel secreted and transmembrane polypeptide for identifying agonists or antagonists of polypeptide, and as molecular weight markers.

PS Claim 2; Fig 25; 195pp; English.

XX The invention relates to an isolated, secreted and transmembrane polypeptide, termed PRO polypeptide, PRO having at least 80 % sequence identity to any one of the 23 100-900 residue amino acid sequences, given in the specification or to a sequence encoded by a nucleic acid molecule

CC deposited under any one of the ATCC accession numbers given in the
CC specification. Also included are an isolated nucleic acid molecule having
CC at least 80 % sequence identity to any one of 23 400-3500 nucleotide
CC sequences given in the specification, (or a nucleotide sequence encoding
CC PRO, a full- length PRO coding sequence, a full-length coding sequence of
CC DNA deposited under any ATCC accession number given in the specification)
CC or at least 80 % identity to a nucleotide sequence encoding PRO, lacking
CC its associated signal peptide, a sequence encoding extracellular domain
CC of PRO with or without its associated signal peptide, a vector comprising
CC the PRO nucleic acid, a host cell comprising the vector, preparation of
CC PRO, a chimeric molecule comprising PRO fused to a heterologous amino
CC acid sequence and an anti-PRO antibody. PRO is useful for identifying
CC ant/agonists or antagonists of PRO, preparing a variant of PRO, as
CC molecular weight markers and PRO nucleic acid is useful for recombinantly
CC expressing those markers. PRO is also useful as therapeutic agent. PRO is
CC useful in assays to identify molecules or proteins which bind to PRO and
CC for identifying inhibitors of PRO. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in generation of
CC antisense RNA and DNA, for generating transgenic animals or knockout
CC animals which in turn are useful in the development and screening of
CC therapeutically useful reagents. PRO nucleic acid is also useful in
CC mapping the gene which encodes the PRO and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, for chromosome
CC identification, as chromosome marker, and for generating probes for PCR,
CC Northern analysis, Southern analysis and Western analysis. The antibody
CC useful in diagnostic assays for PRO, for affinity purification of PRO,
CC and for treating septic shock. PRO or the antibody is useful for the
CC preparation of medicament for treating conditions which is responsive to
CC the PRO polypeptide or anti-PRO antibody. PRO and PRO nucleic acid are
CC useful for tissue typing. The present sequence encodes a PRO protein
XX
SQ Sequence 2242 BP; 606 A; 540 C; 536 G; 559 T; 0 U; 1 Other;

Query Match 100.0%; Score 2241; DB 9; Length 2242;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATGAATACCTCCGAAGCCGCTTGTCTCCAGATGTGAATAGTCCCACTATACCAGCC 60
DB 1 GAATGAATACCTCCGAAGCCGCTTGTCTCCAGATGTGAATAGTCCCACTATACCAGCC 60
QY 61 TCGTCTTCCTCCGGGGACAACGCTGGGTGAGGACAGAGAGATATTAAATGTCACCCCT 120
DB 61 TCGTCTTCCTCCGGGGACAACGCTGGGTGAGGACAGAGAGATATTAAATGTCACCCCT 120
QY 121 CTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTGGAGGTTGGAAAGTTGCTAGA 180
DB 121 CTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTGGAGGTTGGAAAGTTGCTAGA 180
QY 181 GGCTTCAGAACTCCAGCCCTAATGGATCCCAAACCTCGGAGAAATGGTGGCTCCCTGCTGG 240
DB 181 GGCTTCAGAACTCCAGCCCTAATGGATCCCAAACCTCGGAGAAATGGTGGCTCCCTGCTGG 240
QY 241 CTGTGCTGCTGCTGCTGGAGCGCGGATGTTCTCCTCACCCCTCCCGGCCCGCGCGC 300
DB 241 CTGTGCTGCTGCTGCTGGAGCGCGGATGTTCTCCTCACCCCTCCCGGCCCGCGCGC 300
QY 301 TGTTAGAGAAAGTCTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA 360
DB 301 TGTTAGAGAAAGTCTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA 360
QY 361 AGGAGTGGGTGCCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGTTTCAGACAAGAGC 420
DB 361 AGGAGTGGGTGCCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGTTTCAGACAAGAGC 420
QY 421 TCTTCAGAAATGATGGCCCGTGGGTGCGGACACGCTGCAGCGCTGGGGGCCCGTGTGGCCT 480
DB 421 TCTTCAGAAATGATGGCCCGTGGGTGCGGACACGCTGCAGCGCTGGGGGCCCGTGTGGCCT 480
QY 481 CGGTGGACATGGTCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCA 540
DB 481 CGGTGGACATGGTCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCA 540

QY 541 TCCTGGCCGAACCTGGGGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGG 600
DB 541 TCCTGGCCGAACCTGGGGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGG 600
QY 601 ACGTGCAGCCTGCTGACCGGGGCGATGGGTGGCTCACGGACCCCTATGTGTGACGGAGG 660
DB 601 ACGTGCAGCCTGCTGACCGGGGCGATGGGTGGCTCACGGACCCCTATGTGTGACGGAGG 660
QY 661 TAGACGGGAAACTTTATGGACGAGGAGCGACCGACAACAAAGGCCCTGTCTTGGCTTGA 720
DB 661 TAGACGGGAAACTTTATGGACGAGGAGCGACCGACAACAAAGGCCCTGTCTTGGCTTGA 720
QY 721 TCAATGCTGTGAGCGCCTTCAGAGCCCTTGAGCAAGATCTTCTCTGTGAATATCAAATTCA 780
DB 721 TCAATGCTGTGAGCGCCTTCAGAGCCCTTGAGCAAGATCTTCTCTGTGAATATCAAATTCA 780
QY 781 TCATTGAGGGATGGAAGAGGCTGCTGTGTTGCCCTGGAGGAACCTTGTGAAAAAGAAA 840
DB 781 TCATTGAGGGATGGAAGAGGCTGCTGTGTTGCCCTGGAGGAACCTTGTGAAAAAGAAA 840
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DB 841 AGGACCGATTCTTCTGGTGTGACTACATTTGTAATTTTTCAGATAACCTGTGGATCAGCC 900
QY 901 AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGGAACAGCTACTTTCATGGTGGAGGTGA 960
DB 901 AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGGAACAGCTACTTTCATGGTGGAGGTGA 960
QY 961 AATGCAGAGACCAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGG 1020
DB 961 AATGCAGAGACCAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGG 1020
QY 1021 CTGATCTGGTTGCTCTTCTCGGTAGCCTGGTAGACTCGTCTGGTCAATCTCTGGTCCCTG 1080
DB 1021 CTGATCTGGTTGCTCTTCTCGGTAGCCTGGTAGACTCGTCTGGTCAATCTCTGGTCCCTG 1080
QY 1081 GAATCTATGATGAAGTGGTTCCTCTTACAGAAAGAGGAAATAAATACATACAAAGCCATCC 1140
DB 1081 GAATCTATGATGAAGTGGTTCCTCTTACAGAAAGAGGAAATAAATACATACAAAGCCATCC 1140
QY 1141 ATCTAGACCTAGAAGAAATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTTTCGATACTA 1200
DB 1141 ATCTAGACCTAGAAGAAATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTTTCGATACTA 1200
QY 1201 AGGAGGAGATTCTAATGCACCTCTGGAGGTACCCCATCTCTTCTATTTCATGGGATCGAGG 1260
DB 1201 AGGAGGAGATTCTAATGCACCTCTGGAGGTACCCCATCTCTTCTATTTCATGGGATCGAGG 1260
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DB 1321 CAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAACAGGTGACACGACATC 1380
QY 1381 TTGAAGATGTGTTTCTCCAAAAGAAATAGTTCCAAAGATGGTTGTTTCTCCATGACTCTAG 1440
DB 1381 TTGAAGATGTGTTTCTCCAAAAGAAATAGTTCCAAAGATGGTTGTTTCTCCATGACTCTAG 1440
QY 1441 GACTACACCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAAGAGCGA 1500
DB 1441 GACTACACCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAAGAGCGA 1500
QY 1501 TCAGAACAGTGTGTTGGAACAGAACCCAGATATGATCCGGGATGGATCCCAATTG 1560
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QY 1561 CCAAAATGTTCCAGGAGATCGTCCAAAGAGCGTGGTGTCTAATTCGCTGGGAGCTGTTG 1620
DB 1561 CCAAAATGTTCCAGGAGATCGTCCAAAGAGCGTGGTGTCTAATTCGCTGGGAGCTGTTG 1620
QY 1621 ATGATGGAGAACATTTCGAGAAATGAGAAAAATCAACAGGTGGAACTACATAGAGGGAACCA 1680

Db	1621	ATGATGGAGAACATTCGCGAATGAGAAATCAACAGTGGAACACATAGAGGGAACCA	1680	PF	26-DEC-2001; 2001US-00035958.
QY	1681	AATTATTGCTGCCTTTTCTTAGAGATGGCCCGAGCTCCATTAAATCACAAGAACTTCTA	1740	XX	
Db	1681	AATTATTGCTGCCTTTTCTTAGAGATGGCCCGAGCTCCATTAAATCACAAGAACTTCTA	1740	PR	15-MAY-1998; 98US-0085579P.
QY	1741	GTCTGATCTGATCCACTGACAGATTCCACCTCCCCACATCCCTAGACAGGGATGGAATGT	1800	PR	15-DEC-1998; 98US-0112514P.
Db	1741	GTCTGATCTGATCCACTGACAGATTCCACCTCCCCACATCCCTAGACAGGGATGGAATGT	1800	PR	22-DEC-1998; 98US-0113300P.
QY	1801	AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTCCCTTCCATTAAATAATGTCTTG	1860	PR	23-DEC-1998; 98US-0113430P.
Db	1801	AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTCCCTTCCATTAAATAATGTCTTG	1860	PR	23-DEC-1998; 98US-0113605P.
QY	1861	GGATATCTGGATCAGTAATAAATAATTTCAAAGGCACAGATGTTGGAATGTTTAAAGGT	1920	PR	23-DEC-1998; 98US-0113621P.
Db	1861	GGATATCTGGATCAGTAATAAATAATTTCAAAGGCACAGATGTTGGAATGTTTAAAGGT	1920	PR	23-DEC-1998; 98US-0114140P.
QY	1921	CCCCCACTGCACACCTTCCTCAAGTCATAGCTGCTTGCAAGCAACTTGATTTCCCAAGTC	1980	PR	12-JAN-1999; 99US-0115552P.
Db	1921	CCCCCACTGCACACCTTCCTCAAGTCATAGCTGCTTGCAAGCAACTTGATTTCCCAAGTC	1980	PR	22-JAN-1999; 99US-0116843P.
QY	1981	CTGTGCAATAGCCCCAGGATTGGATTCCCTTCCAACCTTTTAGCATATCTCCAACCTTGCA	2040	PR	23-MAR-1999; 99US-0125774P.
Db	1981	CTGTGCAATAGCCCCAGGATTGGATTCCCTTCCAACCTTTTAGCATATCTCCAACCTTGCA	2040	PR	23-MAR-1999; 99US-0125778P.
QY	2041	ATTTGATTGGCATAATCACTCCGGTTTGCTTTCTAGGTCCTCAAGTGCTCGTGACACATA	2100	PR	24-MAR-1999; 99US-0125826P.
Db	2041	ATTTGATTGGCATAATCACTCCGGTTTGCTTTCTAGGTCCTCAAGTGCTCGTGACACATA	2100	PR	31-MAR-1999; 99US-0127035P.
QY	2101	ATCATTCATCCAATGATCGCCTTTGCTTTACCACCTCTTTTCTTATCTTATTAATAAA	2160	PR	05-APR-1999; 99US-0127706P.
Db	2101	ATCATTCATCCAATGATCGCCTTTGCTTTACCACCTCTTTTCTTATCTTATTAATAAA	2160	PR	13-APR-1999; 99US-0129122P.
QY	2161	AATGTTGTTCTCCACCACCTGNCTCCAAAAAATAAAAAAAAAAAAAAAAAAAAAA	2220	PR	21-APR-1999; 99US-0130359P.
Db	2161	AATGTTGTTCTCCACCACCTGNCTCCAAAAAATAAAAAAAAAAAAAAAAAAAAAA	2220	PR	27-APR-1999; 99US-0131270P.
QY	2221	AAAAAAAAAAAAAAAAAAAAA 2242		PR	27-APR-1999; 99US-0131272P.
Db	2221	AAAAAAAAAAAAAAAAAAAAA 2242		PR	27-APR-1999; 99US-0131291P.
RESULT 7				PR	04-MAY-1999; 99US-0132379P.
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ID	AAD59362	standard; cDNA; 2242 BP.		PR	14-MAY-1999; 99WO-US010733.
XX	AC	AAD59362;		PR	25-MAY-1999; 99US-0135750P.
XX	DT	18-DEC-2003 (first entry)		PR	08-JUN-1999; 99US-0138166P.
XX	DE	Human PRO4380 cDNA.		PR	20-JUL-1999; 99US-0144791P.
XX	KW	Human; PRO protein; inflammation; nephropathy; bone disorder; arthritis;		PR	03-AUG-1999; 99US-0146970P.
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XX	OS	Homo sapiens.		PR	02-DEC-1999; 99WO-US028551.
XX	FH	Key	Location/Qualifiers	PR	22-DEC-1999; 99WO-US030720.
FT	CDS	201..1724	/*tag= a	PR	01-MAR-2000; 2000WO-US005601.
FT		/product= "Human PRO protein"		PR	02-MAR-2000; 2000WO-US005841.
FT	sig_peptide	201..278		PR	22-MAY-2000; 2000WO-US014042.
FT	mat_peptide	279..1721	/*tag= b	PR	02-JUN-2000; 2000WO-US015264.
FT		/product= "Mature human PRO protein"		PR	23-AUG-2000; 2000WO-US023522.
FT				PR	24-AUG-2000; 2000WO-US023328.
XX	PN	US2003049733-A1.		PR	01-DEC-2000; 2000WO-US032678.
XX	PD	13-MAR-2003.		PR	20-DEC-2000; 2000WO-US034956.
XX	XX			PR	28-FEB-2001; 2001WO-US006520.
				PR	01-JUN-2001; 2001WO-US017800.
				PR	20-JUN-2001; 2001WO-US019692.
				PR	29-JUN-2001; 2001WO-US021066.
				PR	09-JUL-2001; 2001WO-US021735.
				PR	16-AUG-2001; 2001US-00931836.
				XX	(GETH) GENENTECH INC.
				PA	
				XX	Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
				PI	Stewart TA, Watanabe CK, Wood WI, Zhang Z;
				PI	
				XX	WPI; 2003-585109/55.
				DR	P-PSDB; AAE39109.
				DR	
				XX	New isolated, secreted and transmembrane PRO polypeptides and nucleic
				PT	acids, useful for diagnosing, preventing and/or treating inflammation,
				PT	nephropathies, bone and cartilage disorders, and diabetes.
				XX	Claim 2; Fig 25; 203pp; English.
				PS	
				XX	The invention relates to an isolated nucleic acid that encodes a PRO
				CC	polypeptide. The methods and compositions of the present invention are
				CC	useful for the diagnosis, prevention and/or treatment of inflammation,
				CC	nephropathies, bone and cartilage disorders, such as arthritis and
				CC	disorders that affect glucose or free fatty acid (FFA) uptake, such as
				CC	diabetes, hypoinsulinaemia or hyperinsulinaemia. The PRO polypeptides are
				CC	also useful as molecular weight markers or for chromosome identification.
				CC	The PRO genes are useful as hybridisation probes or for screening
				CC	libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be
				CC	used in gene therapy and antisense therapy. The present sequence is human
				CC	PRO cDNA
				XX	

SQ	Sequence 2242 BP; 606 A; 540 C; 536 G; 559 T; 0 U; 1 Other;									
	Query Match 100.0%; Score 2241; DB 10; Length 2242;									
	Best Local Similarity 100.0%; Pred. No. 0;									
	Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	GAATGAATACCTCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC	60							
Db	1	GAATGAATACCTCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC	60							
QY	61	TCGTCTTCCCTCCGGGGACAACGTTGGTTCAGGACAGAGATATTTAATGTCACCTT	120							
Db	61	TCGTCTTCCCTCCGGGGACAACGTTGGTTCAGGACAGAGATATTTAATGTCACCTT	120							
QY	121	CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTTGGGAAAGTTGCTAGA	180							
Db	121	CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTTGGGAAAGTTGCTAGA	180							
QY	181	GGCTTCAGAACTCAGACCTAATGGATCCCAAACCTCGGGAGAATGGCTGCGTCCCTGCTGG	240							
Db	181	GGCTTCAGAACTCAGACCTAATGGATCCCAAACCTCGGGAGAATGGCTGCGTCCCTGCTGG	240							
QY	241	CTGTGCTGCTGCTGCTGGAGCGCGGCAATGTTCTCCTCACCTCCCGCCCCCGGCGC	300							
Db	241	CTGTGCTGCTGCTGCTGGAGCGCGGCAATGTTCTCCTCACCTCCCGCCCCCGGCGC	300							
QY	301	TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA	360							
Db	301	TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA	360							
QY	361	AGGAGTGGGTGGCCATCGAGAGCGGACTCTGTCCAGCCCTGTGCCCTCGCTTCAGACAAGAGC	420							
Db	361	AGGAGTGGGTGGCCATCGAGAGCGGACTCTGTCCAGCCCTGTGCCCTCGCTTCAGACAAGAGC	420							
QY	421	TCTTCAGAAATGATGGCCGTGGCTGCGGACACGCTGCAGCGCCTGGGGCCCGTGTGGCCT	480							
Db	421	TCTTCAGAAATGATGGCCGTGGCTGCGGACACGCTGCAGCGCCTGGGGCCCGTGTGGCCT	480							
QY	481	CGGTGGACATGGTCTCAGCAGCTGCCGATGGTCAGAGTCTTCCAATACCTCCCGTCA	540							
Db	481	CGGTGGACATGGTCTCAGCAGCTGCCGATGGTCAGAGTCTTCCAATACCTCCCGTCA	540							
QY	541	TCCTGGCCGAACCTGGGGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGG	600							
Db	541	TCCTGGCCGAACCTGGGGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGG	600							
QY	601	ACGTGCAGCCTGCTGACCGGGCGATGGGTGGCTCACGGACCCCTATGTCTGACGGAGG	660							
Db	601	ACGTGCAGCCTGCTGACCGGGCGATGGGTGGCTCACGGACCCCTATGTCTGACGGAGG	660							
QY	661	TAGACGGGAACTTTATGGACGAGGAGCGACCGACAACAAAGGCCCTGTCTTGGCTTGA	720							
Db	661	TAGACGGGAACTTTATGGACGAGGAGCGACCGACAACAAAGGCCCTGTCTTGGCTTGA	720							
QY	721	TCAATGCTGTAGCGCCCTTCAGAGCCCTGGAGCAAGATCTTCCCTGTGAATATCAAAATCA	780							
Db	721	TCAATGCTGTAGCGCCCTTCAGAGCCCTGGAGCAAGATCTTCCCTGTGAATATCAAAATCA	780							
QY	781	TCATTGAGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACCTGTGGAAAAAGAAA	840							
Db	781	TCATTGAGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACCTGTGGAAAAAGAAA	840							
QY	841	AGGACCGGATTTCTCTCTGGTGTGACTACATTTGAATTTTTCAGATAACCTGTGGATCAGCC	900							
Db	841	AGGACCGGATTTCTCTCTGGTGTGACTACATTTGAATTTTTCAGATAACCTGTGGATCAGCC	900							
QY	901	AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGAACAGCTACTTTCATGGTGGAGGTGA	960							
Db	901	AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGAACAGCTACTTTCATGGTGGAGGTGA	960							
QY	961	AATGCAGAGACCAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGG	1020							
Db	961	AATGCAGAGACCAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGG	1020							

QY	1021	CTGATCTGGTTGCTTCTTCGGTAGCCCTGGTAGACTCGTCTGGTCATATCTGGTCCCTG	1080							
Db	1021	CTGATCTGGTTGCTTCTTCGGTAGCCCTGGTAGACTCGTCTGGTCATATCTGGTCCCTG	1080							
QY	1081	GAATCTATGATGAAGTGGTTCTCTTACGAAGAGGAAATAAATACATACAAAGCCATCC	1140							
Db	1081	GAATCTATGATGAAGTGGTTCTCTTACGAAGAGGAAATAAATACATACAAAGCCATCC	1140							
QY	1141	ATCTAGACCTAGAAGAAATACCGGAATAGCAGCCGGGTTGAGAAAATTTCTGTCGATACTA	1200							
Db	1141	ATCTAGACCTAGAAGAAATACCGGAATAGCAGCCGGGTTGAGAAAATTTCTGTCGATACTA	1200							
QY	1201	AGGAGGAGATTCTAATGCACCTCTGGAGTACCCATCTCTTTCTATTTCATGGGATCGAGG	1260							
Db	1201	AGGAGGAGATTCTAATGCACCTCTGGAGTACCCATCTCTTTCTATTTCATGGGATCGAGG	1260							
QY	1261	GCGCGTTTGATGAGCCTGGAACTAAACACATCATACCTGGCCGAGTTATAGGAAAATTTT	1320							
Db	1261	GCGCGTTTGATGAGCCTGGAACTAAACACATCATACCTGGCCGAGTTATAGGAAAATTTT	1320							
QY	1321	CAATCCGCTAGTCCCTCACATGAATGTCTGCGGTGGAAAAACAGGTGACACGACATC	1380							
Db	1321	CAATCCGCTAGTCCCTCACATGAATGTCTGCGGTGGAAAAACAGGTGACACGACATC	1380							
QY	1381	TTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAAACAAGATGGTTGTTCCATGACTCTAG	1440							
Db	1381	TTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAAACAAGATGGTTGTTCCATGACTCTAG	1440							
QY	1441	GACTACACCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGA	1500							
Db	1441	GACTACACCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGA	1500							
QY	1501	TCAGAACAGTGTGTTGGAACAGAACCCAGATATGATCCGGGATGGATCCACCATTTCCAATTG	1560							
Db	1501	TCAGAACAGTGTGTTGGAACAGAACCCAGATATGATCCGGGATGGATCCACCATTTCCAATTG	1560							
QY	1561	CCAAAATGTTCCAGGAGATCGTCCACNAAGAGCGTGGTGCTAAATTCGCTGGGAGCTGTTG	1620							
Db	1561	CCAAAATGTTCCAGGAGATCGTCCACNAAGAGCGTGGTGCTAAATTCGCTGGGAGCTGTTG	1620							
QY	1621	ATGATGGAGAACATTTCGCAGAATGAGAAAATCAACAGGTGGAACATACATAGAGGGAACCA	1680							
Db	1621	ATGATGGAGAACATTTCGCAGAATGAGAAAATCAACAGGTGGAACATACATAGAGGGAACCA	1680							
QY	1681	AATTATTTGCTGCCCTTTTCTTAGAGATGGCCAGCTCCATTAAATCACAAAGAACCTTCTA	1740							
Db	1681	AATTATTTGCTGCCCTTTTCTTAGAGATGGCCAGCTCCATTAAATCACAAAGAACCTTCTA	1740							
QY	1741	GTCTGATCTGATCCACTGACAGATTCACTCCCTCCCCACATCCCTAGACAGGGATGGAATGT	1800							
Db	1741	GTCTGATCTGATCCACTGACAGATTCACTCCCTCCCCACATCCCTAGACAGGGATGGAATGT	1800							
QY	1801	AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCCTTCCATTTAAATGTCTTG	1860							
Db	1801	AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCCTTCCATTTAAATGTCTTG	1860							
QY	1861	GGATATCTGGATCAGTAATAAATAATTTCAAAGGCACAGATGTTGGAAATGGTTTAAGGT	1920							
Db	1861	GGATATCTGGATCAGTAATAAATAATTTCAAAGGCACAGATGTTGGAAATGGTTTAAGGT	1920							
QY	1921	CCCCACTGCACACCTTCCCTCAAGTCATAGCTGCTTGACGAACCTTGATTTCCCCAAGTC	1980							
Db	1921	CCCCACTGCACACCTTCCCTCAAGTCATAGCTGCTTGACGAACCTTGATTTCCCCAAGTC	1980							
QY	1981	CTGTGCAATAGCCCCCAGGATGGATTCTTCCAAACCTTTTAGCATATCTCCAACTTGCA	2040							
Db	1981	CTGTGCAATAGCCCCCAGGATGGATTCTTCCAAACCTTTTAGCATATCTCCAACTTGCA	2040							
QY	2041	ATTTGATTGGCATAATCACTCCGGTTTGCTTTCTAGGTCCTCAAGTCTCGTGACACATA	2100							
Db	2041	ATTTGATTGGCATAATCACTCCGGTTTGCTTTCTAGGTCCTCAAGTCTCGTGACACATA	2100							

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Db      2101 ATCATTCATCCAAATGATCGCCTTTGCTTTACCACCTCTTTCCCTTTTATCTTATTAATAAA 2160
QY      2161 AATGTTGGTCTCCACCACCTGNCCTCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2220
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QY      2221 AAAAAAAAAAAAAAAAAAAAAA 2242
Db      2221 AAAAAAAAAAAAAAAAAAAAAA 2242
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ID      AAD59237 standard; cDNA; 2242 BP.
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AC      AAD59237;
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DT      18-DEC-2003 (first entry)
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DE      Human PRO4380 cDNA.
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KW      Human; diagnosis; inflammation; nephropathy; bone disorder; arthritis;
KW      cartilage disorder; hypoinsulinaemia; hyperinsulinaemia; gene therapy;
KW      antisense therapy; diabetes; PRO; gene; ss.
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XX
FH      Key
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XX
PF      26-DEC-2001; 2001US-00036150.
XX
PR      15-MAY-1998; 98US-0085579P.
PR      15-DEC-1998; 98US-0112514P.
PR      22-DEC-1998; 98US-0113300P.
PR      23-DEC-1998; 98US-0113430P.
PR      23-DEC-1998; 98US-0113605P.
PR      23-DEC-1998; 98US-0113621P.
PR      23-DEC-1998; 98US-0114140P.
PR      12-JAN-1999; 99US-0115552P.
PR      22-JAN-1999; 99US-0116843P.
PR      23-MAR-1999; 99US-0125774P.
PR      23-MAR-1999; 99US-0125778P.
PR      24-MAR-1999; 99US-0125826P.
PR      31-MAR-1999; 99US-0127035P.
PR      05-APR-1999; 99US-0127706P.
PR      13-APR-1999; 99US-0129122P.
PR      21-APR-1999; 99US-0130359P.
PR      27-APR-1999; 99US-0131270P.
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PR      25-MAY-1999; 99US-0135750P.
PR      08-JUN-1999; 99US-0138166P.
PR      20-JUL-1999; 99US-0144791P.
PR      03-AUG-1999; 99US-0146970P.
PR      29-OCT-1999; 99US-0162506P.
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PR      02-DEC-1999; 99WO-US028551.
PR      22-DEC-1999; 99WO-US030720.
PR      01-MAR-2000; 2000WO-US005601.
PR      02-MAR-2000; 2000WO-US005841.
PR      22-MAY-2000; 2000WO-US014042.
PR      02-JUN-2000; 2000WO-US015264.
PR      23-AUG-2000; 2000WO-US023522.
PR      24-AUG-2000; 2000WO-US023328.
PR      01-DEC-2000; 2000WO-US032678.
PR      20-DEC-2000; 2000WO-US034956.
PR      28-FEB-2001; 2001WO-US006520.
PR      01-JUN-2001; 2001WO-US017800.
PR      20-JUN-2001; 2001WO-US019692.
PR      29-JUN-2001; 2001WO-US021066.
PR      09-JUL-2001; 2001WO-US021735.
PR      16-AUG-2001; 2001US-00931836.
XX
XX      (GETH ) GENENTECH INC.
XX
PA
XX
PI      Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI      Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
XX      WPI; 2003-585110/55.
DR      P-PSDB; AAE39046.
XX
PT      New isolated, secreted and transmembrane PRO polypeptides and nucleic
PT      acids, useful for diagnosing, preventing and/or treating inflammation,
PT      nephropathies, bone and cartilage disorders, and diabetes.
XX
PS      Claim 2; Fig 25; 195pp; English.
XX
CC      The present invention relates to novel polypeptides and nucleic acids
CC      encoding them. The methods and compositions of the present invention are
CC      useful for the diagnosis, prevention and/or treatment of inflammation,
CC      nephropathies, bone and cartilage disorders such as arthritis and
CC      disorders that affect glucose or free fatty acid (FFA) uptake such as
CC      diabetes, hypoinsulinaemia and hyperinsulinaemia. The PRO peptides are
CC      useful as molecular weight markers and for chromosome identification. The
CC      PRO genes may also be used in gene therapy and antisense therapy. The
CC      present sequence is human PRO CDNA
XX
SQ      Sequence 2242 BP; 606 A; 540 C; 536 G; 559 T; 0 U; 1 Other;
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Query Match      100.0%; Score 2241; DB 10; Length 2242;
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Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACGAGCC 60
Db      1 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACGAGCC 60
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Db      61 TCGTCTTCTTTCATGGGACTCCCTCTGCCACATTTTTCGAGGTTGGGAAAGTTGCTAGA 180
QY      121 CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTCGAGGTTGGGAAAGTTGCTAGA 180
Db      121 CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTCGAGGTTGGGAAAGTTGCTAGA 180
QY      181 GGCTTCAGAACTCCAGCCTTAATGGATCCCAAACCTCGGAGATGGCTCCCTGCTGG 240
Db      181 GGCTTCAGAACTCCAGCCTTAATGGATCCCAAACCTCGGAGATGGCTCCCTGCTGG 240
QY      241 CTGTGCTGCTGCTGCTGGAGCGCGGCATGTTCTCCTCACCTCCCGCCCCCGGCGC 300
Db      241 CTGTGCTGCTGCTGCTGGAGCGCGGCATGTTCTCCTCACCTCCCGCCCCCGGCGC 300
QY      301 TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCCATCAGGATGAATTTGTGCAGACGCTGA 360
Db      301 TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCCATCAGGATGAATTTGTGCAGACGCTGA 360
QY      361 AGGAGTGGTGGCCCATCGAGAGCGGACTCTGTCCAGCCTGTGCTCGCTTTCAGACAAGAGC 420
Db      361 AGGAGTGGTGGCCCATCGAGAGCGGACTCTGTCCAGCCTGTGCTCGCTTTCAGACAAGAGC 420
```


Db 361 AGGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCCTGTGCCTCGCTTCAGACAAAGAGC 420

QY 421 TCTTCAGAAATGATGGCCGTGGCTGCGGACACGCTGCAGCGCCTGGGGGCCGTGTGGCCT 480

Db 421 TCTTCAGAAATGATGGCCGTGGCTGCGGACACGCTGCAGCGCCTGGGGGCCGTGTGGCCT 480

QY 481 CGGTGGACATGGTCTCAGCAGCTGCCCGATGGTTCAGAGTCTTCCAATACCTCCCGTCA 540

Db 481 CGGTGGACATGGTCTCAGCAGCTGCCCGATGGTTCAGAGTCTTCCAATACCTCCCGTCA 540

QY 541 TCCTGGCCGAACCTGGGAGCGATCCCACGAAAGGCACCGTGTCTTACGGCCACTTGG 600

Db 541 TCCTGGCCGAACCTGGGAGCGATCCCACGAAAGGCACCGTGTCTTACGGCCACTTGG 600

QY 601 ACGTGCAGCCTGTGACCGGGCGATGGGTGGCTACGGACCCCTATGTGCTGACGGAGG 660

Db 601 ACGTGCAGCCTGTGACCGGGCGATGGGTGGCTACGGACCCCTATGTGCTGACGGAGG 660

QY 661 TAGACGGGAAACTTTATGGACGAGGAGCGACCGACAAACAAAGGCCCTGTCTTGGCTTGA 720

Db 661 TAGACGGGAAACTTTATGGACGAGGAGCGACCGACAAACAAAGGCCCTGTCTTGGCTTGA 720

QY 721 TCAATGCTGTAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATTCA 780

Db 721 TCAATGCTGTAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATTCA 780

QY 781 TCATTGAGGGATGGAAGAGGCTGGCTCTGTGCCCTGGAGGAACCTTGGAAAAAGAAA 840

Db 781 TCATTGAGGGATGGAAGAGGCTGGCTCTGTGCCCTGGAGGAACCTTGGAAAAAGAAA 840

QY 841 AGGACCGATTCTCTCTGGTGGACTACATTGTAATTTTCAGATAACCTGTGGATCAGCC 900

Db 841 AGGACCGATTCTCTCTGGTGGACTACATTGTAATTTTCAGATAACCTGTGGATCAGCC 900

QY 901 AAAGGAAGCCAGCAATCACTTATGGAAACCGGGGGAACAGCTACTTCATGGTGGAGTGA 960

Db 901 AAAGGAAGCCAGCAATCACTTATGGAAACCGGGGGAACAGCTACTTCATGGTGGAGTGA 960

QY 961 AATGCAGAGACAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGG 1020

Db 961 AATGCAGAGACAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGG 1020

QY 1021 CTGATCTGGTGTCTTCTCGGTAGCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1080

Db 1021 CTGATCTGGTGTCTTCTCGGTAGCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1080

QY 1081 GAATCTATGATGAAGTGGTTCCTCTTACAGAAGAGGAAATAAATACATACAAAGCCATCC 1140

Db 1081 GAATCTATGATGAAGTGGTTCCTCTTACAGAAGAGGAAATAAATACATACAAAGCCATCC 1140

QY 1141 ATCTAGACCTTAGAAGAATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTTGATACTA 1200

Db 1141 ATCTAGACCTTAGAAGAATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTTGATACTA 1200

QY 1201 AGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCTTTCTAATCATGGGATCGAGG 1260

Db 1201 AGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCTTTCTAATCATGGGATCGAGG 1260

QY 1261 GCGCGTTTGATGAGCCTGGAACTAAACAGTACATACCTGGCCGAGTTATAGGAAATTTT 1320

Db 1261 GCGCGTTTGATGAGCCTGGAACTAAACAGTACATACCTGGCCGAGTTATAGGAAATTTT 1320

QY 1321 CAATCCGCTAGTCCCTCACATGAATGTCTGCGGTGGAAAAACAGGTGACACGACATC 1380

Db 1321 CAATCCGCTAGTCCCTCACATGAATGTCTGCGGTGGAAAAACAGGTGACACGACATC 1380

QY 1381 TTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAAACAAGATGGTGTTCATGACTCTAG 1440

Db 1381 TTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAAACAAGATGGTGTTCATGACTCTAG 1440

QY 1441 GACTACACCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGAGCAAAAAGAGCGGA 1500

Db 1441 GACTACACCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGAGCAAAAAGAGCGGA 1500

QY 1501 TCAGAAACAGTGTTTGGAAACAGAACCCAGATATGATCCGGGATGGATCCACCATTCCAATTG 1560

Db 1501 TCAGAAACAGTGTTTGGAAACAGAACCCAGATATGATCCGGGATGGATCCACCATTCCAATTG 1560

QY 1561 CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTCTAATTCGCTGGGAGCTGTTG 1620

Db 1561 CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTCTAATTCGCTGGGAGCTGTTG 1620

QY 1621 ATGATGGAGAACATTTCGCAGAATGAGAAATCAACAGGTGGAACTACATAGAGGGAACCA 1680

Db 1621 ATGATGGAGAACATTTCGCAGAATGAGAAATCAACAGGTGGAACTACATAGAGGGAACCA 1680

QY 1681 AATTATTTGCTGCCTTTTCTTAGAGATGGCCAGCTCCATTAAATCACAAGAACCTTCTA 1740

Db 1681 AATTATTTGCTGCCTTTTCTTAGAGATGGCCAGCTCCATTAAATCACAAGAACCTTCTA 1740

QY 1741 GTCTGATCTGATCCACTGACAGATTCACTCCCCACATCCCCCTAGACAGGGATGGAATGT 1800

Db 1741 GTCTGATCTGATCCACTGACAGATTCACTCCCCACATCCCCCTAGACAGGGATGGAATGT 1800

QY 1801 AAATATCCAGAGAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTAAANAATGCTTG 1860

Db 1801 AAATATCCAGAGAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTAAANAATGCTTG 1860

QY 1861 GGATATCTGGATCAGTAATAAATATTTCAAAGGCACAGATGTTGGAAATGGTTAAAGGT 1920

Db 1861 GGATATCTGGATCAGTAATAAATATTTCAAAGGCACAGATGTTGGAAATGGTTAAAGGT 1920

QY 1921 CCCCCACTGCACACCTTCCCTCAAGTCATAGCTGCTTGCAACCTTTTAGCATATCTCCAACCTTGCA 2040

Db 1921 CCCCCACTGCACACCTTCCCTCAAGTCATAGCTGCTTGCAACCTTTTAGCATATCTCCAACCTTGCA 2040

QY 2041 ATTTGATTGGCATAATCACTCCGGTTGCTTTCTAGGTCCCTCAAGTGCCTGACACATA 2100

Db 2041 ATTTGATTGGCATAATCACTCCGGTTGCTTTCTAGGTCCCTCAAGTGCCTGACACATA 2100

QY 2101 ATCATTCATCCAATGATCGCTTTGCTTTTACCCTCTTTTATCTTATTAATAAAA 2160

Db 2101 ATCATTCATCCAATGATCGCTTTGCTTTTACCCTCTTTTATCTTATTAATAAAA 2160

QY 2161 AATGTTGGTCTCCACCCTGCTCCCAAAAAA 2242

Db 2161 AATGTTGGTCTCCACCCTGCTCCCAAAAAA 2242

QY 2221 AAAAAAAAAAAAAAAAAAAAAA 2242

Db 2221 AAAAAAAAAAAAAAAAAAAAAA 2242

RESULT 9

ADC29812

ID ADC29812 standard; cDNA; 2242 BP.

XX

AC ADC29812;

XX

DT 18-DEC-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO4380 cDNA.

XX

KW human; secreted and transmembrane protein; PRO; vulnerary; antiarthritic;

.KW antidiabetic; anorectic; antianaemic; dermatological; antiinflammatory;

KW antiallergic; immunosuppressive; gastrointestinal;

KW chondrocyte cell differentiation; glucose uptake stimulator;

KW pancreatic beta cell differentiation; mesangial cell proliferation;

KW tissue typing; chromosome identification; gene therapy;

KW chromosome mapping; gene mapping; sports injury; arthritis; diabetes;

KW obesity; hyper-insulinaemia; hypo-insulinaemia; thalassaemia;

KW Berger disease; Schonlein-Henoch purpura; celiac disease;

KW	dermatitis herpetiformis; Crohn's disease; gene; ss.		acids as given in the specification. (I) is useful for tissue typing, as	
	Homo sapiens.		molecular weight markers or as therapeutic agents. A polynucleotide (II)	
XX	OS		encoding (I) is useful for chromosome identification, gene therapy,	
XX	XX		tissue typing or as hybridisation probes in chromosome and gene mapping.	
PN	US2003092063-A1.		PRO1484, PRO1890, PRO1887, PRO4353, PRO4357, PRO4405, PRO5737 and PRO5990	
XX	15-MAY-2003.		is useful for treating sports injuries and arthritis. PRO1484, PRO1122,	
PD			PRO1889, PRO4357, PRO4380 and PRO4356 are useful for treating diabetes.	
XX	26-DEC-2001; 2001US-00036063.		CC PRO4334, PRO4425, PRO4424, PRO4430, PRO1890, PRO1785 and PRO4422 are	
PF	15-MAY-1998; 98US-0085579P.		useful for treating obesity, diabetes or hyper- or hypo-insulinaemia.	
XX	15-DEC-1998; 98US-0112514P.		CC PRO4352, PRO4354, PRO4408, PRO6030 and PRO4499 are useful for treating	
FR	22-DEC-1998; 98US-0113300P.		CC thalassaemia. PRO4380, PRO4408 and PRO4425 are useful for treating Berger	
FR	23-DEC-1998; 98US-0113430P.		CC disease, Schonlein-Henoch purpura, celiac disease, dermatitis	
FR	23-DEC-1998; 98US-0113605P.		CC herpetiformis or Crohn's disease. This sequence encodes a novel human	
FR	23-DEC-1998; 98US-0114140P.		CC secreted and transmembrane PRO polypeptide.	
FR	12-JAN-1999; 99US-0115552P.		XX	
FR	22-JAN-1999; 99US-0116843P.		SQ	
FR	23-MAR-1999; 99US-0125774P.		Sequence 2242 BP; 606 A; 540 C; 536 G; 559 T; 0 U; 1 Other;	
FR	23-MAR-1999; 99US-0125778P.		Query Match	
FR	24-MAR-1999; 99US-0125826P.		Best Local Similarity 100.0%; Score 2241; DB 10; Length 2242;	
FR	31-MAR-1999; 99US-0127035P.		Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
FR	05-APR-1999; 99US-0127706P.		QY 1 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC 60	
FR	13-APR-1999; 99US-0129122P.		DB 1 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC 60	
FR	21-APR-1999; 99US-0130359P.		QY 61 TCGTCTTCTCCGGGGGACAAACGTGGGTACGGGCACAGAGAGATATTTAATGTCACCCCT 120	
FR	27-APR-1999; 99US-0131270P.		DB 61 TCGTCTTCTCCGGGGGACAAACGTGGGTACGGGCACAGAGAGATATTTAATGTCACCCCT 120	
FR	27-APR-1999; 99US-0131272P.		QY 121 CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTGGAGGTTGGGAAAGTTGCTAGA 180	
FR	04-MAY-1999; 99US-0132371P.		DB 121 CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTGGAGGTTGGGAAAGTTGCTAGA 180	
FR	04-MAY-1999; 99US-0132379P.		QY 181 GGCTTCAGAACTCCAGCCTAATGGATCCAAACTCGGGAGAAATGGTGCCTCCCTGCTGG 240	
FR	04-MAY-1999; 99US-0132383P.		DB 181 GGCTTCAGAACTCCAGCCTAATGGATCCAAACTCGGGAGAAATGGTGCCTCCCTGCTGG 240	
FR	14-MAY-1999; 99WO-US010733.		QY 241 CTGTGCTGCTGCTGTGGAGCGGGCATGTTCTCCTCACCCCTCCCGCCCCCGGCGC 300	
FR	25-MAY-1999; 99US-0135750P.		DB 241 CTGTGCTGCTGCTGTGGAGCGGGCATGTTCTCCTCACCCCTCCCGCCCCCGGCGC 300	
FR	08-JUN-1999; 99US-0138166P.		QY 301 TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA 360	
FR	20-JUL-1999; 99US-0144791P.		DB 301 TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA 360	
FR	03-AUG-1999; 99US-0146970P.		QY 361 AGGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAAGAGC 420	
FR	29-OCT-1999; 99US-0162506P.		DB 361 AGGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAAGAGC 420	
FR	02-DEC-1999; 99WO-US028551.		QY 421 TCTTCAGAAATGATGGCCGTGGCTGCGGACACGCTGCAGCGCCTGGGGCCCCGTGTGGCCT 480	
FR	22-DEC-1999; 99WO-US030720.		DB 421 TCTTCAGAAATGATGGCCGTGGCTGCGGACACGCTGCAGCGCCTGGGGCCCCGTGTGGCCT 480	
FR	01-MAR-2000; 2000WO-US005601.		QY 481 CGGTGGACATGGGTCTCTCAGCAGCTGCCGATGGTTCAGAGTCTTCCAATACCTCCCGTCA 540	
FR	02-MAR-2000; 2000WO-US005841.		DB 481 CGGTGGACATGGGTCTCTCAGCAGCTGCCGATGGTTCAGAGTCTTCCAATACCTCCCGTCA 540	
FR	22-MAY-2000; 2000WO-US014042.		QY 541 TCCTGGCCGAACTGGGGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGG 600	
FR	02-JUN-2000; 2000WO-US015264.		DB 541 TCCTGGCCGAACTGGGGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGG 600	
FR	23-AUG-2000; 2000WO-US023522.		QY 601 ACGTGCAGCCTGTGACCCGGGGCGATGGGTGGTTCACGGACCCCTATGTGTGACGGAGG 660	
FR	24-AUG-2000; 2000WO-US023328.		DB 601 ACGTGCAGCCTGTGACCCGGGGCGATGGGTGGTTCACGGACCCCTATGTGTGACGGAGG 660	
FR	01-DEC-2000; 2000WO-US032678.		QY 661 TAGACGGGAAACTTTTATGGACGAGGAGCGACCGACAAACAAGSCCTGTCTTGGCTTGA 720	
FR	20-DEC-2000; 2000WO-US034956.		DB 661 TAGACGGGAAACTTTTATGGACGAGGAGCGACCGACAAACAAGSCCTGTCTTGGCTTGA 720	
FR	28-FEB-2001; 2001WO-US006520.		QY 721 TCAATGCTGTAGCGCCTTCAGAGCCCTTGAGCAAGATCTTCTGTGAATATCAAATTCA 780	
FR	01-JUN-2001; 2001WO-US017800.		DB 721 TCAATGCTGTAGCGCCTTCAGAGCCCTTGAGCAAGATCTTCTGTGAATATCAAATTCA 780	
FR	20-JUN-2001; 2001WO-US019692.			
FR	29-JUN-2001; 2001WO-US021066.			
FR	09-JUL-2001; 2001WO-US021735.			
FR	16-AUG-2001; 2001US-00931836.			
XX				
PA	(GETH) GENENTECH INC.			
XX	Deenoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;			
PI	Stewart TA, Watanabe CK, Wood WI, Zhang Z;			
PI				
XX	WPI; 2003-765478/72.			
DR	P-PSDB; ADC29813.			
DR				
XX				
PT	Novel isolated PRO polypeptide such as PRO1484, PRO4334, PRO1122,			
PT	PRO1889, PRO1890, PRO1887, PRO1785, useful for treating arthritis,			
PT	obesity, diabetes mellitus, thalassemia, Crohn's disease.			
XX				
PS	Claim 2; SEQ ID NO 56; 200pp; English.			
XX				
CC	The invention describes an isolated secreted and transmembrane PRO			
CC	polypeptide (I) having at least 80% amino acid sequence identity to fully			
CC	defined sequences of 246, 440, 197, 97, 273, 571, 209, 888, 502, 310,			
CC	251, 800, 507, 248, 223, 134, 136, 468, 322, 221, 194, 125 or 339 amino			

QY 781 TCATTGAGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACCTTGTGGA AAAAAGAAA 840
Db 781 TCATTGAGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACCTTGTGGA AAAAAGAAA 840
QY 841 AGGACCGATTCTTCTCTGGTGTGGACTACATTGTAATTTTCAGATAACCTGTGGATCAGCC 900
Db 841 AGGACCGATTCTTCTCTGGTGTGGACTACATTGTAATTTTCAGATAACCTGTGGATCAGCC 900
QY 901 AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGAACAGCTACTTTCATGTGGAGGTGA 960
Db 901 AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGAACAGCTACTTTCATGTGGAGGTGA 960
QY 961 AATGCAGAGACCAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGG 1020
Db 961 AATGCAGAGACCAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGG 1020
QY 1021 CTGATCTGGTTGCTCTTCTCGGTAGCCTGGTAGACTCGTCTGGTCATATCCTTGGTCCCTG 1080
Db 1021 CTGATCTGGTTGCTCTTCTCGGTAGCCTGGTAGACTCGTCTGGTCATATCCTTGGTCCCTG 1080
QY 1081 GAATCTATGATGAAGTGGTTCTCTTACAGAAGAGGAAATAAATACATACAAAGCCATCC 1140
Db 1081 GAATCTATGATGAAGTGGTTCTCTTACAGAAGAGGAAATAAATACATACAAAGCCATCC 1140
QY 1141 ATCTAGACCTAGAGAATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTTCGATACTA 1200
Db 1141 ATCTAGACCTAGAGAATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTTCGATACTA 1200
QY 1201 AGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCTTTCTATTCTATGGGATCGAGG 1260
Db 1201 AGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCTTTCTATTCTATGGGATCGAGG 1260
QY 1261 GCGCGTTTGATGAGCCTGGAACATAAACAGTCAATCCTGGCCGAGTTATAGGAAAATTTT 1320
Db 1261 GCGCGTTTGATGAGCCTGGAACATAAACAGTCAATCCTGGCCGAGTTATAGGAAAATTTT 1320
QY 1321 CAATCCGCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAACAGGTGACACGACATC 1380
Db 1321 CAATCCGCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAACAGGTGACACGACATC 1380
QY 1381 TTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAAAGATGGTTGTTCCATGACTCTAG 1440
Db 1381 TTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAAAGATGGTTGTTCCATGACTCTAG 1440
QY 1441 GACTACACCCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGA 1500
Db 1441 GACTACACCCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGA 1500
QY 1501 TCAGAACAGTGTGTTGGAACAGAACCCAGATATGATCGGGATGGATCCACCATTCCAATTG 1560
Db 1501 TCAGAACAGTGTGTTGGAACAGAACCCAGATATGATCGGGATGGATCCACCATTCCAATTG 1560
QY 1561 CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGCTAATTCGCGTGGGAGCTGTTG 1620
Db 1561 CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGCTAATTCGCGTGGGAGCTGTTG 1620
QY 1621 ATGATGGAGAACATTCCGAGAAATGAGAAAATCAACAGGTGGAACTACATAGAGGGAACCA 1680
Db 1621 ATGATGGAGAACATTCCGAGAAATGAGAAAATCAACAGGTGGAACTACATAGAGGGAACCA 1680
QY 1681 AATTATTGCTGCTCTTTTCTTAGAGATGGCCAGCTCCATTAATCACAAGAACCTTCTA 1740
Db 1681 AATTATTGCTGCTCTTTTCTTAGAGATGGCCAGCTCCATTAATCACAAGAACCTTCTA 1740
QY 1741 GTCTGATCTGATCCACTGACAGATTACCTCCCCACATCCCTAGACAGGGATGGAATGT 1800
Db 1741 GTCTGATCTGATCCACTGACAGATTACCTCCCCACATCCCTAGACAGGGATGGAATGT 1800
QY 1801 AAATATCCAGAGAATTTGGGTCTAGTATAGTACATTTCCCTTCCATTTAAATGTCTTG 1860
Db 1801 AAATATCCAGAGAATTTGGGTCTAGTATAGTACATTTCCCTTCCATTTAAATGTCTTG 1860
QY 1861 GGATATCTGGATCAGTAATAAAATATTTCAAAGGCACAGATGTTGGAAATGTTTAAGGT 1920

Db 1861 GGATATCTGGATCAGTAATAAAATATTTCAAAGGCACAGATGTTGGAATGGTTTAAGGT 1920
QY 1921 CCCCCACTGCACACCTTCCCTCAAGTCATAGCTGCTTGCAGCAACCTTGATTTCCCCAAGTC 1980
Db 1921 CCCCCACTGCACACCTTCCCTCAAGTCATAGCTGCTTGCAGCAACCTTGATTTCCCCAAGTC 1980
QY 1981 CTGTGCAATAGCCCCCAGGATTGGATTCCCTCCAAACCTTTTAGCATATCTCCAAACCTTGCA 2040
Db 1981 CTGTGCAATAGCCCCCAGGATTGGATTCCCTCCAAACCTTTTAGCATATCTCCAAACCTTGCA 2040
QY 2041 ATTTGATTGGCATAATCACTCCGGTTTGCTTTCTAGGTCCCTCAAGTGTCTCGTGACACATA 2100
Db 2041 ATTTGATTGGCATAATCACTCCGGTTTGCTTTCTAGGTCCCTCAAGTGTCTCGTGACACATA 2100
QY 2101 ATCATTCATCCAATGATCGCCTTTTGCTTTTACCACTCTTTTCTTTTATCTTATTAATAAAA 2160
Db 2101 ATCATTCATCCAATGATCGCCTTTTGCTTTTACCACTCTTTTCTTTTATCTTATTAATAAAA 2160
QY 2161 AATGTTGGTCTCCACCACTGNCCTCCAAAAA AAAAAAAAAAAAAAAAAAAAAA 2220
Db 2161 AATGTTGGTCTCCACCACTGNCCTCCAAAAA AAAAAAAAAAAAAAAAAAAAAA 2220
QY 2221 AAAAAAAAAAAAAAAAAAAAAA 2242
Db 2221 AAAAAAAAAAAAAAAAAAAAAA 2242
RESULT 10
ACA06168
ID ACA06168 standard; cdNA; 2242 BP.
XX ACA06168;
AC ACA06168;
XX 02-JUN-2003 (first entry)
XX cDNA encoding human PRO polypeptide #13.
DE Human; secreted and transmembrane protein; bone disorder; obesity;
XX cartilage disorder; sports injury; arthritis; diabetes mellitus;
KW hypo-insulinaemia; obesity; hyper-insulinaemia; thalassaemia;
KW haemoglobin-associated disorder; kidney disorder; Berger disease;
KW mesangial cell function; nephropathy; Schonlein-Henoch purpura;
KW celiac disease; dermatitis herpetiformis; Crohn's disease; anorectic;
KW antiarthritic; antidiabetic; antianaemic; nephrotropic; antiinflammatory;
KW gene therapy; gene; ss.
XX Homo sapiens.
OS US2003032061-A1.
PN 13-FEB-2003.
XX 26-DEC-2001; 2001US-00036214.
PF 15-MAY-1998; 98US-0085579P.
XX 15-DEC-1998; 98US-0112514P.
PR 22-DEC-1998; 98US-0113300P.
PR 23-DEC-1998; 98US-0113430P.
PR 23-DEC-1998; 98US-0113605P.
PR 23-DEC-1998; 98US-0113621P.
PR 23-DEC-1998; 98US-0114140P.
PR 12-JAN-1999; 99US-0115552P.
PR 22-JAN-1999; 99US-0116843P.
PR 23-MAR-1999; 99US-0125774P.
PR 23-MAR-1999; 99US-0125778P.
PR 24-MAR-1999; 99US-0125826P.
PR 31-MAR-1999; 99US-0127035P.
PR 05-APR-1999; 99US-0127706P.
PR 13-APR-1999; 99US-0129122P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.

PR 27-APR-1999; 99US-0131291P.
PR 04-MAY-1999; 99US-0132371P.
PR 04-MAY-1999; 99US-0132379P.
PR 04-MAY-1999; 99US-0132383P.
PR 14-MAY-1999; 99WO-US010733.
PR 25-MAY-1999; 99US-0135750P.
PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99WO-US028551.
PR 22-DEC-1999; 99WO-US030720.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 16-AUG-2001; 2001US-00931836.
XX
PA (GETH) GENENTECH INC.
XX
PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-341962/32.
DR P-PSDB; ABU69115.
XX
PT Novel isolated PRO polypeptides e.g., PRO4334, PRO1122, PRO1889, PRO1890,
PT PRO1887, PRO1785, PRO4353, useful for treating sports injuries,
PT arthritis, diabetes, obesity, hyper- or hypo-insulinemia.
XX
PS Claim 2; Fig 25; 194pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful in diagnosing or treating
CC various bone and/or cartilage disorders (e.g. sports injuries,
CC arthritis), various insulin deficient states (e.g. diabetes mellitus,
CC hypo-insulinaemia), obesity, hyper-insulinaemia, haemoglobin-associated
CC disorders (e.g. thalassaemias), kidney disorders associated with
CC decreased mesangial cell function (e.g. Berger disease), or other
CC nephropathies associated with Schonlein-Henoch purpura, celiac disease,
CC dermatitis herpetiformis or Crohn's disease. The PRO polynucleotide
CC sequences may be used as hybridisation probes in chromosome and gene
CC mapping, or in generating antisense RNA and DNA. They are also useful in
CC preparing PRO polypeptides, in assays to identify other proteins or
CC molecules involved in binding reaction, to generate transgenic animals or
CC knockout animals, which in turn are useful in the development and
CC screening of therapeutically useful reagents, for chromosome
CC identification, and tissue typing. The PRO polypeptides and nucleic acid
CC molecules are also useful in gene therapy, and as molecular weight
CC markers for protein electrophoresis purposes. Anti-PRO antibodies may be
CC used in diagnostic assays for PRO polypeptides, or for the affinity
CC purification of the polypeptides from recombinant cell culture or natural
CC sources. The present sequence represents a cDNA encoding a human PRO
CC polypeptide of the invention
XX
SQ Sequence 2242 BP; 606 A; 540 C; 536 G; 559 T; 0 U; 1 Other;

Query Match 100.0%; Score 2241; DB 10; Length 2242;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAATGAATACTCCGAAGCCGCTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC 60

QY

Db 1 GAATGAATACTCCGAAGCCGCTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC 60
QY 61 TCGTCTTCCCTCCGGGGACAAACGTGGTCAAGGACAGAGATATTAATGTCAACCT 120
Db 61 TCGTCTTCCCTCCGGGGACAAACGTGGTCAAGGACAGAGATATTAATGTCAACCT 120
QY 121 CTTGGGCTTTCATGGGACTCCCTCTGCCACATTTTGGAGTTGGAAAGTTGCTAGA 180
Db 121 CTTGGGCTTTCATGGGACTCCCTCTGCCACATTTTGGAGTTGGAAAGTTGCTAGA 180
QY 181 GGCTTCAGAACTCCAGCCTAATGGATCCAAACTCGGAGAAATGGCTGCCCTCCCTGCTGG 240
Db 181 GGCTTCAGAACTCCAGCCTAATGGATCCAAACTCGGAGAAATGGCTGCCCTCCCTGCTGG 240
QY 241 CTGTGCTGCTGCTGTGGAGCGCGGCATGTTCTCCTCACCTCCCGCCCCCGGCGC 300
Db 241 CTGTGCTGCTGCTGTGGAGCGCGGCATGTTCTCCTCACCTCCCGCCCCCGGCGC 300
QY 301 TGTTAGAGAAAGTCTTCAGTACATTGACCTCCATCAGGATGAATTTGTGACAGCGCTGA 360
Db 301 TGTTAGAGAAAGTCTTCAGTACATTGACCTCCATCAGGATGAATTTGTGACAGCGCTGA 360
QY 361 AGGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCCCTCGCTTCAGACAAGAGC 420
Db 361 AGGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCCCTCGCTTCAGACAAGAGC 420
QY 421 TCTTCAGAAATGATGGCCGTGGCTGCGGACACGCTGCAGCGCTGGGGGCCCCGTGTGGCCT 480
Db 421 TCTTCAGAAATGATGGCCGTGGCTGCGGACACGCTGCAGCGCTGGGGGCCCCGTGTGGCCT 480
QY 481 CGGTGGACATGGGTCTTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCA 540
Db 481 CGGTGGACATGGGTCTTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCA 540
QY 541 TCTGGCCGAACCTGGGAGCGATCCACGAAAGGACCGTGTGCTTCTACGGCCACTTGG 600
Db 541 TCTGGCCGAACCTGGGAGCGATCCACGAAAGGACCGTGTGCTTCTACGGCCACTTGG 600
QY 601 ACCTGCAGCCTGCTGACCGGGCGATGGGTGGCTCAGGACCCCTATGTGTGACGGAGG 660
Db 601 ACCTGCAGCCTGCTGACCGGGCGATGGGTGGCTCAGGACCCCTATGTGTGACGGAGG 660
QY 661 TAGACGGGAAACTTTATGACGAGGAGCGACCGACACAAAGGCCCTGTCTTGGCTTGA 720
Db 661 TAGACGGGAAACTTTATGACGAGGAGCGACCGACACAAAGGCCCTGTCTTGGCTTGA 720
QY 721 TCAATGCTGTAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATCA 780
Db 721 TCAATGCTGTAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATCA 780
QY 781 TCATTGAGGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACTTGTGAAAAAGAAA 840
Db 781 TCATTGAGGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACTTGTGAAAAAGAAA 840
QY 841 AGGACCGATTCTTCTCTGGTGTGACTACATTGTAATTCAGATAACCTGTGGATCAGCC 900
Db 841 AGGACCGATTCTTCTCTGGTGTGACTACATTGTAATTCAGATAACCTGTGGATCAGCC 900
QY 901 AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGGAACAGCTACTTCATGGTGGAGTGA 960
Db 901 AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGGAACAGCTACTTCATGGTGGAGTGA 960
QY 961 AATGCAGAGACCAGGATTTTCACTCAGGAACCTTGGTGGCATCCTTCATGAACCAATGG 1020
Db 961 AATGCAGAGACCAGGATTTTCACTCAGGAACCTTGGTGGCATCCTTCATGAACCAATGG 1020
QY 1021 CTGATCTGGTGTCTTCTCGGTAGCCTGGTAGACTCGTGTGTCATATCCTGGTCCCTG 1080
Db 1021 CTGATCTGGTGTCTTCTCGGTAGCCTGGTAGACTCGTGTGTCATATCCTGGTCCCTG 1080
QY 1081 GAATCTATGATGAAGTGGTTCCTCTTACAGAAGAGGAAATTAATACATACAAAGCCATCC 1140

Db 1081 GAATCTATGATGAAGTGGTTCCCTCTTACAGAAAGAGGAAATAAAATACATACAAAGCCATCC 1140

QY 1141 ATCTAGACCTAGAAGATACCGGAATAGCAGCGGTTGAGAAATTTCTGTTGATACTA 1200

Db 1141 ATCTAGACCTAGAAGATACCGGAATAGCAGCGGTTGAGAAATTTCTGTTGATACTA 1200

QY 1201 AGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCTTTCTATTCTATTCATGGATCGAGG 1260

Db 1201 AGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCTTTCTATTCTATTCATGGATCGAGG 1260

QY 1261 GCGCGTTTGATGAGCCTTGGAACTAAACAGTCTATCTGCGCCGAGTTATAGGAAATTTT 1320

Db 1261 GCGCGTTTGATGAGCCTTGGAACTAAACAGTCTATCTGCGCCGAGTTATAGGAAATTTT 1320

QY 1321 CAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAACAGGTGACACGACATC 1380

Db 1321 CAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAACAGGTGACACGACATC 1380

QY 1381 TTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAAACAAGATGGTTGTTTCCATGACTCTAG 1440

Db 1381 TTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAAACAAGATGGTTGTTTCCATGACTCTAG 1440

QY 1441 GACTACACCCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGA 1500

Db 1441 GACTACACCCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGA 1500

QY 1501 TCAGAACAGTGTGTTGGAACAGAACCCAGATATGATCCGGGATGGATCCACCATTCCAATTG 1560

Db 1501 TCAGAACAGTGTGTTGGAACAGAACCCAGATATGATCCGGGATGGATCCACCATTCCAATTG 1560

QY 1561 CCAAAATGTTCCAGGAGATCGTCCCAAGAGCGTGGTGCTAATTCGCGTGGGAGCTGTTG 1620

Db 1561 CCAAAATGTTCCAGGAGATCGTCCCAAGAGCGTGGTGCTAATTCGCGTGGGAGCTGTTG 1620

QY 1621 ATGATGGAGAACATTCGCAGAAATGAGAAAAATCAACAGGTGGAACTACATAGAGGGAACCA 1680

Db 1621 ATGATGGAGAACATTCGCAGAAATGAGAAAAATCAACAGGTGGAACTACATAGAGGGAACCA 1680

QY 1681 AATTATTGCTGCTGCTTTTCTTAGAGATGGCCAGCTCCATTAATCACAAGAACCTTCTA 1740

Db 1681 AATTATTGCTGCTGCTTTTCTTAGAGATGGCCAGCTCCATTAATCACAAGAACCTTCTA 1740

QY 1741 GTCTGATCTGATCCACTGACAGATTACCTCCCCACATCCCTAGACAGGATGGAATGT 1800

Db 1741 GTCTGATCTGATCCACTGACAGATTACCTCCCCACATCCCTAGACAGGATGGAATGT 1800

QY 1801 AAATATCCAGAGAATTTGGGTCTAGTATAGTACATTTCCCTTCCATTTAAATGTCTTG 1860

Db 1801 AAATATCCAGAGAATTTGGGTCTAGTATAGTACATTTCCCTTCCATTTAAATGTCTTG 1860

QY 1861 GGATATCTGGATCAGTAATAAAATATTTCAAAGGCACAGATGTTGGAATGTTTAAGGT 1920

Db 1861 GGATATCTGGATCAGTAATAAAATATTTCAAAGGCACAGATGTTGGAATGTTTAAGGT 1920

QY 1921 CCCCACCTGCACACCTTCTCAAGTCAATAGCTGTTGCAGCAACTTGATTTCCCAAGTC 1980

Db 1921 CCCCACCTGCACACCTTCTCAAGTCAATAGCTGTTGCAGCAACTTGATTTCCCAAGTC 1980

QY 1981 CTGTGCAATAGCCCCAGGATGGATTCCCTTCCAACTTTTAGCATATCTCCAACCTTGCA 2040

Db 1981 CTGTGCAATAGCCCCAGGATGGATTCCCTTCCAACTTTTAGCATATCTCCAACCTTGCA 2040

QY 2041 ATTATTGATGGCATAATCACTCCGGTTTGCTTTCTAGGTCTCAAGTGCTCGTGACACATA 2100

Db 2041 ATTATTGATGGCATAATCACTCCGGTTTGCTTTCTAGGTCTCAAGTGCTCGTGACACATA 2100

QY 2101 ATCATTTCCATCCAATGATCGCCTTTTGCTTTTACCCTTTTCCCTTTTATCTTATTATAAAA 2160

Db 2101 ATCATTTCCATCCAATGATCGCCTTTTGCTTTTACCCTTTTCCCTTTTATCTTATTATAAAA 2160

QY 2161 AATGTTGGTCTCCACCCTGCTCCCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2220

Db 2161 AATGTTGGTCTCCACCCTGCTCCCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2220

QY 2221 AAAAAAAAAAAAAAAAAAAAAA 2242

Db 2221 AAAAAAAAAAAAAAAAAAAAAA 2242

RESULT 11

ADF09255

ID ADF09255 standard; cDNA; 2242 BP.

XX

AC ADF09255;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human secreted and transmembrane protein PRO4380 cDNA.

XX

KW cytostatic; gene therapy; human; secreted and transmembrane; PRO; cancer;

XX

KW tumour; chromosome mapping; gene mapping; therapeutic reagent; gene; ss.

OS Homo sapiens.

XX

PN US2003134327-A1.

PD 17-JUL-2003.

XX

PF 26-DEC-2001; 2001US-00035977.

XX

PR 15-MAY-1998; 98US-0085579P.

PR 15-DEC-1998; 98US-0112514P.

PR 22-DEC-1998; 98US-0113300P.

PR 23-DEC-1998; 98US-0113430P.

PR 23-DEC-1998; 98US-0113605P.

PR 23-DEC-1998; 98US-0113621P.

PR 23-DEC-1998; 98US-0114140P.

PR 12-JAN-1999; 99US-0115552P.

PR 22-JAN-1999; 99US-0116843P.

PR 23-MAR-1999; 99US-0125774P.

PR 23-MAR-1999; 99US-0125778P.

PR 24-MAR-1999; 99US-0125826P.

PR 31-MAR-1999; 99US-0127035P.

PR 05-APR-1999; 99US-0127706P.

PR 13-APR-1999; 99US-0129122P.

PR 21-APR-1999; 99US-0130359P.

PR 27-APR-1999; 99US-0131270P.

PR 27-APR-1999; 99US-0131272P.

PR 27-APR-1999; 99US-0131291P.

PR 04-MAY-1999; 99US-0132371P.

PR 04-MAY-1999; 99US-0132379P.

PR 04-MAY-1999; 99US-0132383P.

PR 14-MAY-1999; 99WO-US010733.

PR 25-MAY-1999; 99US-0135750P.

PR 08-JUN-1999; 99US-0138166P.

PR 20-JUL-1999; 99US-0144791P.

PR 03-AUG-1999; 99US-0146970P.

PR 29-OCT-1999; 99US-0162506P.

PR 02-DEC-1999; 99WO-US028551.

PR 22-DEC-1999; 99WO-US030720.

PR 01-MAR-2000; 2000WO-US005601.

PR 02-MAR-2000; 2000WO-US005841.

PR 22-MAY-2000; 2000WO-US014042.

PR 02-JUN-2000; 2000WO-US015264.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-JUN-2001; 2001WO-US017800.

PR 20-JUN-2001; 2001WO-US019692.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.

PR 16-AUG-2001; 2001US-00931836.

XX

PA (GETH) GENENTECH INC.

XX Desnoyers L, Baton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2004-031325/03.
DR P-PSDB; ADF09256.
XX Twenty three nucleic acids encoding PRO polypeptides, useful in
PT chromosome and gene mapping, in generating antisense RNA and DNA and in
PT gene therapy.
XX Claim 2; SEQ ID NO 56; 261pp; English.
XX The invention describes 23 nucleic acids encoding human secreted and
CC transmembrane PRO polypeptides. The PRO polypeptides and nucleic acids
CC are useful for the therapeutic treatment of cancerous tumours. The PRO
CC polynucleotide is useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA, and in gene therapy. The polynucleotide may also
CC be used in preparing PRO polypeptides by recombinant techniques, and in
CC generating either transgenic animals or knock-out animals which, in turn,
CC are useful in the development and screening of therapeutically useful
CC reagents. This sequence encodes novel human secreted and transmembrane
CC protein PRO1484.
XX
SQ Sequence 2242 BP; 606 A; 540 C; 536 G; 559 T; 0 U; 1 Other;
Query Match 100.0%; Score 2241; DB 12; Length 2242;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCC 60
DB 1 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCC 60
QY 61 TCGTCTTCCCTCCGGGGACAACGTTGGGTACGGGCACAGAGAGATATTAATGTCAACCCT 120
DB 61 TCGTCTTCCCTCCGGGGACAACGTTGGGTACGGGCACAGAGAGATATTAATGTCAACCCT 120
QY 121 CTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTGTGGAGTTGGGAAAGTTGCTAGA 180
DB 121 CTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTGTGGAGTTGGGAAAGTTGCTAGA 180
QY 181 GGCTTCAGAACTCCAGCCTAATGGATCCCAAACCTCGGAGAAATGGCTGCTCCCTGCTGG 240
DB 181 GGCTTCAGAACTCCAGCCTAATGGATCCCAAACCTCGGAGAAATGGCTGCTCCCTGCTGG 240
QY 241 CTGTGCTGCTGCTGTGGAGCGCGGCATGTTCTCCTCACCCCTCCCGCCCCCGGCGC 300
DB 241 CTGTGCTGCTGCTGTGGAGCGCGGCATGTTCTCCTCACCCCTCCCGCCCCCGGCGC 300
QY 301 TGTAGAGAAAGTCTTCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA 360
DB 301 TGTAGAGAAAGTCTTCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA 360
QY 361 AGGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAAGAGC 420
DB 361 AGGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAAGAGC 420
QY 421 TCTTCAGAAATGATGGCGTGGCTCGGACACGCTGCAGCGCCTGGGGCCCCGTGGCCCT 480
DB 421 TCTTCAGAAATGATGGCGTGGCTCGGACACGCTGCAGCGCCTGGGGCCCCGTGGCCCT 480
QY 481 CGGTGGACATGGGTCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCA 540
DB 481 CGGTGGACATGGGTCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCA 540
QY 541 TCCTGGCCGAACCTGGGGAGCGATCCACGAAAGCCACCGTGTGCTTCTACGGCCACTTGG 600
DB 541 TCCTGGCCGAACCTGGGGAGCGATCCACGAAAGCCACCGTGTGCTTCTACGGCCACTTGG 600
QY 601 ACGTGCAGCCTGCTGACCGGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGG 660
DB 601 ACGTGCAGCCTGCTGACCGGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGG 660

DB 601 ACGTGCAGCCTGCTGACCGGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGG 660
QY 661 TAGACGGGAAACTTTATGGACGAGGAGCGACCCGACAAACAAAGGCCCTGTCTTGGCTTGA 720
DB 661 TAGACGGGAAACTTTATGGACGAGGAGCGACCCGACAAACAAAGGCCCTGTCTTGGCTTGA 720
QY 721 TCAATGCTGTAGCGCCTTCAGAGCCCTTGAGCAAGATCTTCTCTGTGAATATCAAAATTCA 780
DB 721 TCAATGCTGTAGCGCCTTCAGAGCCCTTGAGCAAGATCTTCTCTGTGAATATCAAAATTCA 780
QY 781 TCATTGAGGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACCTTGGAAGAAAGAA 840
DB 781 TCATTGAGGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACCTTGGAAGAAAGAA 840
QY 841 AGGACCGATTCTTCTCTGGTGTGGACTACATTGTAATTTTCAGATAACCTTGGATCAGCC 900
DB 841 AGGACCGATTCTTCTCTGGTGTGGACTACATTGTAATTTTCAGATAACCTTGGATCAGCC 900
QY 901 AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGAAACAGTACTTTCATGGTGGAGGTGA 960
DB 901 AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGAAACAGTACTTTCATGGTGGAGGTGA 960
QY 961 AATGCAGAGACCAGGATTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGG 1020
DB 961 AATGCAGAGACCAGGATTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGG 1020
QY 1021 CTGATCTGTTGCTCTCTCGGTAGCCTGTAGACTCGTCTGGTCATATCCTGGTCCCTG 1080
DB 1021 CTGATCTGTTGCTCTCTCGGTAGCCTGTAGACTCGTCTGGTCATATCCTGGTCCCTG 1080
QY 1081 GAATCTATGATGAAGTGGTTCCTTACAGAAAGAGGAAATAAATACATACAAAGCCATCC 1140
DB 1081 GAATCTATGATGAAGTGGTTCCTTACAGAAAGAGGAAATAAATACATACAAAGCCATCC 1140
QY 1141 ATCTAGACCTAGAAGATACCGGAATAGCAGCCGGTTGAGAAATTTCTGTTCGATACTA 1200
DB 1141 ATCTAGACCTAGAAGATACCGGAATAGCAGCCGGTTGAGAAATTTCTGTTCGATACTA 1200
QY 1201 AGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCTTCTATTTCATGGGATCGAGG 1260
DB 1201 AGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCTTCTATTTCATGGGATCGAGG 1260
QY 1261 GCGCTTTGATGAGCCTGGAACATAAAACAGTCAATACCTGGCCGAGTTATAGGAAAATTTT 1320
DB 1261 GCGCTTTGATGAGCCTGGAACATAAAACAGTCAATACCTGGCCGAGTTATAGGAAAATTTT 1320
QY 1321 CAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAACAGGTGACACGACATC 1380
DB 1321 CAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAACAGGTGACACGACATC 1380
QY 1381 TTGAAGATGTGTTCTCCAAAAGAAAAATAGTTCCAAACAAGATGGTTGTTTCCATGACTCTAG 1440
DB 1381 TTGAAGATGTGTTCTCCAAAAGAAAAATAGTTCCAAACAAGATGGTTGTTTCCATGACTCTAG 1440
QY 1441 GACTACACCCGTGGATTGCAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGA 1500
DB 1441 GACTACACCCGTGGATTGCAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGA 1500
QY 1501 TCAGAACAGTGTGTTGGAAACAGAACCATATGATCCGGGATGGATCCACCATTCCCAATTG 1560
DB 1501 TCAGAACAGTGTGTTGGAAACAGAACCATATGATCCGGGATGGATCCACCATTCCCAATTG 1560
QY 1561 CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGTCTAATTCGCTGGGAGCTGTTG 1620
DB 1561 CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGTCTAATTCGCTGGGAGCTGTTG 1620
QY 1621 ATGATGGAAACATTCCGAGAATGAGAAAAATCAACAGGTGGAACTACATAGAGGGAACCA 1680
DB 1621 ATGATGGAAACATTCCGAGAATGAGAAAAATCAACAGGTGGAACTACATAGAGGGAACCA 1680
QY 1681 AATTATTTGCTGCTCTTTTCTTAGAGATGGCCCGAGCTCCATTAAATCAAGAACCTTCTA 1740
DB 1681 AATTATTTGCTGCTCTTTTCTTAGAGATGGCCCGAGCTCCATTAAATCAAGAACCTTCTA 1740

QY 1741 GTCTGATCTGATCCACTGACAGATTTCACCTCCCCCAGCATCCCTAGACAGGGATGGAATGT 1800
Db 1741 GTCTGATCTGATCCACTGACAGATTTCACCTCCCCCAGCATCCCTAGACAGGGATGGAATGT 1800
QY 1801 AAATATCCAGAGAATTTGGGTCTAGTATAGTACATTTCCCTTCCATTTAAATGTCTTG 1860
Db 1801 AAATATCCAGAGAATTTGGGTCTAGTATAGTACATTTCCCTTCCATTTAAATGTCTTG 1860
QY 1861 GGATATCTGGATCAGTAATAAATATTTCAAAGGACAGATGTTGGAATGTTTAAGGT 1920
Db 1861 GGATATCTGGATCAGTAATAAATATTTCAAAGGACAGATGTTGGAATGTTTAAGGT 1920
QY 1921 CCCCCACTGCACACCTTCTCAAGTCATAGCTGCTTGCAGCAACTTGATTTCCCCCAAGTC 1980
Db 1921 CCCCCACTGCACACCTTCTCAAGTCATAGCTGCTTGCAGCAACTTGATTTCCCCCAAGTC 1980
QY 1981 CTGTGCAATAGCCCCAGGATTGGATTCCTTCCAACCTTTTAGCATATCTCCAACCTTGCA 2040
Db 1981 CTGTGCAATAGCCCCAGGATTGGATTCCTTCCAACCTTTTAGCATATCTCCAACCTTGCA 2040
QY 2041 ATTTGATTGGCATAATCACTCCGGTTTGCTTTCTAGGTCCCTCAAGTCTCGTGACACATA 2100
Db 2041 ATTTGATTGGCATAATCACTCCGGTTTGCTTTCTAGGTCCCTCAAGTCTCGTGACACATA 2100
QY 2101 ATCATTTCCATCCAATGATCGCCTTTTGCTTTTACCACCTTTTCCCTTTTATCTTATTAATAA 2160
Db 2101 ATCATTTCCATCCAATGATCGCCTTTTGCTTTTACCACCTTTTCCCTTTTATCTTATTAATAA 2160
QY 2161 AATGTTGGTCTCCACCAGTGNCTCCAAAAAIAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2220
Db 2161 AATGTTGGTCTCCACCAGTGNCTCCAAAAAIAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2220
QY 2221 AAAAAAAAAAAAAAAAAAAAAA 2242
Db 2221 AAAAAAAAAAAAAAAAAAAAAA 2242

RESULT 12
ABLS8476
ID ABL58476 standard; cDNA; 2784 BP.
XX AC ABL58476;
XX DT 30-JUL-2002 (first entry)
XX DE Human metalloprotease, 55054 cDNA sequence.
XX KW 55054; human; metalloprotease; neural cell; cerebral injury; vulnerary;
XX OS Homo sapiens.
XX FT Key Location/Qualifiers
XX CDS 602..2125
XX FT /*tag= a
XX FT /product= "metalloprotease 55054"
XX FT /note= "the coding sequence (ABL58477) is specifically
XX FT claimed"
PN WO200226948-A2.
XX PD 04-APR-2002.
XX PF 25-SEP-2001; 2001WO-US030016.
XX PR 25-SEP-2000; 2000US-0235055P.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Kapeller-Libermann R;
XX WPI; 2002-405051/43.
DR

DR P-PSDB; ABB07950.
XX Identifying modulator of neural cell growth or transition metal
PT neurotoxicity, involves contacting test compound with novel human
PT metalloprotease polypeptide and determining if the polypeptide binds the
PT test compound.
XX Claim 6; Fig 1A-D; 105pp; English.
PS The invention provides a method for identifying a modulator of neural
XX cell growth, cerebral injury or wound healing, transition metal
CC neurotoxicity, histamine production, neural/hepatic cell proliferation or
CC degradation of extracellular matrix, neurotransmitter or soluble
CC intracellular/extracellular dipeptide. The method involves contacting a
CC test compound and metalloprotease polypeptide, selected from a human
CC metalloprotease polypeptide, termed 55054, and determining if 55054 binds
CC the test compound. The metalloprotease, 55054 is useful for making a
CC pharmaceutical composition for inhibiting the ability of a cell selected
CC from a neural cell such as glial cell or neuron (a sensory neuron or
CC olfactory sensory neuron), astrocyte, oligodendrocyte and ensheathing
CC cell, to cleave a polypeptide. The present sequence represents a cDNA
CC encoding the human metalloprotease, 55054
XX
SQ Sequence 2784 BP; 682 A; 680 C; 666 G; 726 T; 0 U; 30 Other;

Query Match 97.4%; Score 2182.8; DB 6; Length 2784;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2184; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCC 60
Db 402 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCC 461
QY 61 TCGTCTTCTTCCGGGGGACAACTGGGTGAGGACAGAGAGATATTTAATGTACCCCT 120
Db 462 TCGTCTTCTTCCGGGGGACAACTGGGTGAGGACAGAGAGATATTTAATGTACCCCT 521
QY 121 CTTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTTGGGAAAGTTGCTAGA 180
Db 522 CTTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTTGGGAAAGTTGCTAGA 581
QY 181 GGCTTCAGAACTCCAGCCTAATGGATCCAAACTCGGGAGAAATGGCTGCTCCCTGCTGG 240
Db 582 GGCTTCAGAACTCCAGCCTAATGGATCCAAACTCGGGAGAAATGGCTGCTCCCTGCTGG 641
QY 241 CTGTGCTGCTGCTGCTGGAGCGGCGATGTTCTCCTACCCCTCCCGCCCCCGGCGC 300
Db 642 CTGTGCTGCTGCTGCTGGAGCGGCGATGTTCTCCTACCCCTCCCGCCCCCGGCGC 701
QY 301 TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGAGACGCTGA 360
Db 702 TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGAGACGCTGA 761
QY 361 AGGAGTGGGTGGCCCATCGAGAGCGACTCTGTCCAGCCTGTGCTTTCAGACAAGAGC 420
Db 762 AGGAGTGGGTGGCCCATCGAGAGCGACTCTGTCCAGCCTGTGCTTTCAGACAAGAGC 821
QY 421 TCTTCAGAAATGATGGCCGTGGCTGCGGACACGCTGCAGCGCCTGGGGGCCCCGTGTGGCCT 480
Db 822 TCTTCAGAAATGATGGCCGTGGCTGCGGACACGCTGCAGCGCCTGGGGGCCCCGTGTGGCCT 881
QY 481 CGGTGGACATGGGTCTCAGCAGCTGCCGATGGTTCAGAGTCTTCCAAATACCTCCCGTCA 540
Db 882 CGGTGGACATGGGTCTCAGCAGCTGCCGATGGTTCAGAGTCTTCCAAATACCTCCCGTCA 941
QY 541 TCCTGGCCGAAGTGGGAGCGATCCACGAAAGGACCCGTGTGCTTCTACGGCCACTTGG 600
Db 942 TCCTGGCCGAAGTGGGAGCGATCCACGAAAGGACCCGTGTGCTTCTACGGCCACTTGG 1001
QY 601 ACGTGCAGCCTGCTGACCCGGGGCGATGGGTGGCTCA CGGACCCCTATGTGCTGACGGAGG 660
Db 1002 ACGTGCAGCCTGCTGACCCGGGGCGATGGGTGGCTCA CGGACCCCTATGTGCTGACGGAGG 1061

QY 661 TAGACGGGAAACTTTATGGACGAGGCGGACCGACAACAAAGGCCCTGTCTTGGCTTGA 720
Db 1062 TAGACGGGAAACTTTATGGACGAGGCGGACCGACAACAAAGGCCCTGTCTTGGCTTGA 1121
QY 721 TCAATGCTGTAGCGCCTTCAGAGCCCTTGAGCAAGATCTCCTGTGAATATCAAAATCA 780
Db 1122 TCAATGCTGTAGCGCCTTCAGAGCCCTTGAGCAAGATCTCCTGTGAATATCAAAATCA 1181
QY 781 TCATTGAGGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACTTGTGGAAGAA 840
Db 1182 TCATTGAGGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACTTGTGGAAGAA 1241
QY 841 AGGACCGATTCTTCTCTGGTGTGGACTACATTTGTAATTTTCAGATAAACCTGTGGATCAGCC 900
Db 1242 AGGACCGATTCTTCTCTGGTGTGGACTACATTTGTAATTTTCAGATAAACCTGTGGATCAGCC 1301
QY 901 AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGAAACAGCTACTTTCATGGTGGAGTGA 960
Db 1302 AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGAAACAGCTACTTTCATGGTGGAGTGA 1361
QY 961 AATGCAGAGACGAGGATTTTCACTCAGGAACCTTTTGGTGGCATCCTTTCATGAACCAATGG 1020
Db 1362 AATGCAGAGACGAGGATTTTCACTCAGGAACCTTTTGGTGGCATCCTTTCATGAACCAATGG 1421
QY 1021 CTGATCTGGTGTCTTCTCGGTAGCCTGGTAGACTCGTCTGGTGCATATCCTGGTCCCTG 1080
Db 1422 CTGATCTGGTGTCTTCTCGGTAGCCTGGTAGACTCGTCTGGTGCATATCCTGGTCCCTG 1481
QY 1081 GAATCTATGATGAAGTGGTTCCTCTTACAGAAGAGGAAATAAATACATACAAAGCCATCC 1140
Db 1482 GAATCTATGATGAAGTGGTTCCTCTTACAGAAGAGGAAATAAATACATACAAAGCCATCC 1541
QY 1141 ATCTAGACCTAGAAGAAATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTTGATACTA 1200
Db 1542 ATCTAGACCTAGAAGAAATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTTGATACTA 1601
QY 1201 AGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCTTCTAATTCATGGGATCGAGG 1260
Db 1602 AGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCTTCTAATTCATGGGATCGAGG 1661
QY 1261 GCGCGTTTGATGAGCCTGGAACCTAAACAGTCACTACCTGGCCGAGTTATAGGAAATTTT 1320
Db 1662 GCGCGTTTGATGAGCCTGGAACCTAAACAGTCACTACCTGGCCGAGTTATAGGAAATTTT 1721
QY 1321 CAATCCGCTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAACACAGGTGACACGACATC 1380
Db 1722 CAATCCGCTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAACACAGGTGACACGACATC 1781
QY 1381 TTGAAGATGTGTTCTCCAAAGAAATAGTTTCCAAAGATGGTTGTTTCCATGACTCTAG 1440
Db 1782 TTGAAGATGTGTTCTCCAAAGAAATAGTTTCCAAAGATGGTTGTTTCCATGACTCTAG 1841
QY 1441 GACTACACCCGTTGATGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAGAGCGGA 1500
Db 1842 GACTACACCCGTTGATGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAGAGCGGA 1901
QY 1501 TCAGAACAGTGTGTTGGAACAGAACCCAGATATGATCCGGGATGGATCCACATTCCAATTG 1560
Db 1902 TCAGAACAGTGTGTTGGAACAGAACCCAGATATGATCCGGGATGGATCCACATTCCAATTG 1961
QY 1561 CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGCTAATTCGCTGGGASCTGTTG 1620
Db 1962 CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGCTAATTCGCTGGGAGCTGTTG 2021
QY 1621 ATGATGGAGAACATTCGCCAGAAATGAGAAATCAACAGGTGGAACCTACATAGAGGGAACCA 1680
Db 2022 ATGATGGAGAACATTCGCCAGAAATGAGAAATCAACAGGTGGAACCTACATAGAGGGAACCA 2081
QY 1681 AATTATTTGCTGCTCTTTTCTTAGAGATGGCCCGCTCCATTAATCACAAGAACCTTCTA 1740
Db 2082 AATTATTTGCTGCTCTTTTCTTAGAGATGGCCCGCTCCATTAATCACAAGAACCTTCTA 2141
QY 1741 GTCTGATCTGATCCACTGACAGATTACCTCCCCCACATCCCTAGACAGGGGATGGAATGT 1800

Db 2142 GTCTGATCTGATCCACTGACAGATTCACTCCCCACATCCCTAGACAGGATGGAATGT 2201
QY 1801 AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTG 1860
Db 2202 AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTG 2261
QY 1861 GGATATCTGGATCAGTAATAAATAATTTCAAAGGCACAGATGTTGGAATGGTTTAAGGT 1920
Db 2262 GGATATCTGGATCAGTAATAAATAATTTCAAAGGCACAGATGTTGGAATGGTTTAAGGT 2321
QY 1921 CCCCCACTGCACACCTTCTCAAGTCAATAGTGTGCTTGAGCAATTTCCCCAAGTC 1980
Db 2322 CCCCCACTGCACACCTTCTCAAGTCAATAGTGTGCTTGAGCAATTTCCCCAAGTC 2381
QY 1981 CTGTGCAATAGCCCCCAGGATTGGATTCCCTTCCAAACCTTTTAGCATATCTCCTCAACCTTGCA 2040
Db 2382 CTGTGCAATAGCCCCCAGGATTGGATTCCCTTCCAAACCTTTTAGCATATCTCCTCAACCTTGCA 2441
QY 2041 ATTTGATTGGCATATCACTCCGGTTTGTCTTCTAGTCTCTCAAGTGTCTGCTGACACATA 2100
Db 2442 ATTTGATTGGCATATCACTCCGGTTTGTCTTCTAGTCTCTCAAGTGTCTGCTGACACATA 2501
QY 2101 ATCATTTCCATCCAATGATCGCCTTTGCTTTTACCACCTCTTTCCCTTTTATCTTATTAATAA 2160
Db 2502 ATCATTTCCATCCAATGATCGCCTTTGCTTTTACCACCTCTTTCCCTTTTATCTTATTAATAA 2561
QY 2161 AATGTTGGTCTCCACCACCTGNCCTCCA 2187
Db 2562 AATGTTGGTCTCCACCACCTGACTACAA 2588

RESULT 13

ADF90847

ID ADF90847 standard; DNA; 2851 BP.

XX ADF90847;

AC ADF90847;

XX 26-FEB-2004 (first entry)

DT Human hepatic-fibrosis disease marker SEQ ID 309.

XX Hepatic fibrosis; marker; chronic hepatitis; liver cirrhosis;

DE Hepatic carcinoma; human; ds.

XX Homo sapiens.

OS JP2003259877-A.

XX 16-SEP-2003.

PD 11-MAR-2002; 2002JP-00065013.

XX 11-MAR-2002; 2002JP-00065013.

XX (SUMU) SUMITOMO SEIYAKU KK.

PA WPI; 2003-821598/77.

XX Hepatic fibrosis disease markers comprising polynucleotides or

PT antibodies, useful for improved diagnosis, screening and developing drugs

PT to treat hepatitis, to control cirrhosis and carcinoma.

XX Claim 1; SEQ ID NO 309; 313pp; Japanese.

PS The present invention relates to hepatic-fibrosis disease markers

XX (ADF90539-ADF90871) and related proteins (ADF90872-ADF90917). The

CC sequences are useful for detecting and treating hepatic fibrosis caused

CC by alcohol consumption, virus infection, etc., and the associated chronic

CC hepatitis, etc. leading to liver cirrhosis and hepatic carcinoma. The

CC markers allow the cause of hepatic fibrosis to be clarified (diagnostic

CC precision), so more suitable treatments can be developed and given.

XX

SQ	Sequence 2851 BP; 717 A; 712 C; 659 G; 763 T; 0 U; 0 Other;									
	Query Match 97.4%; Score 2182.8; DB 10; Length 2851;									
	Best Local Similarity 99.9%; Pred. No. 0;									
	Matches 2184; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
QY	1	GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC	60							
Db	159	GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC	218							
QY	61	TCGTCTTCTTCCGGGGGACAAACGTGGGTACGGGCACAGAGAGATATTTAATGTCAACCCT	120							
Db	219	TCGTCTTCTTCCGGGGGACAAACGTGGGTACGGGCACAGAGAGATATTTAATGTCAACCCT	278							
QY	121	CTTGGGGCTTTTCATGGGACTCCCTCTGCCCACATTTTGTGGAGTTGGGAAAGTTGCTAGA	180							
Db	279	CTTGGGGCTTTTCATGGGACTCCCTCTGCCCACATTTTGTGGAGTTGGGAAAGTTGCTAGA	338							
QY	181	GGCTTCAGAACTCCAGCCTAATGGATCCCAAACTCGGGAGAAATGGCTGCGTCCCTGCTGG	240							
Db	339	GGCTTCAGAACTCCAGCCTAATGGATCCCAAACTCGGGAGAAATGGCTGCGTCCCTGCTGG	398							
QY	241	CTGTGCTGCTGCTGTGGAGCGCGGCATGTTCTCCTCACCCCTCCCCCGCCCCCGGCGC	300							
Db	399	CTGTGCTGCTGCTGTGGAGCGCGGCATGTTCTCCTCACCCCTCCCCCGCCCCCGGCGC	458							
QY	301	TGTTAGAGAAAGCTTTCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA	360							
Db	459	TGTTAGAGAAAGCTTTCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA	518							
QY	361	AGGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAAGAGC	420							
Db	519	AGGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAAGAGC	578							
QY	421	TCTTCAGAAATGATGGCGTGGCTGCGGACACGCTGACGCGCCTGGGGCCCGTGTGGCCT	480							
Db	579	TCTTCAGAAATGATGGCGTGGCTGCGGACACGCTGACGCGCCTGGGGCCCGTGTGGCCT	638							
QY	481	CGGTGGACATGGGTCTTCAGCAGCTGCCCGATGGTCAAGAGTCTTCCAATACCTCCCGTCA	540							
Db	639	CGGTGGACATGGGTCTTCAGCAGCTGCCCGATGGTCAAGAGTCTTCCAATACCTCCCGTCA	698							
QY	541	TCCTGGCCGAACCTGGGAGCGATCCACGAAAGSCACCGTGTGCTTCTACGSCCACTTGG	600							
Db	699	TCCTGGCCGAACCTGGGAGCGATCCACGAAAGSCACCGTGTGCTTCTACGSCCACTTGG	758							
QY	601	ACGTGCAGCCTGCTGACCGGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGG	660							
Db	759	ACGTGCAGCCTGCTGACCGGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGG	818							
QY	661	TAGACGGGAAACTTTATGGACGAGGAGCGACCGACAAACAAAGGCCCTGTCTGGCTTGA	720							
Db	819	TAGACGGGAAACTTTATGGACGAGGAGCGACCGACAAACAAAGGCCCTGTCTGGCTTGA	878							
QY	721	TCAATGCTGTAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCCCTGTGAATATCAAAATTCA	780							
Db	879	TCAATGCTGTAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCCCTGTGAATATCAAAATTCA	938							
QY	781	TCATTGAGGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACCTTGTGGAAGAAAGAAA	840							
Db	939	TCATTGAGGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACCTTGTGGAAGAAAGAAA	998							
QY	841	AGGACCGATTCTTCTCTGCTGTGGACTACATTGTAATTTTCAGATAACCTGTGGATCAGCC	900							
Db	999	AGGACCGATTCTTCTCTGCTGTGGACTACATTGTAATTTTCAGATAACCTGTGGATCAGCC	1058							
QY	901	AAAGGAAGCCAGCAATCACTTATGGAACCCCGGGGGAACAGCTACTTTCATGTGTGGAGTGA	960							
Db	1059	AAAGGAAGCCAGCAATCACTTATGGAACCCCGGGGGAACAGCTACTTTCATGTGTGGAGTGA	1118							
QY	961	AATGCAGAGACCAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTTCATGAACCAATGG	1020							
Db	1119	AATGCAGAGACCAGGATTTTCACTCAGGAACCTTTGGTGGCATCCTTTCATGAACCAATGG	1178							

QY	1021	CTGATCTGGTTGCTCTTCTCGGTAGCCCTGGTAGACTCGTCTGGTCATATCCTGGTCCCTG	1080							
Db	1179	CTGATCTGGTTGCTCTTCTCGGTAGCCCTGGTAGACTCGTCTGGTCATATCCTGGTCCCTG	1238							
QY	1081	GAATCTATGATGAAGTGGTTCCTCTTACAGAAAGAGAAATAAATACATACAAAAGCCATCC	1140							
Db	1239	GAATCTATGATGAAGTGGTTCCTCTTACAGAAAGAGAAATAAATACATACAAAAGCCATCC	1298							
QY	1141	ATCTAGACCTAGAAGAATACCGGAATAGCAGCCGGGTTGAGAAAATTTCTGTTTCGATACTA	1200							
Db	1299	ATCTAGACCTAGAAGAATACCGGAATAGCAGCCGGGTTGAGAAAATTTCTGTTTCGATACTA	1358							
QY	1201	AGGAGGAGATTCTAATGCACCTCTGGAGTACCCATCTCTTTCTATTTCATGGGATCGAGG	1260							
Db	1359	AGGAGGAGATTCTAATGCACCTCTGGAGTACCCATCTCTTTCTATTTCATGGGATCGAGG	1418							
QY	1261	GCGCGTTTGTAGAGCCTGGAACTAAACAGTCAATACCTGGCCGAGTTATAGGAAAAATTTT	1320							
Db	1419	GCGCGTTTGTAGAGCCTGGAACTAAACAGTCAATACCTGGCCGAGTTATAGGAAAAATTTT	1478							
QY	1321	CAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAACAGGTGACACGACATC	1380							
Db	1479	CAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAACAGGTGACACGACATC	1538							
QY	1381	TTGAAGATGTGTTCTCCAAAAGAAATAGTCCAAACAAGATGGTTGTTTCCATGACTCTAG	1440							
Db	1539	TTGAAGATGTGTTCTCCAAAAGAAATAGTCCAAACAAGATGGTTGTTTCCATGACTCTAG	1598							
QY	1441	GACTACACCCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAAGAGCGA	1500							
Db	1599	GACTACACCCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAAGAGCGA	1658							
QY	1501	TCAGAACAGTGTTTGGAACAGAACCCAGATATGATCCGGGATGGATCCACCATTCCAAATTG	1560							
Db	1659	TCAGAACAGTGTTTGGAACAGAACCCAGATATGATCCGGGATGGATCCACCATTCCAAATTG	1718							
QY	1561	CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGCTAAATCCGCTGGGAGCTGTTG	1620							
Db	1719	CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGCTAAATCCGCTGGGAGCTGTTG	1778							
QY	1621	ATGATGGAGAACATTCCGAGAATGAGAAAAATCAACAGGTGGAACCTACATAGAGGGAACCA	1680							
Db	1779	ATGATGGAGAACATTCCGAGAATGAGAAAAATCAACAGGTGGAACCTACATAGAGGGAACCA	1838							
QY	1681	AATTATTTGCTGCCCTTTTCTTAGAGATGGCCCCAGCTCCATTAAATCAAGAACCTTCTA	1740							
Db	1839	AATTATTTGCTGCCCTTTTCTTAGAGATGGCCCCAGCTCCATTAAATCAAGAACCTTCTA	1898							
QY	1741	GTCTGATCTGATCCACTGACAGATTCACTCCCTCCACATCCCTAGACAGGATGGAATGT	1800							
Db	1899	GTCTGATCTGATCCACTGACAGATTCACTCCCTCCACATCCCTAGACAGGATGGAATGT	1958							
QY	1801	AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTAAAAATGTCTTG	1860							
Db	1959	AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTAAAAATGTCTTG	2018							
QY	1861	GGATATCTCGATCAGTAATAAAATATTTCAAAGGCACAGATGTTGGAAATGGTTTAAGGT	1920							
Db	2019	GGATATCTCGATCAGTAATAAAATATTTCAAAGGCACAGATGTTGGAAATGGTTTAAGGT	2078							
QY	1921	CCCCCACTGCACACCTTCTCAAGTCAATAGCTGCTTGCAGCAACCTTGATTTCCCCAAGTC	1980							
Db	2079	CCCCCACTGCACACCTTCTCAAGTCAATAGCTGCTTGCAGCAACCTTGATTTCCCCAAGTC	2138							
QY	1981	CTGTGCAATAGCCCCAGGATTGGATTCTTCCAAACCTTTTAGCATATCTCCAAACCTTGCA	2040							
Db	2139	CTGTGCAATAGCCCCAGGATTGGATTCTTCCAAACCTTTTAGCATATCTCCAAACCTTGCA	2198							
QY	2041	ATTTGATTGGCATAAATCACTCCGGTTTGTCTTAGGTCTCTCAAGTGTCTGTGACACATA	2100							
Db	2199	ATTTGATTGGCATAAATCACTCCGGTTTGTCTTAGGTCTCTCAAGTGTCTGTGACACATA	2258							

QY 1170 AGCCGGGTGAGAAATTTCTGTTTCGATACCTAAGGAGGAGATTCTAATGCACCTCTGGAGG 1229
Db |||||||
QY 1141 AGCCGGGTGAGAAATTTCTGTTTCGATACCTAAGGAGGAGATTCTAATGCACCTCTGGAGG 1200
Db |||||||
QY 1230 TACCCATCTCTTTCTATTTCATGGATCGAGGGCGGTTTGTATGAGCCTGGAACATAAACA 1289
Db |||||||
QY 1201 TACCCATCTCTTTCTATTTCATGGATCGAGGGCGGTTTGTATGAGCCTGGAACATAAACA 1260
Db |||||||
QY 1290 GTCATACCTGGCCGAGTTATAGGAAATTTTCAATCCGTTCTAGTCCCTCACATGAATGTG 1349
Db |||||||
QY 1261 GTCATACCTGGCCGAGTTATAGGAAATTTTCAATCCGTTCTAGTCCCTCACATGAATGTG 1320
Db |||||||
QY 1350 TCTGCGGTGGAATAACAGGTGACACGACATCTTGAAGATGTGTTCTCCAAAGAAATAGT 1409
Db |||||||
QY 1321 TCTGCGGTGGAATAACAGGTGACACGACATCTTGAAGATGTGTTCTCCAAAGAAATAGT 1380
Db |||||||
QY 1410 TCCAACAAGATGGTTGTTTCCATGACTCTAGGACTACACCCGTTGATTGCAAAATATTGAT 1469
Db |||||||
QY 1381 TCCAACAAGATGGTTGTTTCCATGACTCTAGGACTACACCCGTTGATTGCAAAATATTGAT 1440
Db |||||||
QY 1470 GACACCCAGTATCTCGCAGCAAAAGAGCGATCAGAACAGTGTGTTGGAACAGAACCCAGAT 1529
Db |||||||
QY 1441 GACACCCAGTATCTCGCAGCAAAAGAGCGATCAGAACAGTGTGTTGGAACAGAACCCAGAT 1500
Db |||||||
QY 1530 ATGATCCGGGATGATCCACCATTTCCAATTTGCCAAATGTTCCAGGAGATCGTCCACAAG 1589
Db |||||||
QY 1501 ATGATCCGGGATGATCCACCATTTCCAATTTGCCAAATGTTCCAGGAGATCGTCCACAAG 1560
Db |||||||
QY 1590 AGCGTGTGCTAATTCGCTGGGAGCTGTTGATGATGGAGAACATTCGAGAAATGAGAAA 1649
Db |||||||
QY 1561 AGCGTGTGCTAATTCGCTGGGAGCTGTTGATGATGGAGAACATTCGAGAAATGAGAAA 1620
Db |||||||
QY 1650 ATCAACAGGTGGAATACTACATAGAGGGAACCAAAATATTGCTGCCTTTTCTTAGAGATG 1709
Db |||||||
QY 1621 ATCAACAGGTGGAATACTACATAGAGGGAACCAAAATATTGCTGCCTTTTCTTAGAGATG 1680
Db |||||||
QY 1710 GCCAGCTCCATTAATCAAGAACCCTTCTAGTCTGATCTGATCCACTGCAGATTCACC 1769
Db |||||||
QY 1681 GCCAGCTCCATTAATCAAGAACCCTTCTAGTCTGATCTGATCCACTGCAGATTCACC 1740
Db |||||||
QY 1770 TCCCCCAGATCCTTAGACAGGGATGGAATGAAATATCCAGAGAAATTTGGGTCTAGTATA 1829
Db |||||||
QY 1741 TCCCCCAGATCCTTAGACAGGGATGGAATGAAATATCCAGAGAAATTTGGGTCTAGTATA 1800
Db |||||||
QY 1830 GTACATTTTCCCTTCCATTTAAATGCTTTGGGATATCTGGATCAGTAATAAATATTTC 1889
Db |||||||
QY 1801 GTACATTTTCCCTTCCATTTAAATGCTTTGGGATATCTGGATCAGTAATAAATATTTC 1860
Db |||||||
QY 1890 AAAGGCACAGATGTTGGAATGTTTAAAGTCCCTCCCTGACACACCTTCTCAAGTCATA 1949
Db |||||||
QY 1861 AAAGGCACAGATGTTGGAATGTTTAAAGTCCCTCCCTGACACACCTTCTCAAGTCATA 1920
Db |||||||
QY 1950 GCTGCTTGACCAACTTGATTTCCCAAGTCTGTGCAATAGCCCCAGGATTCCT 2009
Db |||||||
QY 1921 GCTGCTTGACCAACTTGATTTCCCAAGTCTGTGCAATAGCCCCAGGATTCCT 1980
Db |||||||
QY 2010 TCCAACCTTTTAGCATATCTCCAACCTTGCAATTTGATTGGCAATATCACTCCGTTTGC 2069
Db |||||||
QY 1981 TCCAACCTTTTAGCATATCTCCAACCTTGCAATTTGATTGGCAATATCACTCCGTTTGC 2040
Db |||||||
QY 2070 TTTCTAGGCTCAAGTCTGTCGACACATAATCATTCATCCATGATCGCCTTTGCTT 2129
Db |||||||
QY 2041 TTTCTAGGCTCAAGTCTGTCGACACATAATCATTCATCCATGATCGCCTTTGCTT 2100
Db |||||||
QY 2130 TACCACCTTTTCTTTTATCTTATTAATAAATGTTGGTCTCCACACTGNCCTCCCAA 2189
Db |||||||
QY 2101 TACCACCTTTTCTTTTATCTTATTAATAAATGTTGGTCTCCACACTGAAACAAAA 2160
Db |||||||
QY 2190 AA 2230
Db |||||||
QY 2161 AA 2201
Db |||||||

RESULT 15
AAC84452

ID AAC84452 standard; cDNA; 2235 BP.

XX
AC AAC844452;

XX
DT 02-APR-2001 (first entry)

XX
DE Nucleotide sequence of mddt cDNA clone ID No: 436857.2.

XX
KW Molecule for disease detection and treatment; mddt; human; cirrhosis;
cell proliferative disorder; arteriosclerosis; bursitis; hepatitis;
connective tissue disease; myelofibrosis; cancer; leukemia; autoimmune;
acquired immunodeficiency syndrome; AIDS; Addison's disease; allergy;
anemia; bronchitis; gout; Hashimoto's thyroiditis; multiple sclerosis;
cytostatic; immunomodulator; anti-inflammatory; gene therapy; ss.

XX
OS Homo sapiens.

XX
PN WO200075298-A2.

XX
PD 14-DEC-2000.

XX
PF 01-JUN-2000; 2000WO-US015344.

XX
PR 03-JUN-1999; 99US-0137412P.

XX
PR 05-AUG-1999; 99US-0147500P.

XX
PR 05-AUG-1999; 99US-0147501P.

XX
PR 05-AUG-1999; 99US-0147542P.

XX
PA (INCY-) INCYTE GENOMICS INC.

XX
PI Hodgson DM, Lincoln SE, Russo FD, Spiro PA, Banville SC;
Bratcher SR, Dufour GE, Cohen HJ, Rosen BH, Hillman JL;
Jones AL, Yu JY, Greenawalt LB, Panzer SR, Roseberry AM, Wright RJ;
Daniels SE;

XX
DR WPI; 2001-071068/08.

XX
PT New polypeptide and polynucleotide molecules for disease detection and
treatment are useful in diagnosis and gene therapy of proliferative
disorders (e.g. breast cancer), autoimmune and inflammatory disorders
(e.g. AIDS or allergy).

XX
PS Claim 1; Page 95-96; 99pp; English.

XX
CC Sequences AAC84445-C84458 are new isolated polynucleotide molecules for
disease detection and treatment (mddt). The mddt polynucleotides are
useful for diagnosing or treating disorders associated with disease
detection and treatment molecules. These diseases include cell
proliferative disorders (e.g. arteriosclerosis, bursitis, cirrhosis,
hepatitis, mixed connective tissue disease, myelofibrosis, or cancers
such as leukemia, or breast or brain cancers), autoimmune or inflammatory
disorders (e.g. acquired immunodeficiency syndrome (AIDS), Addison's
disease, allergies, anemia, autoimmune haemolytic anemia, bronchitis,
gout, Hashimoto's thyroiditis, multiple sclerosis or cancers). The mddt
are especially useful for somatic or germline gene therapy. The mddt may
also be used to detect the presence of, or to quantify the amount of, an
mddt-related polynucleotide in a sample. The mddt are also useful for
isolating full length cDNA sequences utilizing hybridization and/or
amplification procedures, for generating hybridization probes useful in
chromosomal mapping of naturally occurring genomic sequences, as
molecular weight markers, or for monitoring the progress of disorders
associated with abnormal levels of mddt expression or evaluating the
efficacy of a particular treatment. The recombinant nucleic acids are
useful as part of a viral vector (e.g. based on a vaccinia virus) for
vaccinating a mammal and inducing a protective immunological response in
the mammal. The MDDT polypeptides are useful for screening molecules that
bind to or are bound by the polypeptides, i.e. for screening agonists,
antagonists or modulators of MDDT

XX
SQ Sequence 2235 BP; 557 A; 543 C; 536 G; 568 T; 0 U; 31 Other;

Query Match		95.8%;	Score 2147.4;	DB 4;	Length 2235;		
Best Local Similarity		98.5%;	Pred. No. 0;				
Matches 2148; Conservative		0;	Mismatches	32;	Indels	0;	Gaps 0;
Qy	1	GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGGAATAGCTCCACATATACCAGCC	60				
Db	56	GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGGAATAGCTCCACATATACCAGCC	115				
Qy	61	TCGTCTTCCTTCCGGGGACAAAGCTGGGTGAGGACAGAGAGATATTTAATGTCAACCT	120				
Db	116	TCGTCTTCCTTCCGGGGACAAAGCTGGGTGAGGACAGAGAGATATTTAATGTCAACCT	175				
Qy	121	CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTCGAGGTTGGGAAAGTTGCTAGA	180				
Db	176	CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTCGAGGTTGGGAAAGTTGCTAGA	235				
Qy	181	GGTTTCAGAACTCCAGCCTAATGGATCCCAAACCTCGGAGAAATGGCTGCCCTCCCTGG	240				
Db	236	GGTTTCAGAACTCCAGCCTAATGGATCCCAAACCTCGGAGAAATGGCTGCCCTCCNNNNNN	295				
Qy	241	CTGTGCTGCTGCTGCTGGAGCGCGGCATGTTCTCTCACCCCTCCCGCCCCCGGCGC	300				
Db	296	NNNNNNNNNNNNNNNNNNNGCGGCATGTTCTCTCTCACCCCTCCCGCCCCCGGCGC	355				
Qy	301	TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA	360				
Db	356	TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA	415				
Qy	361	AGGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTCGCTTCAGACAAAGAGC	420				
Db	416	AGGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTCGCTTCAGACAAAGAGC	475				
Qy	421	TCITTCAAAATGATGGCCGTGGCTCGGACACGCTGCAGCGCCTGGGGCCCGTGTGGCCT	480				
Db	476	TCITTCAAAATGATGGCCGTGGCTTCGGGACACGCTGCAGCGCCTGGGGCCCGTGTGGCCT	535				
Qy	481	CGGTGACATGGGTCTTCAGCAGCTGCCCCGATGGTCAGAGTCTTCCAAATACCTCCCGTCA	540				
Db	536	CGGTGACATGGGTCTTCAGCAGCTGCCCCGATGGTCAGAGTCTTCCAAATACCTCCCGTCA	595				
Qy	541	TCCTGGCCGAACCTGGGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGG	600				
Db	596	TCCTGGCCGAACCTGGGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGG	655				
Qy	601	ACGTGCAGCCTGTGACCGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGG	660				
Db	656	ACGTGCAGCCTGTGACCGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGG	715				
Qy	661	TAGACGGGAAACTTTATGGACGAGGACGACCGACAACAAAGGCCCTGTCTTGGCTTGA	720				
Db	716	TAGACGGGAAACTTTATGGACGAGGACGACCGACAACAAAGGCCCTGTCTTGGCTTGA	775				
Qy	721	TCAATGCTGTAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAATTCA	780				
Db	776	TCAATGCTGTAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAATTCA	835				
Qy	781	TCATTGAGGGATGGAAGAGGCTGGCTGTGTCCTGGAGGAACTTGTGGAAAAAGAAA	840				
Db	836	TCATTGAGGGATGGAAGAGGCTGGCTGTGTCCTGGAGGAACTTGTGGAAAAAGAAA	895				
Qy	841	AGGACCGATTCTTCTCTGGTGTGACTACATTGTAATTTTCAGATAAACCTGTGGATCAGCC	900				
Db	896	AGGACCGATTCTTCTCTGGTGTGACTACATTGTAATTTTCAGATAAACCTGTGGATCAGCC	955				
Qy	901	AAAGGAAGCCAGCAATCACTTATGGAAACCGGGGGAACAGCTACTTTCATGGTGGAGTGA	960				
Db	956	AAAGGAAGCCAGCAATCACTTACGGAAACCGGGGGAACAGCTACTTTCATGGTGGAGTGA	1015				
Qy	961	AATGCAGAGACAGGATTTTTCACCTCAGGAACCTTTGGTGGCATCCTTTCATGAACCAATGG	1020				
Db	1016	AATGCAGAGACAGGATTTTTCACCTCAGGAACCTTTGGTGGCATCCTTTCATGAACCAATGG	1075				

Qy	1021	CTGATCTGGTTGCTCTTCTCGGTAGCCTGGTAGACTCGTCTGGTCATATCCTGGTCCCTG	1080
Db	1076	CTGATCTGGTTGCTCTTCTCGGTAGCCTGGTAGACTCGTCTGGTCATATCCTGGTCCCTG	1135
Qy	1081	GAATCTATGATGAAGTGGTTCCTCTTACAGAAAGAGGAAATAAATACATACAAAGCATCC	1140
Db	1136	GAATCTATGATGAAGTGGTTCCTCTTACAGAAAGAGGAAATAAATACATACAAAGCATCC	1195
Qy	1141	ATCTAGACCTAGAAATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTTCGATACTA	1200
Db	1196	ATCTAGACCTAGAAATACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTTCGATACTA	1255
Qy	1201	AGGAGGAGATTCTAATGACCTCTGGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGG	1260
Db	1256	AGGAGGAGATTCTAATGACCTCTGGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGG	1315
Qy	1261	GCGCGTTTGATGAGCCTGGAACTAAAAACAGTCTATACCTGGCCGAGTTTATAGGAAAAATTT	1320
Db	1316	GCGCGTTTGATGAGCCTGGAACTAAAAACAGTCTATACCTGGCCGAGTTTATAGGAAAAATTT	1375
Qy	1321	CAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAACAGGTGACACGACATC	1380
Db	1376	CAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAACAGGTGACACGACATC	1435
Qy	1381	TTGAAGATGTGTTCTCCAAAAAGAAATAGTTCCAAAGATGGTTGTTTCCATGACTCTAG	1440
Db	1436	TTGAAGATGTGTTCTCCAAAAAGAAATAGTTCCAAAGATGGTTGTTTCCATGACTCTAG	1495
Qy	1441	GACTACACCCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAAGAGCGA	1500
Db	1496	GACTACACCCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAAGAGCGA	1555
Qy	1501	TCAGAAACAGTGTGTTGGAAACAGAACCATATGATCCGGGATGGATCCACCAATTCCTAATTG	1560
Db	1556	TCAGAAACAGTGTGTTGGAAACAGAACCATATGATCCGGGATGGATCCACCAATTCCTAATTG	1615
Qy	1561	CCAAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGCTAATTCGCTGGGAGCTGTTG	1620
Db	1616	CCAAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGCTAATTCGCTGGGAGCTGTTG	1675
Qy	1621	ATGATGGAGAACATTCGAGAATGAGAAAAATCAACAGGTGGAACTACATAGAGGGAACCA	1680
Db	1676	ATGATGGAGAACATTCGAGAATGAGAAAAATCAACAGGTGGAACTACATAGAGGGAACCA	1735
Qy	1681	AATTATTGCTGCCCTTTTCTTAGAGATGGCCAGCTCCCATTAATCACAAGAACCTTCTA	1740
Db	1736	AATTATTGCTGCCCTTTTCTTAGAGATGGCCAGCTCCCATTAATCACAAGAACCTTCTA	1795
Qy	1741	GTCTGATCTGATCCACTGCAGATTCACCTCCCCACATCCCTAGACAGGGATGGAATGT	1800
Db	1796	GTCTGATCTGATCCACTGCAGATTCACCTCCCCACATCCCTAGACAGGGATGGAATGT	1855
Qy	1801	AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAAAATGCTTG	1860
Db	1856	AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAAAATGCTTG	1915
Qy	1861	GGATATCTGGATCAGTAATAAAATATTTCAAAGGCACAGATGTTGGAAATGGTTTAAGGT	1920
Db	1916	GGATATCTGGATCAGTAATAAAATATTTCAAAGGCACAGATGTTGGAAATGGTTTAAGGT	1975
Qy	1921	CCCCACTGCACACCTTCTCAAGTCATAGCTGCTTGACGAACTTGATTTCCCCCAAGTC	1980
Db	1976	CCCCACTGCACACCTTCTCAAGTCATAGCTGCTTGACGAACTTGATTTCCCCCAAGTC	2035
Qy	1981	CTGTGCAATAGCCCCAGGATTCCTTCCAAACCTTTTAGCATATCTCCAAACCTTGCA	2040
Db	2036	CTGTGCAATAGCCCCAGGATTCCTTCCAAACCTTTTAGCATATCTCCAAACCTTGCA	2095
Qy	2041	ATTTGATTTGGCATAATCACTCCGTTTGTCTTCTAGGTCCTCAAGTCTCGTGACACATA	2100
Db	2096	ATTTGATTTGGCATAATCACTCCGTTTGTCTTCTAGGTCCTCAAGTCTCGTGACACATA	2155
Qy	2101	ATCATTCACATCCAATGATCGCCCTTGTGCTTTTACCACCTCTTTTCCCTTTTATCTTATAATAAA	2160

Db 2156 ATCATTCATCCAAATGATCGCCTTTGCTTTACCACTCTTCCCTTTATCTATTATAATAA 2215
QY 2161 AATGTTGGTCTCCACCACTG 2180
Db 2216 AATGTTGGTCTCCACCACTG 2235

RESULT 16

AAZ65270
ID AAZ65270 standard; DNA; 2152 BP.
XX AAZ65270;
AC AAZ65270;
XX AAZ65270;
DT 23-MAR-2000 (first entry)
XX Human secreted protein gene 21.
DE Human;
XX Human; secreted protein; cancer; tumour; developmental abnormality;
KW foetal deficiency; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW therapy; chromosome 18q22-23; ds.
XX Homo sapiens.
OS
XX WO9958660-A1.
PN
XX 18-NOV-1999.
PD
XX 06-MAY-1999; 99WO-US009847.
PF
XX 12-MAY-1998; 98US-0085093P.
PR 12-MAY-1998; 98US-0085094P.
PR 12-MAY-1998; 98US-0085105P.
PR 12-MAY-1998; 98US-0085180P.
PR 18-MAY-1998; 98US-0085906P.
PR 18-MAY-1998; 98US-0085920P.
PR 18-MAY-1998; 98US-0085921P.
PR 18-MAY-1998; 98US-0085922P.
PR 18-MAY-1998; 98US-0085923P.
PR 18-MAY-1998; 98US-0085924P.
PR 18-MAY-1998; 98US-0085925P.
PR 18-MAY-1998; 98US-0085927P.
PR 18-MAY-1998; 98US-0085928P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR, Lafleur DW;
PI Endress GA, Ebner R;
XX WPI; 2000-062296/05.
DR P-PSDB; AAY76144.
XX
PT New isolated human genes and the secreted polypeptides they encode,
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
PS Claim 1; Page 309; 475pp; English.
XX
CC AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
CC This sequence was found to be present on human chromosome 18q22-23.
CC AAY76124 to AAY76223 represent the secreted proteins encoded by the 97
CC human genes. The genes and their corresponding secreted polypeptides are
CC useful for preventing, treating or ameliorating medical conditions, e.g.
CC by protein or gene therapy. Also pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new genes. Specific uses are
CC described for each of the 97 genes, based on which tissues they are most
CC highly expressed in, and include developing products for the diagnosis or

CC treatment of cancer, tumours, developmental abnormalities and foetal
CC deficiencies, blood disorders, diseases of the immune system, autoimmune
CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
CC also useful for identifying their binding partners. The sequences shown
CC in AAY76224 to AAY76424 represent fragments of the secreted proteins
XX
SQ Sequence 2152 BP; 541 A; 526 C; 531 G; 553 T; 0 U; 1 Other;
Query Match 95.3%; Score 2135.6; DB 3; Length 2152;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2148; Conservative 1; Mismatches 0; Indels 3; Gaps 1;
QY 19 CCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCCTCGTCTTCTTCCGGGG 78
Db 1 CCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCCTCGTCTTCTTCCGGGG 60
QY 79 ACAACGTGGTTCAGGGCACAGAGAGATATTAAATGTCAACCTCTTGGGGCTTTCATGGGA 138
Db 61 ACAACGTGGTTCAGGGCACAGAGAGATATTAAATGTCAACCTCTTGGGGCTTTCATGGGA 120
QY 139 CTCCCTCTGCCACATTTTGGAGGTGGGAAAGTTGCTAGAGGCTCAGAACTCCAGCC 198
Db 121 CTCCCTCTGCCACATTTTGGAGGTGGGAAAGTTGCTAGAGGCTCAGAACTCCAGCC 180
QY 199 TAATGGATCCCAAACTCGGAGAAATGGCTGCTCCCTCGTGGCTG---TGCTGCTGCTGC 255
Db 181 TAATGGATCCCAAACTCGGAGAAATGGCTGCTCCCTCGTGGCTGCTGCTGCTGCTGC 240
QY 256 TGCTGGAGCGCGGCATGTTCTCTCACCTCCCGCCCCCGCGCTGTTAGAGAAAGTCT 315
Db 241 TGCTGGAGCGCGGCATGTTCTCTCACCTCCCGCCCCCGCGCTGTTAGAGAAAGTCT 300
QY 316 TCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGAGTGGGTGGCCA 375
Db 301 TCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGAGTGGGTGGCCA 360
QY 376 TCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCCAGACAAGAGCTCTTTCAGAAATGATGG 435
Db 361 TCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCCAGACAAGAGCTCTTTCAGAAATGATGG 420
QY 436 CCGTGGTTCGGACACGCTGCAGCGCTGGGGGGCCCGTGTGGCTCGGTGGACATGGGTC 495
Db 421 CCGTGGTTCGGACACGCTGCAGCGCTGGGGGGCCCGTGTGGCTCGGTGGACATGGGTC 480
QY 496 CTCAGCAGTCCCGATGGTTCAGAGTCTTCCAATACCTCCCGTCATCCTGGCCGGAACCTGG 555
Db 481 CTCAGCAGTCCCGATGGTTCAGAGTCTTCCAATACCTCCCGTCATCCTGGCCGGAACCTGG 540
QY 556 GGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGGCCACTTGGAGCTGCAGCCTGCTG 615
Db 541 GGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGGCCACTTGGAGCTGCAGCCTGCTG 600
QY 616 ACCGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACGGGAAACTTT 675
Db 601 ACCGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACGGGAAACTTT 660
QY 676 ATGGACGAGGAGCGACCGACAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCG 735
Db 661 ATGGACGAGGAGCGACCGACAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCG 720
QY 736 CCTTCAGAGCCTCGAGCAAGATCTTCTGTGAATATCAAATTCATCATTTAGGGGATGG 795
Db 721 CCTTCAGAGCCTCGAGCAAGATCTTCTGTGAATATCAAATTCATCATTTAGGGGATGG 780
QY 796 AAGAGGCTGGCTCTGTTGCCCTGGAGAACTTGTGGAAAAAGAAAGACCGATTCTTCT 855
Db 781 AAGAGGCTGGCTCTGTTGCCCTGGAGAACTTGTGGAAAAAGAAAGACCGATTCTTCT 840
QY 856 CTGGTGGACTACATTGTAATTTTCAGATAACCTGTGGATCAGCCAAAGGAAGCCAGCAA 915

Db 841 CTGCTGTGGACTACATTGTAAATTCAGATAAACCTGTGGATCAGCCAAAGGAAGCCAGCAA 900

Qy 916 TCACCTTATGGAACCCGGGGAAACAGCTACTTTCATGTTGGAGGTGAAATGCAGAGACCAGG 975

Db 901 TCACCTTATGGAACCCGGGGAAACAGCTACTTTCATGTTGGAGGTGAAATGCAGAGACCAGG 960

Qy 976 ATTTTCACTCAGGAACCTTTTGGTGGCATCCTTTCATGAACCAATGGCTGATCTGGTTGCTC 1035

Db 961 ATTTTCACTCAGGAACCTTTTGGTGGCATCCTTTCATGAACCAATGGCTGATCTGGTTGCTC 1020

Qy 1036 TTCTCGGTAGCCTGGTAGACTCGTCTGGTCATATCCTGTGCCCTGGAAATCTATGATGAAG 1095

Db 1021 TTCTCGGTAGCCTGGTAGACTCGTCTGGTCATATCCTGTGCCCTGGAAATCTATGATGAAG 1080

Qy 1096 TGGTTCCTCTTACAGAAGAGGAATAAATACATACAAAGCCATCCATCTAGACCTAGAAAG 1155

Db 1081 TGGTTCCTCTTACAGAAGAGGAATAAATACATACAAAGCCATCCATCTAGACCTAGAAAG 1140

Qy 1156 AATACCGGAATAGCAGCCGGGTTGAGAAAATTTCTGTTCCGATACTAAGGAGGAGATTCTAA 1215

Db 1141 AATACCGGAATAGCAGCCGGGTTGAGAAAATTTCTGTTCCGATACTAAGGAGGAGATTCTAA 1200

Qy 1216 TGCACCTCTGGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGGGCGGCTTTTGATGAGC 1275

Db 1201 TGCACCTCTGGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGGGCGGCTTTTGATGAGC 1260

Qy 1276 CTGGAACATAAACAGTCATACCTGGCCGAGTTATAGGAAAATTTTCAATCCGTCGTAGTCC 1335

Db 1261 CTGGAACATAAACAGTCATACCTGGCCGAGTTATAGGAAAATTTTCAATCCGTCGTAGTCC 1320

Qy 1336 CTCACATGAATGTGTCTGCGGTGGAAAAAACAGGTGACACGACATCTTGAAGATGTGTCT 1395

Db 1321 CTCACATGAATGTGTCTGCGGTGGAAAAAACAGGTGACACGACATCTTGAAGATGTGTCT 1380

Qy 1396 CCAAAAGAAAATAGTTTCCAACAAGATGGTTGTTTCCATGACTCTAGGACTACACCCGTGGA 1455

Db 1381 CCAAAAGAAAATAGTTTCCAACAAGATGGTTGTTTCCATGACTCTAGGACTACACCCGTGGA 1440

Qy 1456 TTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGACGGATCAGAACAGTGTG 1515

Db 1441 TTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGACGGATCAGAACAGTGTG 1500

Qy 1516 GAACAGAACCCAGATATGATCCGGGATGGATCCACCATTCCAATTCCAAATGTTCCAGG 1575

Db 1501 GAACAGAACCCAGATATGATCCGGGATGGATCCACCATTCCAATTCCAAATGTTCCAGG 1560

Qy 1576 AGATCGTCCACAAGACCGTGTGCTAAATCCGCTGGGAGCTGTTGATGATGGAGAACATT 1635

Db 1561 AGATCGTCCACAAGACCGTGTGCTAAATCCGCTGGGAGCTGTTGATGATGGAGAACATT 1620

Qy 1636 CGCAGAATGAGAAAAATCAACAGGTGGAACTACATAGAGGGAACCAAAATATTGTCGTGCT 1695

Db 1621 CGCAGAATGAGAAAAATCAACAGGTGGAACTACATAGAGGGAACCAAAATATTGTCGTGCT 1680

Qy 1696 TTTTCTTAGAGATGGCCAGCTCCATTAAATCACAAGAACCTTCTAGTCTGATCTGATCCA 1755

Db 1681 TTTTCTTAGAGATGGCCAGCTCCATTAAATCACAAGAACCTTCTAGTCTGATCTGATCCA 1740

Qy 1756 CTGACAGATTACCTCCCCACATCCCTAGACAGGGATGGAATGTAATATCCAGAGAAAT 1815

Db 1741 CTGACAGATTACCTCCCCACATCCCTAGACAGGGATGGAATGTAATATCCAGAGAAAT 1800

Qy 1816 TTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTTTAAAGTCTTTGGGATATCTGGATCAG 1875

Db 1801 TTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTTTAAAGTCTTTGGGATATCTGGATCAG 1860

Qy 1876 TAATAAAATATTTCAAAGGCACAGATGTTGAAATGGTTTAAAGTCCCCCCTGCACACC 1935

Db 1861 TAATAAAATATTTCAAAGGCACAGATGTTGAAATGGTTTAAAGTCCCCCCTGCACACC 1920

Qy 1936 TTCCTCAAGTCATAGCTGTTGACGAACCTTGATTTCCCCCAAGTCCTGTGCAATAGCCCC 1995

Db 1921 TTCCTCAAGTCATAGCTGTTGACGAACCTTGATTTCCCCCAAGTCCTGTGCAATAGCCCC 1980

Qy 1996 AGGATTGGATTCCTTCCAAACCTTTTAGCATATCTCCAACCTTGCAATTTGATTGGCATAA 2055

Db 1981 AGGATTGGATTCCTTCCAAACCTTTTAGCATATCTCCAACCTTGCAATTTGATTGGCATAA 2040

Qy 2056 TCACTCCGGTTTGCTTTCTAGGTCTCTCAAGTGCTCGTGACACATAATCATTCATCCAAT 2115

Db 2041 TCACTCCGGTTTGCTTTCTAGGTCTCTCAAGTGCTCGTGACACATAATCATTCATCCAAT 2100

Qy 2116 GATCGCCTTTGCTTTACCACTCTTTTCCTTTTATCTTAAATAAAAAATGTTG 2167

Db 2101 GATCGCCTTTGCTTTACCACTCTTTTCCTTTTATCTTAAATAAAAAATGTTG 2152

RESULT 17
ACC50470

ID ACC50470 standard; cDNA; 2152 BP.

XX ACC50470;

XX 12-JUN-2003 (first entry)

XX Human secreted protein coding sequence, SEQ ID 137.

XX Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;

KW vulnerary; antiinflammatory; nootropic; neuroprotective;

KW antiparkinsonian; gene therapy; human; cardiovascular disorder; gene; ss.

XX Homo sapiens.

XX WO200295010-A2.

XX 28-NOV-2002.

XX 19-MAR-2002; 2002WO-US0009785.

XX 21-MAR-2001; 2001US-0277340P.

PR 19-JUL-2001; 2001US-0306171P.

PR 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2003-129429/12.

XX Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia.

PS Claim 21; SEQ ID NO 137; 1881pp; English.

XX The present invention relates to novel human secreted proteins (ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary arteriosclerosis and myocardial ischaemia), neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, renal disorders, proliferative disorders and/or cancerous diseases and conditions, for wound healing and epithelial cell proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts, to prevent skin aging or hair loss, to stimulate growth and differentiation of haematopoietic cells and bone marrow cells when used in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in

Db 2041 TCACTCCGGTTTGCTTCTAGTCTCCTCAAGTGTCTCGTGACACATAATCATTCATCCAAT 2100
QY 2116 GATCGCCTTTGCTTTACCACTCTTTCCTTTTATCTTATTAATAAAAAATGTTG 2167
Db 2101 GATCGCCTTTGCTTTACCACTCTTTCCTTTTATCTTATTAATAAAAAATGTTG 2152

RESULT 18
ABZ71261
ID ABZ71261 standard; cDNA; 2152 BP.
XX ABZ71261;
AC
XX
DT 03-APR-2003 (first entry)
XX Human secreted protein-encoding gene 72 cDNA clone HHPEN62, SEQ ID NO:82.
DE
XX Human; secreted protein; digestive disorder; gastrointestinal disorder;
KW mouth; oesophagus; stomach; small intestine; large intestine; liver;
KW biliary tract; pancreas; cancer; tumour; hyperproliferative disorder;
KW immune disorder; inflammation; infection; wound healing; drug screening;
KW chromosome identification; chromosome mapping; cytostatic;
KW antiinflammatory; immunosuppressive; vulnery; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200276488-A1.
XX
PD 03-OCT-2002.
XX
PF 19-MAR-2002; 2002WO-US008276.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
PI
XX WPI; 2003-029900/02.
DR P-PSDB; ABR00082.
XX
PT New human secreted proteins and nucleic acids, useful for detecting,
PT preventing, diagnosing, prognosticating, treating and/or ameliorating
PT e.g. gastrointestinal diseases and disorders, or cancers.
XX
PS Claim 21; Page 800-801; 1216pp; English.
PS
CC ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted
CC protein genes, and ABP00011-ABP00299 represent the proteins they encode.
CC ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The
CC invention also encompasses antibodies specific for the secreted proteins,
CC the use of the secreted proteins in drug screening, and recombinant
CC vectors and host cells comprising a nucleic acid of the invention. The
CC secreted proteins, nucleic acids encoding them, antibodies or antibody
CC fragments specific for the secreted proteins, and modulators of protein
CC activity are useful for diagnosing, treating, ameliorating or preventing
CC digestive disorders. Such conditions include disorders of the mouth,
CC oesophagus, stomach, small intestine, large intestine, liver, biliary
CC tract and pancreas, and include cancers of these organs and tissues. The
CC secreted proteins and their nucleic acids may also be used in the
CC treatment of immune disorders, inflammation, infection,
CC hyperproliferative disorders, and to promote wound healing. Nucleic acids
CC of the invention may be used for chromosome identification, chromosome
CC mapping, in gene therapy, for identifying individuals from minute
CC biological samples, as hybridisation probes, and as molecular weight
CC markers. The present sequence represents a human secreted protein-
XX encoding cDNA clone of the invention

Sequence 2152 BP; 541 A; 526 C; 531 G; 553 T; 0 U; 1 Other;

Query Match 95.3%; Score 2135.6; DB 8; Length 2152;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2148; Conservative 1; Mismatches 0; Indels 3; Gaps 1;
QY 19 CCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCCTCGTCTTCCTTCGGGGG 78
Db 1 CCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCCTCGTCTTCCTTCGGGGG 60
QY 79 ACAACGTGGTTCAGGCACAGAGAGATATTTAATGTACCCCTCTTGGGGCTTTCATGGGA 138
Db 61 ACAACGTGGTTCAGGCACAGAGAGATATTTAATGTACCCCTCTTGGGGCTTTCATGGGA 120
QY 139 CTCCCTCTGCCACATTTTGGAGGTTGGGAAAGTTGCTAGAGGCTTCAGAACTCCAGCC 198
Db 121 CTCCCTCTGCCACATTTTGGAGGTTGGGAAAGTTGCTAGAGGCTTCAGAACTCCAGCC 180
QY 199 TAATGGATCCCAAACCTCGGGAGAAATGGTGCCTCGCTGGCTG--TGCTGCTGCTGC 255
Db 181 TAATGGATCCCAAACCTCGGGAGAAATGGTGCCTCGCTGGCTGCTGCTGCTGCTGC 240
QY 256 TGCTGGAGCGCGCATGTTCTCTCACCCCTCCCGCCCCCGGCGCTGTTAGAGAAAGTCT 315
Db 241 TGCTGGAGCGCGCATGTTCTCTCACCCCTCCCGCCCCCGGCGCTGTTAGAGAAAGTCT 300
QY 316 TCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGGAGTGGGTGGCCA 375
Db 301 TCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGGAGTGGGTGGCCA 360
QY 376 TCGAGAGCGACTCTGTCCAGCCTGTGCCCTCGCTTCAGACAAAGAGCTCTTCAGAAATGATGG 435
Db 361 TCGAGAGCGACTCTGTCCAGCCTGTGCCCTCGCTTCAGACAAAGAGCTCTTCAGAAATGATGG 420
QY 436 CCGTGGCTGCGGACACCGCTGCAGCGCCTGGGGGCCCGTGTGGCCTCGGTGGACATGGGTC 495
Db 421 CCGTGGCTGCGGACACCGCTGCAGCGCCTGGGGGCCCGTGTGGCCTCGGTGGACATGGGTC 480
QY 496 CTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCATCCTGGCCCGAACTGG 555
Db 481 CTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCATCCTGGCCCGAACTGG 540
QY 556 GGAGCGATCCACGAAAGGACCGTGTGCTTCTACGGCCACTTGGACGTGCAGCCTGCTG 615
Db 541 GGAGCGATCCACGAAAGGACCGTGTGCTTCTACGGCCACTTGGACGTGCAGCCTGCTG 600
QY 616 ACCGGGCGATGGTGGCTCACGGACCCCTATGTGTGACGGAGGTAGACGGGAACTTT 675
Db 601 ACCGGGCGATGGTGGCTCACGGACCCCTATGTGTGACGGAGGTAGACGGGAACTTT 660
QY 676 ATGACGAGGAGCGACCGCAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCG 735
Db 661 ATGACGAGGAGCGACCGCAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCG 720
QY 736 CCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAATTCATATTGAGGGGATGG 795
Db 721 CCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAATTCATATTGAGGGGATGG 780
QY 796 AAGAGGCTGGCTCTGTTGCCCTGGAGGAACTTGTGGAAAAAGAACCCGATTCTTCT 855
Db 781 AAGAGGCTGGCTCTGTTGCCCTGGAGGAACTTGTGGAAAAAGAACCCGATTCTTCT 840
QY 856 CTGTTGTGGACTACATTGTAATTTTCAGATAACCTGTGGATCAGCCAAAGGAAGCCAGCAA 915
Db 841 CTGTTGTGGACTACATTGTAATTTTCAGATAACCTGTGGATCAGCCAAAGGAAGCCAGCAA 900
QY 916 TCACCTATGGAACCCGGGGGAACAGCTACTTTCATGGTGGAGGTGAAATGCAGAGACCAGG 975
Db 901 TCACCTATGGAACCCGGGGGAACAGCTACTTTCATGGTGGAGGTGAAATGCAGAGACCAGG 960
QY 976 ATTTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGGCTGATCTGGTTGCTC 1035
Db 961 ATTTTCACTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGGCTGATCTGGTTGCTC 1020
QY 1036 TTCTCGGTAGCCTGGTAGACTCGTCTGGTGCATATCCTGGTCCCTGGAATCTATGATGAAG 1095

Db 1021 TTCTCGGTAGCCTGGTAGACTCGTCTGGTCAATATCCTGGTCCCTGGAATCTATGATGAAG 1080
QY TGGTTCTCTTACAGAGAGGAAATAAATACATACATACAAAAGCCATCCATCTAGACCTAGAAG 1155
Db TGGTTCTCTTACAGAGAGGAAATAAATACATACATACAAAAGCCATCCATCTAGACCTAGAAG 1140
QY AATACCGGAATAGCAGCCGGTTGAGAAATTTCTGTTTCGATACATAAGAGGAGAGATTCTAA 1215
Db AATACCGGAATAGCAGCCGGTTGAGAAATTTCTGTTTCGATACATAAGAGGAGAGATTCTAA 1200
QY TGCACCTCTGGAGGTACCCATCTCTTTCTATTATCATGGGATCGAGGGCGGTTGATGAGC 1275
Db TGCACCTCTGGAGGTACCCATCTCTTTCTATTATCATGGGATCGAGGGCGGTTGATGAGC 1260
QY CTGGAACATAAAGTCACTACCTGGCCGAGTTATAGGAAATTTTCAATCCGTCTAGTCC 1335
Db CTGGAACATAAAGTCACTACCTGGCCGAGTTATAGGAAATTTTCAATCCGTCTAGTCC 1320
QY CTCACATGAATGTCTGCGGTGGAATAACAGTGACACGACATCTTTGAAGATGTGTTCT 1395
Db CTCACATGAATGTCTGCGGTGGAATAACAGTGACACGACATCTTTGAAGATGTGTTCT 1380
QY CCAAAGAAATAGTTCCAAACAAGATGGTTGTTCCATGACTCTAGGACTACACCCGTGGA 1455
Db CCAAAGAAATAGTTCCAAACAAGATGGTTGTTCCATGACTCTAGGACTACACCCGTGGA 1440
QY TTGCAATATTGTAGACACCCAGTATCTCGAGCAAAAAGAGCGATCAGAACAGTGTGTTG 1515
Db TTGCAATATTGTAGACACCCAGTATCTCGAGCAAAAAGAGCGATCAGAACAGTGTGTTG 1500
QY GAACAGAACCCAGATATGATCCGGATGGATCCACCATTCCAATTGCCAAATGTTCCAGG 1575
Db GAACAGAACCCAGATATGATCCGGATGGATCCACCATTCCAATTGCCAAATGTTCCAGG 1560
QY AGATCGTCCACAAGAGCGTGGTGCTAATTCGCTGGGAGCTGTTGATGATGGAGAACATT 1635
Db AGATCGTCCACAAGAGCGTGGTGCTAATTCGCTGGGAGCTGTTGATGATGGAGAACATT 1620
QY CGCAGAATGAGAAATCAACAGGTGGAACCTACATAGAGGGAACCAATATTGCTGCCT 1695
Db CGCAGAATGAGAAATCAACAGGTGGAACCTACATAGAGGGAACCAATATTGCTGCCT 1680
QY TTTTCTTAGAGATGGCCAGCTCCATTATACAAAGAACCTTCTAGTCTGATCTGATCCA 1755
Db TTTTCTTAGAGATGGCCAGCTCCATTATACAAAGAACCTTCTAGTCTGATCTGATCCA 1740
QY CTGACAGATTACCTCCCCACATCCCTAGCAGGGATGGAATGTAATATCCAGAGAAT 1815
Db CTGACAGATTACCTCCCCACATCCCTAGCAGGGATGGAATGTAATATCCAGAGAAT 1800
QY TTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTGGGATATCTGGATCAG 1875
Db TTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTGGGATATCTGGATCAG 1860
QY TAATAAAATATTTCAAAGGCACAGATGTTGGAATGGTTTAAGGTCCCCCACTGCACACC 1935
Db TAATAAAATATTTCAAAGGCACAGATGTTGGAATGGTTTAAGGTCCCCCACTGCACACC 1920
QY TTCCTCAAGTCATAGCTGCTTGCAGCAACTTGATTTCCCAAGTCCCTGTGCAATAGCCCC 1995
Db TTCCTCAAGTCATAGCTGCTTGCAGCAACTTGATTTCCCAAGTCCCTGTGCAATAGCCCC 1980
QY AGGATTGGATTCTTCCAAACCTTTTAGCATATCTCCAAACCTTGCAATTTGATTTGGCATAA 2055
Db AGGATTGGATTCTTCCAAACCTTTTAGCATATCTCCAAACCTTGCAATTTGATTTGGCATAA 2040
QY TCACTCCGGTTTGCTTTCTAGGTCTCTCAAGTGCTCGTGACACATAATCAATCCATCCAAT 2115
Db TCACTCCGGTTTGCTTTCTAGGTCTCTCAAGTGCTCGTGACACATAATCAATCCATCCAAT 2100
QY GATCGCCTTTGCTTTTACCACTCTTTCCCTTTTATCTTATTATAAAAAATGTTG 2167
|||||:|||||

Db 2101 GATCGCCTTTGCTTTACCAAYCTTTCCCTTTTATCTTATTATAAAAAATGTTG 2152
RESULT 19
ADB91167
ID ADB91167 standard; cDNA; 2152 BP.
XX
AC ADB91167;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human secreted protein cDNA #SEQ ID 113.
XX
KW Secreted protein; gene therapy; antidiabetic; diabetes; human; ss.
XX
OS Homo sapiens.
XX
PN WO2003004622-A2.
XX
PD 16-JAN-2003.
XX
PF 19-MAR-2002; 2002WO-US008124.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-229407/22.
XX
PT Nucleic acid encoding a human secreted protein is useful in diagnosing or
treating diabetes or conditions related to diabetes.
XX
PS Claim 9; SEQ ID NO 113; 1537pp; English.
XX
CC The invention relates to isolated nucleic acid molecules ADB91065-
ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-
ADB91834. Also disclosed is a recombinant vector comprising a
polynucleotide of the invention, and a recombinant host cell comprising
the recombinant vector. The polypeptide of the invention is useful in
identifying a binding partner by contacting the polypeptide with a
binding partner, and determining whether the binding partner increases or
decreases activity of the polypeptide. The polypeptide, polynucleotide,
antibody or its fragment, agonist or antagonist are useful for preparing
a pharmaceutical composition for diagnosing or treating diabetes or
conditions related to diabetes. The present sequence is that of the human
immunoglobulin Fc portion used to generate fusion proteins, increasing
the stability of the fused protein as compared to the secreted protein
only. Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2152 BP; 541 A; 526 C; 531 G; 553 T; 0 U; 1 Other;

Query Match 95.3%; Score 2135.6; DB 9; Length 2152;
Best Local Similarity 99.8%; Pred.No. 0;
Matches 2148; Conservative / 1; Mismatches 0; Indels 3; Gaps 1;

QY 19 CCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCCTCGTCTTCCGGGGG 78
|||||
Db 1 CCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCCTCGTCTTCCGGGGG 60
QY 79 ACAACGTGGTCCAGGCACAGAGAGATTTAATGTCAACCCTCTTGGGGCTTTTCATGGGA 138
|||||
Db 61 ACAACGTGGTCCAGGCACAGAGAGATTTAATGTCAACCCTCTTGGGGCTTTTCATGGGA 120
QY 139 CTCCTCTGCGCACATTTTTTGGAGGTTGGGAAAGTTGCTAGAGGCTTCAGAACTCCAGCC 198
|||||
Db 121 CTCCTCTGCGCACATTTTTTGGAGGTTGGGAAAGTTGCTAGAGGCTTCAGAACTCCAGCC 180

QY	199	TAATGGATCCCAAACCTCGGGAGAAATGGCTGCGTCCCTGCTGGCTG--TGCTGCTGCTGC	255
Dd	181	TAATGGATCCCAAACCTCGGGAGAAATGGCTGCGTCCCTGCTGGCTGTGCTGCTGCTGCTGC	240
QY	256	TGCTGGAGCGCGCATGTTCTCCTCACCCCTCCC CGCCCCCGGCGCTGTTAGAGAAAAGTC	315
Dd	241	TGCTGGAGCGCGCATGTTCTCCTCACCCCTCCC CGCCCCCGGCGCTGTTAGAGAAAAGTC	300
QY	316	TCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGAGTGGGTGGCCA	375
Dd	301	TCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGAGTGGGTGGCCA	360
QY	376	TCGAGAGCGACTCTGTCCAGCCCTGCGCTCGCTTTCAGACAAGAGTCTTTCAGAATGATGG	435
Dd	361	TCGAGAGCGACTCTGTCCAGCCCTGCGCTCGCTTTCAGACAAGAGTCTTTCAGAATGATGG	420
QY	436	CCGTGGCTGCGGACACGCTGCAGCGCTTGGGGGCCCGTGTGGCCTCGGTGGACATGGGTC	495
Dd	421	CCGTGGCTGCGGACACGCTGCAGCGCTTGGGGGCCCGTGTGGCCTCGGTGGACATGGGTC	480
QY	496	CTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCATCCTGGCCGGAACCTGG	555
Dd	481	CTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCATCCTGGCCGGAACCTGG	540
QY	556	GGAGCGATCCCAACGAAAGGCACCGTGTGCTTCTACGGCCACTTGGACGTGCAGCCTGCTG	615
Dd	541	GGAGCGATCCCAACGAAAGGCACCGTGTGCTTCTACGGCCACTTGGACGTGCAGCCTGCTG	600
QY	616	ACCGGGCGATGGGTGGCTCACGGA CCCCTATGTGCTGACGGAGGTACACGGGAACTTT	675
Dd	601	ACCGGGCGATGGGTGGCTCACGGA CCCCTATGTGCTGACGGAGGTACACGGGAACTTT	660
QY	676	ATGACGAGGAGCGAACCGACAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCG	735
Dd	661	ATGACGAGGAGCGAACCGACAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCG	720
QY	736	CCTTCAGAGCCCTGGAGCAAGATCTTCCGTGGAATATCAAAATTCATATTGAGGGATGG	795
Dd	721	CCTTCAGAGCCCTGGAGCAAGATCTTCCGTGGAATATCAAAATTCATATTGAGGGATGG	780
QY	796	AAGAGGCTGGCTCTGTTGCCCTGGAGGAACCTTGTGAAAAAAGAAAGACCAGATCTTCT	855
Dd	781	AAGAGGCTGGCTCTGTTGCCCTGGAGGAACCTTGTGAAAAAAGAAAGACCAGATCTTCT	840
QY	856	CTGGTGTGGACTACATTGTAATTTTCAGATAACCTGTGGATCAGCCAAAGGAAGCCAGCAA	915
Dd	841	CTGGTGTGGACTACATTGTAATTTTCAGATAACCTGTGGATCAGCCAAAGGAAGCCAGCAA	900
QY	916	TCACCTTATGGAA CCGGGGGAACAGCTACTTTCATGGTGGAGGTGAAATGCAGAGACCAGG	975
Dd	901	TCACCTTATGGAA CCGGGGGAACAGCTACTTTCATGGTGGAGGTGAAATGCAGAGACCAGG	960
QY	976	ATTTTCACTCAGGAACCTTTGGTGGCATCCCTCATGAACCAATGGCTGATCTGGTTGCTC	1035
Dd	961	ATTTTCACTCAGGAACCTTTGGTGGCATCCCTCATGAACCAATGGCTGATCTGGTTGCTC	1020
QY	1036	TTCTCGGTAGCCTGGTAGACTCGTCTGGTCATATCCTGGTCCCTGGAATCTATGATGAAG	1095
Dd	1021	TTCTCGGTAGCCTGGTAGACTCGTCTGGTCATATCCTGGTCCCTGGAATCTATGATGAAG	1080
QY	1096	TGGTTCCTCTTACAGAAAGAGGAAATAAATACATACAAAGCCATCCATCTAGACCTAGAAG	1155
Dd	1081	TGGTTCCTCTTACAGAAAGAGGAAATAAATACATACAAAGCCATCCATCTAGACCTAGAAG	1140
QY	1156	AATACCGGAA TAGCAGCCGGTTGAGAAAATTTCTGTTGATAC TAAGGAGGAGATTCTAA	1215
Dd	1141	AATACCGGAA TAGCAGCCGGTTGAGAAAATTTCTGTTGATAC TAAGGAGGAGATTCTAA	1200
QY	1216	TGCACCTCTGGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGGGCGGTTTTGATGAGC	1275
Dd	1201	TGCACCTCTGGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGGGCGGTTTTGATGAGC	1260
QY	1276	CTGGAACTAAAA CAGTCATACCTGGCCGAGTTATAGGAAAAATTTTCAATCCCGTCTAGTCC	1335

Db	1261	CTGGAAC TAAACAGTCTATACCTGGCCGAGTTATAGGAAAATTTTCAATCCGTC TAGTCC	1320
QY	1336	CTCACATGAATGTGTCTGCGGTGGAACACAGGTGACACGACATCTTGAAGATGTGTTCT	1395
Dd	1321	CTCACATGAATGTGTCTGCGGTGGAACACAGGTGACACGACATCTTGAAGATGTGTTCT	1380
QY	1396	CCAAAAGAAAATAGTTCCAACAAGATGGTTGTTTCCATGACTCTAGGACTACACCCGTTGGA	1455
Dd	1381	CCAAAAGAAAATAGTTCCAACAAGATGGTTGTTTCCATGACTCTAGGACTACACCCGTTGGA	1440
QY	1456	TTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGATCAGAACAGTGTGTTG	1515
Dd	1441	TTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGATCAGAACAGTGTGTTG	1500
QY	1516	GAACAGAAC CAGATATGATCCGGATGGATCCA CATTCCAATTGCCAAAATGTTCCAGG	1575
Dd	1501	GAACAGAAC CAGATATGATCCGGATGGATCCA CATTCCAATTGCCAAAATGTTCCAGG	1560
QY	1576	AGATCGTCCACAAGAGCGTGTGCTAAATTCGCTGGAGCTGTTGATGGAGAACATT	1635
Dd	1561	AGATCGTCCACAAGAGCGTGTGCTAAATTCGCTGGAGCTGTTGATGGAGAACATT	1620
QY	1636	CGCAGAA TGAGAAAATCAACAGGTGGAAC TACATAGAGGGAACCAAATTAATTGCTGCCT	1695
Dd	1621	CGCAGAA TGAGAAAATCAACAGGTGGAAC TACATAGAGGGAACCAAATTAATTGCTGCCT	1680
QY	1696	TTTTCTTAGAGATGGCCCCAGCTCCATTAATCACAAGAACCTTCTAGTCTGATCTGATCCA	1755
Dd	1681	TTTTCTTAGAGATGGCCCCAGCTCCATTAATCACAAGAACCTTCTAGTCTGATCTGATCCA	1740
QY	1756	CTGACAGATTCACCTCCCCACATCCCTAGACAGGGATGGAATGTAATATCCAGAGAAT	1815
Dd	1741	CTGACAGATTCACCTCCCCACATCCCTAGACAGGGATGGAATGTAATATCCAGAGAAT	1800
QY	1816	TTGGGTCTAGTATAGTACATTTTCCCTTCCATTAAAATGTCTTGGATATCTGGATCAG	1875
Dd	1801	TTGGGTCTAGTATAGTACATTTTCCCTTCCATTAAAATGTCTTGGATATCTGGATCAG	1860
QY	1876	TAATAAAATATTCAAAGGCACAGATGTTGGAAAATGGTTTAAGGTCCCCACCTGCACACC	1935
Dd	1861	TAATAAAATATTCAAAGGCACAGATGTTGGAAAATGGTTTAAGGTCCCCACCTGCACACC	1920
QY	1936	TTCTCTCAAGTTCATAGCTGCTTGACAGCAACTTGATTTCCCAAGTCTCTGCAATAGCCCC	1995
Dd	1921	TTCTCTCAAGTTCATAGCTGCTTGACAGCAACTTGATTTCCCAAGTCTCTGCAATAGCCCC	1980
QY	1996	AGGATTGGATTCTCTTCCAACTTTTAGCATATCTCCAACCTTGCAATTTGATTTGGCATAA	2055
Dd	1981	AGGATTGGATTCTCTTCCAACTTTTAGCATATCTCCAACCTTGCAATTTGATTTGGCATAA	2040
QY	2056	TCACTCCGGTTTGCTTTTCTAGGTCTCAAGTGCTCGTGACACATAATCATTCATCCCAAT	2115
Dd	2041	TCACTCCGGTTTGCTTTTCTAGGTCTCAAGTGCTCGTGACACATAATCATTCATCCCAAT	2100
QY	2116	GATCGCCTTTGCTTTTACCACCTCTTTCCCTTTTATCTTTATTAATAAAAAATGTTG	2167
Dd	2101	GATCGCCTTTGCTTTTACCACCTCTTTCCCTTTTATCTTTATTAATAAAAAATGTTG	2152

RESULT 20

ADC73537

ID ADC73537 standard; DNA; 2152 BP.

ADC73537;

ADC73537;

01-JAN-2004 (first entry)

01-JAN-2004 (first entry)

Human secreted protein-related DNA - SEQ ID 170.

xx antihaemic: antirheumatic: antiarthritic: antiinflammatory; antithyroid;
vw

antianaemic; antirheumatic; antiarthritic; antiinflammatory; antidiabetic: immunosuppressive: dermatological: nephrotoxic; kw

kW antidiabetic; immunosuppressive; dermatological; nephrotoxic; antiviral; antiparasitic; antibacterial; virucide;
kW antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;

OV 1276 CTGGAACATAAACAGTCATACCTGGCCGAGTTATAGGAAATTTCAATCCGCTAGTCC 1335

PR	17-AUG-1998;	98US-0096768P.
PR	17-AUG-1998;	98US-0096773P.
PR	17-AUG-1998;	98US-0096791P.
PR	17-AUG-1998;	98US-0096867P.
PR	17-AUG-1998;	98US-0096891P.
PR	17-AUG-1998;	98US-0096894P.
PR	17-AUG-1998;	98US-0096895P.
PR	17-AUG-1998;	98US-0096897P.
PR	18-AUG-1998;	98US-0096949P.
PR	18-AUG-1998;	98US-0096950P.
PR	18-AUG-1998;	98US-0096959P.
PR	18-AUG-1998;	98US-0096960P.
PR	18-AUG-1998;	98US-0097022P.
PR	19-AUG-1998;	98US-0097141P.
PR	20-AUG-1998;	98US-0097218P.
PR	24-AUG-1998;	98US-0097661P.
PR	26-AUG-1998;	98US-0097952P.
PR	26-AUG-1998;	98US-0097954P.
PR	26-AUG-1998;	98US-0097955P.
PR	26-AUG-1998;	98US-0097971P.
PR	26-AUG-1998;	98US-0097974P.
PR	26-AUG-1998;	98US-0097978P.
PR	26-AUG-1998;	98US-0097979P.
PR	26-AUG-1998;	98US-0097986P.
PR	26-AUG-1998;	98US-0098014P.
PR	31-AUG-1998;	98US-0098525P.
PR	16-SEP-1998;	98US-0100634P.
PR	16-SEP-1998;	98WO-US019330.
PR	17-SEP-1998;	98US-0100858P.
PR	17-SEP-1998;	98WO-US019437.
PR	07-OCT-1998;	98WO-US021141.
PR	01-DEC-1998;	98WO-US025108.
PR	22-DEC-1998;	98US-0113296P.
PR	05-JAN-1999;	99WO-US000106.
PR	08-MAR-1999;	99WO-US005028.
PR	12-MAR-1999;	99US-0123957P.
PR	02-JUN-1999;	99WO-US012252.
PR	23-JUN-1999;	99US-0141037P.
PR	07-JUL-1999;	99US-0143048P.
PR	20-JUL-1999;	99US-0144758P.
PR	26-JUL-1999;	99US-0145698P.
PR	28-JUL-1999;	99US-0146222P.
PR	17-AUG-1999;	99US-0149396P.
PR	15-SEP-1999;	99WO-US021090.
PR	15-SEP-1999;	99WO-US021547.
PR	08-OCT-1999;	99US-0158663P.
PR	30-NOV-1999;	99WO-US028313.
PR	01-DEC-1999;	99WO-US028301.
PR	16-DEC-1999;	99WO-US028634.
PR	20-DEC-1999;	99WO-US030095.
PR	05-JAN-2000;	99WO-US030911.
PR	06-JAN-2000;	2000WO-US000219.
PR	11-FEB-2000;	2000WO-US000376.
PR	22-FEB-2000;	2000WO-US003565.
PR	24-FEB-2000;	2000WO-US004914.
PR	24-FEB-2000;	2000WO-US005004.
PR	02-MAR-2000;	2000WO-US005841.
PR	10-MAR-2000;	2000WO-US006319.
PR	15-MAR-2000;	2000WO-US006884.
PR	20-MAR-2000;	2000WO-US007377.
PR	30-MAR-2000;	2000WO-US008439.
PR	15-MAY-2000;	2000WO-US013358.
PR	17-MAY-2000;	2000WO-US013705.
PR	22-MAY-2000;	2000WO-US014042.
PR	30-MAY-2000;	2000WO-US014941.
PR	02-JUN-2000;	2000WO-US015264.
PR	23-JUN-2000;	2000US-0213637P.
PR	28-JUL-2000;	2000WO-US020710.
PR	11-AUG-2000;	2000WO-US022031.
PR	23-AUG-2000;	2000WO-US023522.
PR	24-AUG-2000;	2000WO-US023328.

Query Match
Best Local Similarity 3.0%; Score 66.6; DB 8; Length 2846;
Matches 87; Conservative 71.3%; Pred. No. 0.00023;
Mismatches 0; Indels 0; Gaps 0;

Qy	2121	CCTTTGCTTTACCACCTCTTTCCTTTTATCTTATTAATAAAATGTTGGTCTCCACCACCTG	2180
Db	2653	CCTTTTCCTTCCCACTCTCTGTACACATTTTAATAAAATAAGGTTGGCTTCTGAACCTA	2712
Qy	2181	NCTCCCAA	2240
Db	2713	CAAA	2772
Qy	2241	AA 2242	
Db	2773	AA 2774	

RESULT 353
ACA72548
ID ACA72548 standard; cDNA; 2846 BP.
XX
AC ACA72548;
XX
DT 02-JUL-2003 (first entry)
XX
DE Human PRO polynucleotide #85.
XX
KW Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;
KW cancer; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour; TNF-alpha;
KW tumour necrosis factor-alpha; chondrocyte cell.
XX
OS Homo sapiens.
XX
PN US2003022295-A1.
XX
PD 30-JAN-2003.
XX
PF 19-JUN-2002; 2002US-00175752.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-007886P.
PR 11-MAR-1998; 98US-0078939P.
PR 20-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.

